



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 12:55 AM UTC

PDB ID : 1M7K / pdb_00001m7k
Title : Solution Structure of the SODD BAG Domain
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Oschkinat, H.
Deposited on : 2002-07-22

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

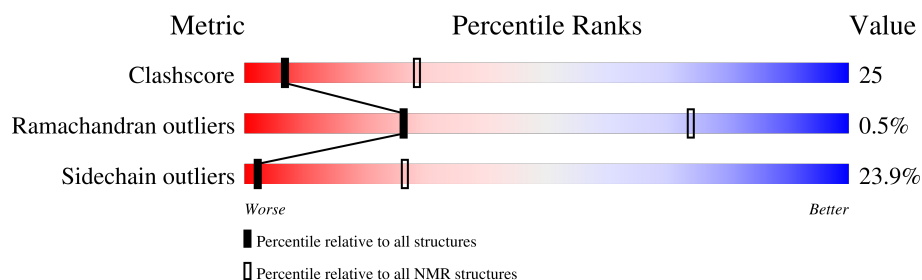
1 Overall quality at a glance

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	99	43% 34% •• 18%

2 Ensemble composition and analysis

This entry contains 20 models. Model 1 is the overall representative, medoid model (most similar to other models).

The following residues are included in the computation of the global validation metrics.

Well-defined (core) protein residues			
Well-defined core	Residue range (total)	Backbone RMSD (Å)	Medoid model
1	A:379-A:456 (78)	0.62	1

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 2 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1343 atoms, of which 688 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Silencer of Death Domains.

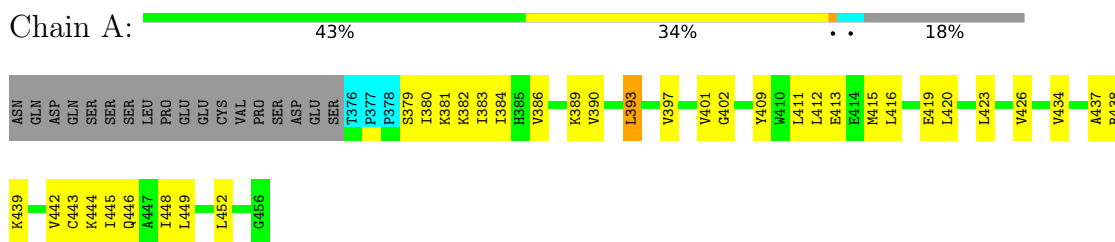
Mol	Chain	Residues	Atoms						Trace
1	A	81	Total	C	H	N	O	S	0
			1343	418	688	107	128	2	

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: Silencer of Death Domains

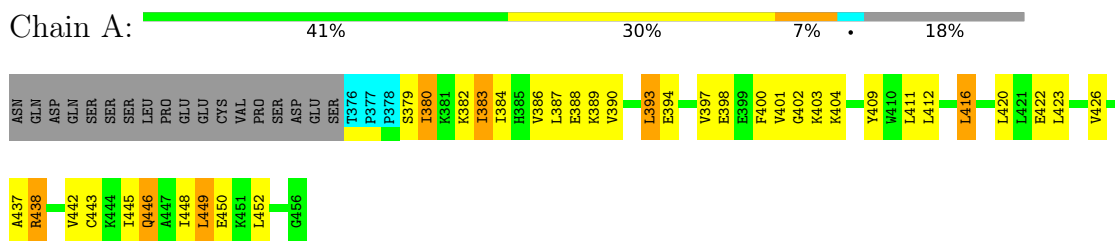


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1 (medoid)

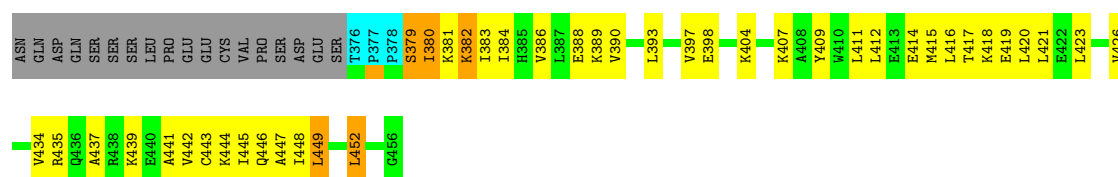
- Molecule 1: Silencer of Death Domains



4.2.2 Score per residue for model 2

- Molecule 1: Silencer of Death Domains

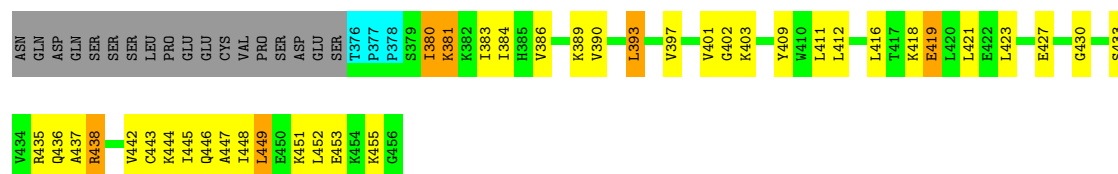




4.2.3 Score per residue for model 3

- Molecule 1: Silencer of Death Domains

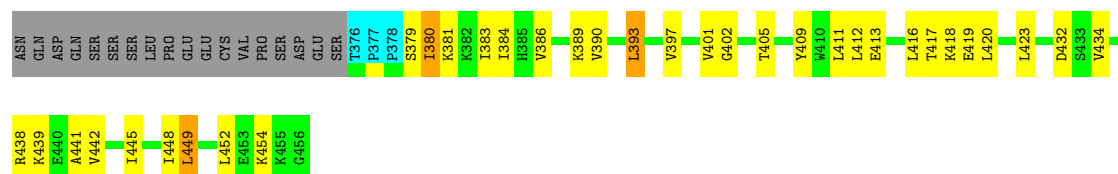
Chain A: 39% 33% 6% 18%



4.2.4 Score per residue for model 4

- Molecule 1: Silencer of Death Domains

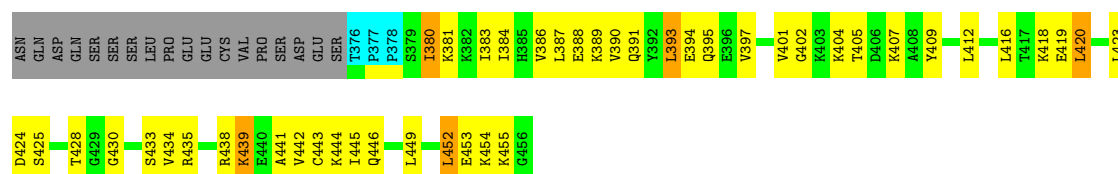
Chain A: 44% 31% 18%



4.2.5 Score per residue for model 5

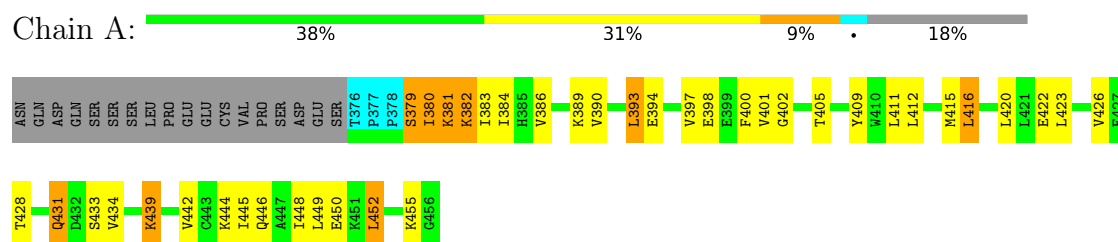
- Molecule 1: Silencer of Death Domains

Chain A: 32% 41% 5% 18%



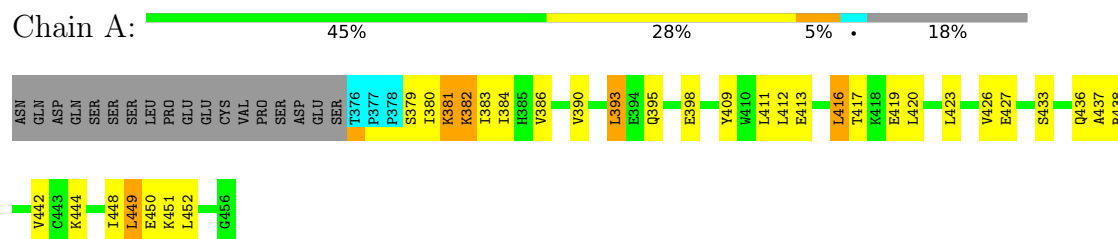
4.2.6 Score per residue for model 6

- Molecule 1: Silencer of Death Domains



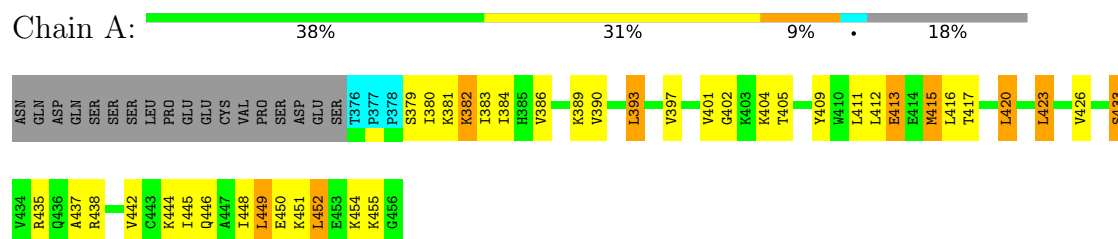
4.2.7 Score per residue for model 7

- Molecule 1: Silencer of Death Domains



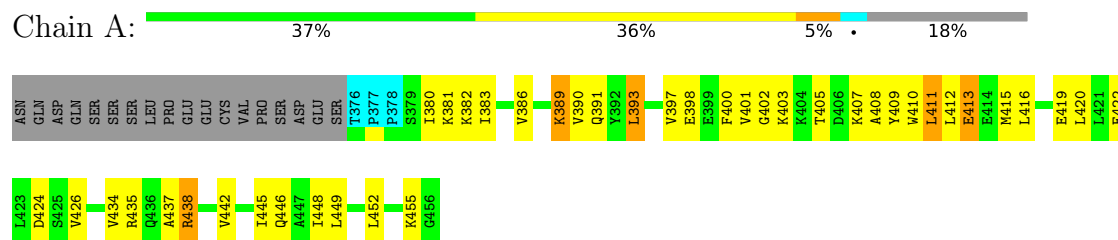
4.2.8 Score per residue for model 8

- Molecule 1: Silencer of Death Domains



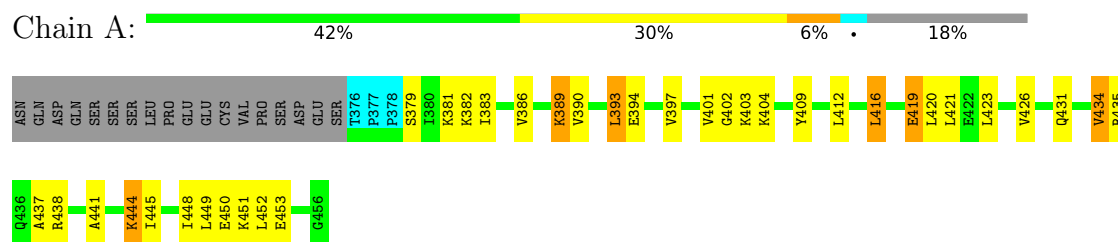
4.2.9 Score per residue for model 9

- Molecule 1: Silencer of Death Domains



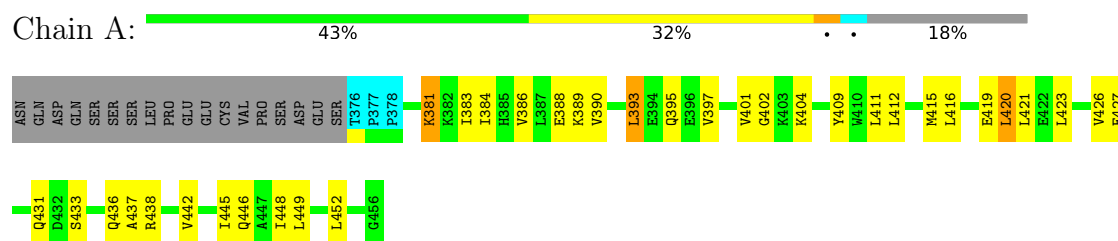
4.2.10 Score per residue for model 10

• Molecule 1: Silencer of Death Domains



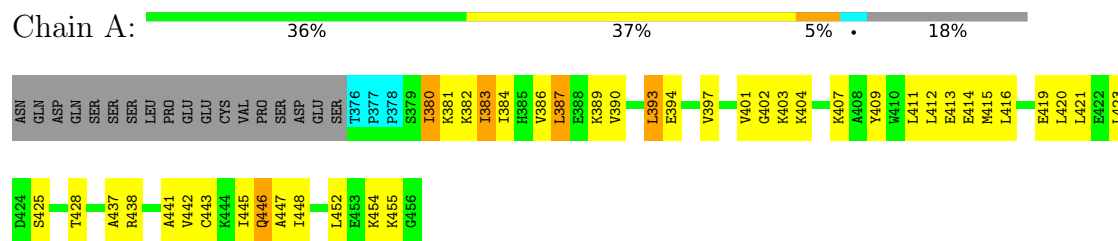
4.2.11 Score per residue for model 11

• Molecule 1: Silencer of Death Domains



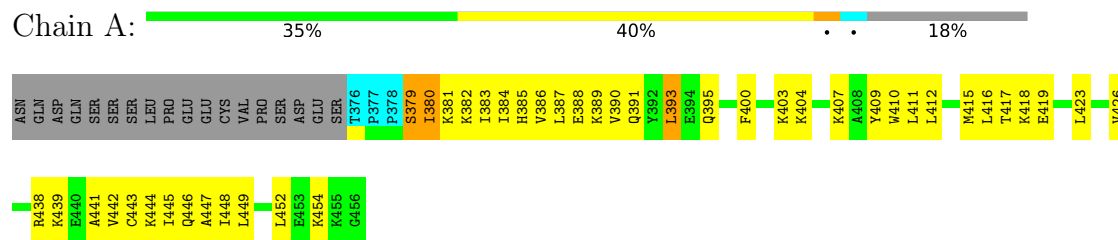
4.2.12 Score per residue for model 12

• Molecule 1: Silencer of Death Domains



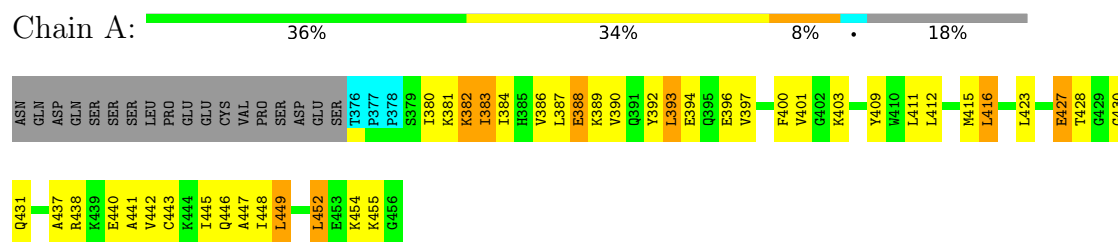
4.2.13 Score per residue for model 13

• Molecule 1: Silencer of Death Domains



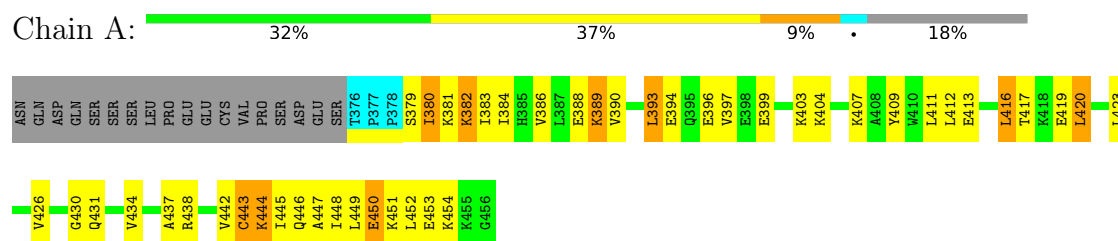
4.2.14 Score per residue for model 14

- Molecule 1: Silencer of Death Domains



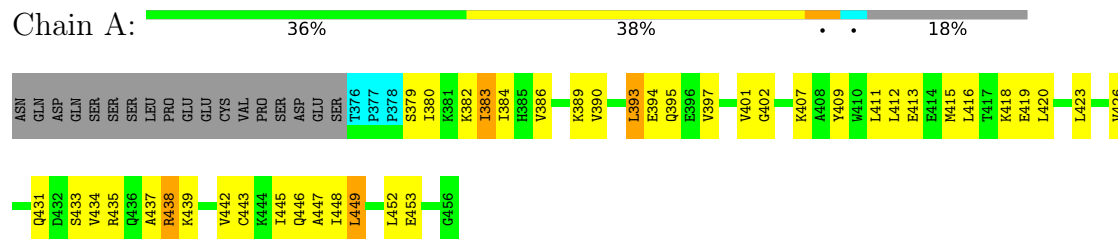
4.2.15 Score per residue for model 15

- Molecule 1: Silencer of Death Domains



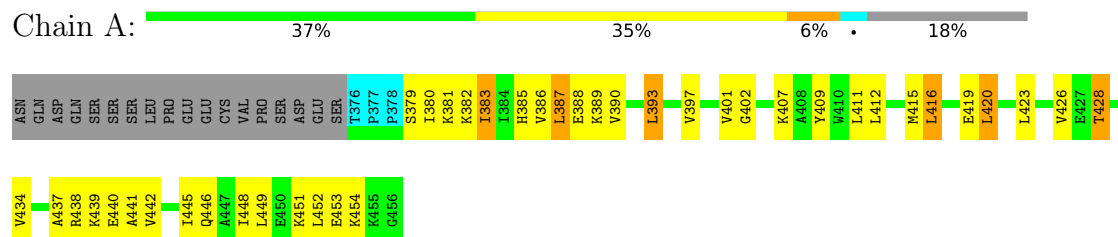
4.2.16 Score per residue for model 16

- Molecule 1: Silencer of Death Domains



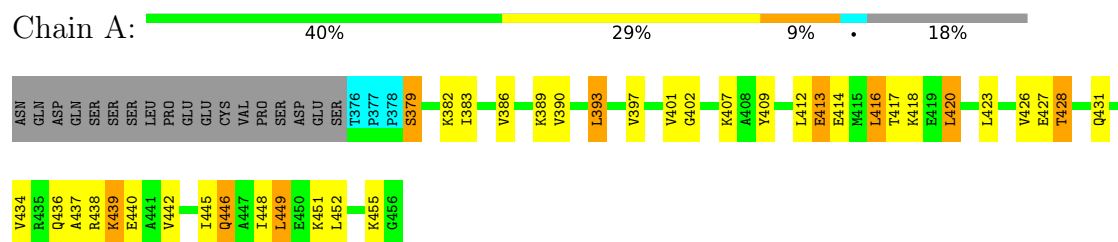
4.2.17 Score per residue for model 17

- Molecule 1: Silencer of Death Domains



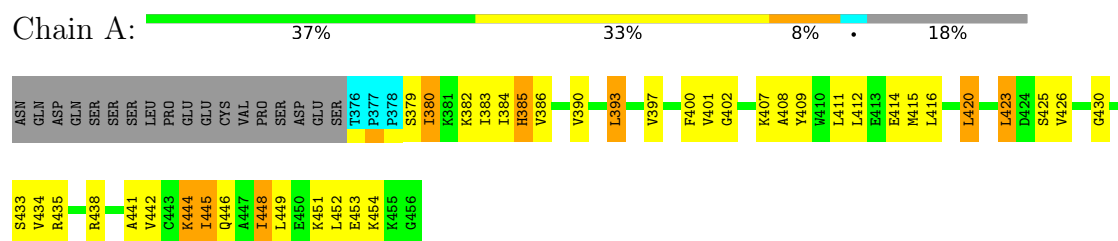
4.2.18 Score per residue for model 18

• Molecule 1: Silencer of Death Domains



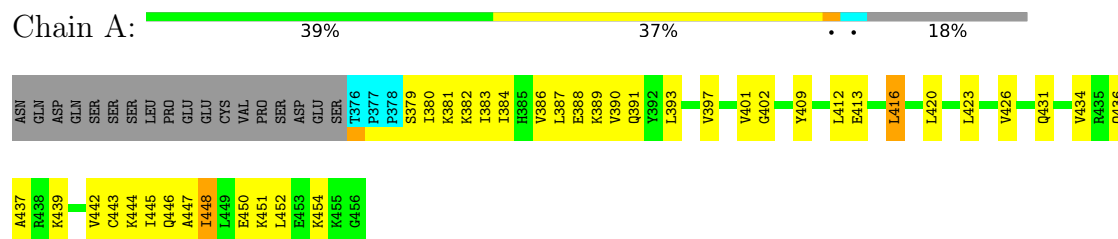
4.2.19 Score per residue for model 19

• Molecule 1: Silencer of Death Domains



4.2.20 Score per residue for model 20

• Molecule 1: Silencer of Death Domains



5 Refinement protocol and experimental data overview ⓘ

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

Of the 400 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
CNS	refinement	1.1

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	634	667	666	32±7
All	All	12680	13340	13320	644

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 25.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:386:VAL:HG21	1:A:423:LEU:HD13	1.05	1.18	15	4
1:A:416:LEU:HD21	1:A:448:ILE:HD13	1.04	1.27	7	6
1:A:386:VAL:HG21	1:A:423:LEU:HD12	0.99	1.31	6	4
1:A:393:LEU:HD22	1:A:416:LEU:HD13	0.98	1.33	18	3
1:A:416:LEU:HD23	1:A:448:ILE:HD11	0.97	1.32	20	1
1:A:420:LEU:HD11	1:A:445:ILE:HD13	0.94	1.37	15	4
1:A:383:ILE:HD13	1:A:437:ALA:HB1	0.90	1.42	1	4
1:A:412:LEU:HD13	1:A:452:LEU:HD11	0.88	1.44	18	8
1:A:420:LEU:HD21	1:A:445:ILE:HD13	0.88	1.43	8	2
1:A:416:LEU:CD2	1:A:448:ILE:HD11	0.83	2.04	20	1
1:A:386:VAL:HG21	1:A:423:LEU:CD1	0.83	2.03	15	3
1:A:416:LEU:HD13	1:A:449:LEU:HD12	0.81	1.51	16	3
1:A:383:ILE:HD11	1:A:426:VAL:HG21	0.81	1.53	8	4
1:A:383:ILE:HD11	1:A:441:ALA:HB3	0.80	1.54	5	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:438:ARG:O	1:A:442:VAL:HG23	0.80	1.77	8	14
1:A:386:VAL:O	1:A:390:VAL:HG23	0.79	1.77	9	19
1:A:383:ILE:HD13	1:A:437:ALA:CB	0.79	2.08	16	5
1:A:393:LEU:O	1:A:397:VAL:HG23	0.79	1.77	12	7
1:A:382:LYS:O	1:A:386:VAL:HG23	0.78	1.78	15	2
1:A:412:LEU:HD13	1:A:452:LEU:HD21	0.78	1.56	20	9
1:A:428:THR:OG1	1:A:434:VAL:HG11	0.78	1.79	5	1
1:A:416:LEU:HD21	1:A:448:ILE:CD1	0.77	2.09	9	4
1:A:423:LEU:O	1:A:426:VAL:HG12	0.77	1.79	16	8
1:A:379:SER:OG	1:A:434:VAL:HG21	0.77	1.80	17	3
1:A:416:LEU:HD21	1:A:448:ILE:HG23	0.77	1.57	8	3
1:A:444:LYS:O	1:A:448:ILE:HD12	0.76	1.80	19	1
1:A:383:ILE:HD12	1:A:434:VAL:HG22	0.76	1.58	10	2
1:A:409:TYR:CE1	1:A:452:LEU:HD11	0.76	2.15	14	2
1:A:416:LEU:HG	1:A:449:LEU:HD13	0.75	1.56	10	1
1:A:420:LEU:HD11	1:A:445:ILE:CD1	0.75	2.12	15	1
1:A:397:VAL:HG21	1:A:448:ILE:HG13	0.75	1.59	8	6
1:A:383:ILE:HD11	1:A:438:ARG:CA	0.75	2.12	17	1
1:A:448:ILE:HD12	1:A:449:LEU:N	0.73	1.98	15	1
1:A:386:VAL:HG21	1:A:423:LEU:HD23	0.73	1.59	3	1
1:A:383:ILE:HG21	1:A:437:ALA:HB1	0.73	1.57	10	5
1:A:397:VAL:HG12	1:A:412:LEU:HD13	0.73	1.58	19	4
1:A:380:ILE:O	1:A:380:ILE:HD13	0.73	1.83	19	1
1:A:380:ILE:CD1	1:A:383:ILE:HD11	0.73	2.13	3	1
1:A:383:ILE:HD11	1:A:434:VAL:HG13	0.73	1.59	10	2
1:A:416:LEU:HD22	1:A:448:ILE:CD1	0.72	2.15	15	1
1:A:416:LEU:HD23	1:A:449:LEU:CD1	0.72	2.13	8	3
1:A:393:LEU:HD13	1:A:416:LEU:CD1	0.72	2.14	17	3
1:A:390:VAL:HG22	1:A:419:GLU:OE2	0.71	1.85	5	1
1:A:379:SER:HB3	1:A:426:VAL:HG23	0.71	1.60	8	4
1:A:409:TYR:CE2	1:A:452:LEU:HD23	0.71	2.20	6	1
1:A:393:LEU:HD23	1:A:412:LEU:HD23	0.71	1.63	1	9
1:A:381:LYS:HA	1:A:384:ILE:HD12	0.71	1.62	7	6
1:A:382:LYS:O	1:A:386:VAL:HG22	0.71	1.85	8	4
1:A:409:TYR:CE1	1:A:452:LEU:HD22	0.70	2.21	9	15
1:A:386:VAL:HG12	1:A:419:GLU:OE1	0.70	1.86	11	1
1:A:393:LEU:CD2	1:A:416:LEU:HD13	0.70	2.16	1	3
1:A:383:ILE:HD11	1:A:441:ALA:CB	0.70	2.15	5	3
1:A:428:THR:HG23	1:A:434:VAL:HG12	0.70	1.62	17	1
1:A:449:LEU:HD12	1:A:450:GLU:N	0.70	2.01	15	1
1:A:390:VAL:HG11	1:A:444:LYS:CG	0.69	2.17	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:397:VAL:CG1	1:A:412:LEU:HD22	0.69	2.16	20	4
1:A:386:VAL:CG2	1:A:423:LEU:HD12	0.69	2.15	6	3
1:A:400:PHE:CD1	1:A:412:LEU:HD11	0.69	2.23	9	1
1:A:416:LEU:CD2	1:A:448:ILE:HD13	0.69	2.15	9	3
1:A:386:VAL:HG21	1:A:423:LEU:CD2	0.68	2.19	3	1
1:A:412:LEU:CD1	1:A:452:LEU:HD21	0.68	2.18	16	3
1:A:393:LEU:HD22	1:A:416:LEU:CD2	0.68	2.18	7	3
1:A:420:LEU:HD12	1:A:445:ILE:HD12	0.68	1.64	9	2
1:A:386:VAL:HG11	1:A:423:LEU:HD13	0.68	1.63	7	1
1:A:379:SER:HB2	1:A:434:VAL:HG11	0.68	1.66	17	3
1:A:393:LEU:HD11	1:A:415:MET:HB3	0.67	1.65	14	2
1:A:383:ILE:HD11	1:A:426:VAL:CG2	0.67	2.18	8	1
1:A:386:VAL:CG1	1:A:423:LEU:HD21	0.67	2.19	16	1
1:A:383:ILE:CD1	1:A:437:ALA:HB1	0.67	2.17	1	4
1:A:393:LEU:HD11	1:A:415:MET:CG	0.67	2.19	13	4
1:A:387:LEU:HD21	1:A:440:GLU:OE2	0.67	1.90	14	1
1:A:380:ILE:O	1:A:384:ILE:HG23	0.67	1.89	16	1
1:A:409:TYR:CE1	1:A:452:LEU:HD23	0.67	2.25	5	1
1:A:438:ARG:O	1:A:442:VAL:HG13	0.67	1.90	5	1
1:A:397:VAL:HG21	1:A:448:ILE:CG1	0.67	2.20	11	4
1:A:383:ILE:HG21	1:A:437:ALA:CB	0.67	2.20	7	7
1:A:420:LEU:HD21	1:A:445:ILE:CD1	0.67	2.18	8	1
1:A:397:VAL:HG13	1:A:412:LEU:HD22	0.67	1.67	20	1
1:A:420:LEU:CD1	1:A:445:ILE:HD12	0.66	2.21	9	2
1:A:386:VAL:HG23	1:A:419:GLU:HG2	0.66	1.66	16	1
1:A:380:ILE:HD12	1:A:433:SER:HB2	0.66	1.65	7	1
1:A:386:VAL:HG23	1:A:419:GLU:HB3	0.66	1.66	7	1
1:A:416:LEU:HD21	1:A:448:ILE:CG2	0.66	2.20	8	5
1:A:383:ILE:O	1:A:387:LEU:HD23	0.66	1.90	12	1
1:A:412:LEU:HD13	1:A:452:LEU:CD1	0.65	2.21	15	3
1:A:393:LEU:HD22	1:A:416:LEU:HD22	0.65	1.67	7	3
1:A:386:VAL:HG11	1:A:423:LEU:HD21	0.65	1.68	16	1
1:A:383:ILE:HD11	1:A:438:ARG:CB	0.65	2.22	17	1
1:A:445:ILE:HD12	1:A:446:GLN:N	0.65	2.07	11	13
1:A:416:LEU:HD13	1:A:449:LEU:CD1	0.65	2.20	16	2
1:A:380:ILE:CG1	1:A:384:ILE:HD11	0.65	2.22	5	7
1:A:416:LEU:HG	1:A:449:LEU:HD12	0.64	1.67	14	2
1:A:383:ILE:HD13	1:A:434:VAL:HA	0.64	1.69	6	1
1:A:420:LEU:HG	1:A:445:ILE:HG21	0.64	1.67	17	2
1:A:386:VAL:CB	1:A:423:LEU:HD21	0.64	2.22	16	1
1:A:382:LYS:HB2	1:A:426:VAL:HG23	0.64	1.70	2	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:428:THR:HG21	1:A:438:ARG:HD3	0.64	1.68	17	1
1:A:393:LEU:HD13	1:A:416:LEU:HD12	0.64	1.69	17	3
1:A:383:ILE:CD1	1:A:434:VAL:HG13	0.64	2.23	9	2
1:A:393:LEU:O	1:A:397:VAL:HG22	0.63	1.93	9	1
1:A:386:VAL:HG11	1:A:423:LEU:HB2	0.63	1.71	6	3
1:A:380:ILE:HG12	1:A:384:ILE:HD11	0.63	1.69	5	7
1:A:397:VAL:CG1	1:A:452:LEU:HD11	0.63	2.23	20	3
1:A:390:VAL:HG11	1:A:444:LYS:HB3	0.63	1.70	20	1
1:A:382:LYS:CB	1:A:426:VAL:HG23	0.62	2.24	20	2
1:A:393:LEU:O	1:A:397:VAL:HG13	0.62	1.94	9	1
1:A:397:VAL:HG12	1:A:452:LEU:HD11	0.62	1.72	20	3
1:A:393:LEU:HD22	1:A:416:LEU:HG	0.62	1.70	9	5
1:A:390:VAL:HG22	1:A:419:GLU:OE1	0.62	1.93	10	1
1:A:379:SER:CB	1:A:426:VAL:HG23	0.62	2.25	18	3
1:A:411:LEU:HD12	1:A:412:LEU:N	0.62	2.10	15	12
1:A:452:LEU:HD22	1:A:452:LEU:O	0.61	1.96	14	1
1:A:413:GLU:HA	1:A:416:LEU:HD12	0.61	1.72	4	3
1:A:383:ILE:CD1	1:A:426:VAL:HG21	0.61	2.24	7	2
1:A:386:VAL:HG11	1:A:423:LEU:HB3	0.61	1.71	19	4
1:A:403:LYS:HG2	1:A:405:THR:HG22	0.61	1.71	9	1
1:A:409:TYR:HA	1:A:412:LEU:HD12	0.61	1.72	20	9
1:A:386:VAL:CG2	1:A:423:LEU:HD13	0.61	2.11	15	1
1:A:379:SER:OG	1:A:426:VAL:HG22	0.60	1.96	16	1
1:A:383:ILE:HD12	1:A:387:LEU:HD12	0.60	1.72	1	1
1:A:383:ILE:O	1:A:387:LEU:HD12	0.60	1.96	17	1
1:A:383:ILE:HD11	1:A:438:ARG:HA	0.59	1.73	17	1
1:A:393:LEU:HD11	1:A:415:MET:HG3	0.59	1.73	2	1
1:A:379:SER:HA	1:A:426:VAL:HG23	0.59	1.74	6	3
1:A:397:VAL:HG11	1:A:448:ILE:HG23	0.59	1.73	19	1
1:A:409:TYR:CD1	1:A:452:LEU:HD22	0.59	2.32	16	8
1:A:397:VAL:HG13	1:A:452:LEU:HG	0.59	1.75	8	4
1:A:386:VAL:HG23	1:A:419:GLU:HB2	0.59	1.72	13	1
1:A:412:LEU:HD13	1:A:452:LEU:CD2	0.59	2.26	17	4
1:A:397:VAL:HG12	1:A:412:LEU:HD22	0.59	1.74	1	2
1:A:393:LEU:HD22	1:A:416:LEU:HD23	0.59	1.75	15	1
1:A:390:VAL:HG13	1:A:416:LEU:HD11	0.59	1.75	19	1
1:A:420:LEU:HD23	1:A:424:ASP:OD2	0.59	1.98	5	1
1:A:416:LEU:HD21	1:A:448:ILE:HG21	0.59	1.74	10	1
1:A:383:ILE:CG2	1:A:437:ALA:HB1	0.58	2.28	10	7
1:A:416:LEU:HD22	1:A:448:ILE:HG21	0.58	1.73	19	1
1:A:386:VAL:HG23	1:A:419:GLU:CG	0.58	2.29	3	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:393:LEU:HD22	1:A:416:LEU:CD1	0.57	2.21	1	3
1:A:420:LEU:HA	1:A:423:LEU:HD23	0.57	1.75	8	1
1:A:383:ILE:HD11	1:A:426:VAL:CB	0.57	2.28	8	1
1:A:379:SER:OG	1:A:434:VAL:HG11	0.57	2.00	19	2
1:A:397:VAL:HG23	1:A:452:LEU:HG	0.57	1.77	5	2
1:A:416:LEU:HD23	1:A:449:LEU:HD12	0.56	1.76	1	4
1:A:393:LEU:HD11	1:A:415:MET:HG2	0.56	1.77	17	5
1:A:383:ILE:HD12	1:A:437:ALA:CB	0.56	2.29	20	2
1:A:420:LEU:CD1	1:A:445:ILE:HD13	0.56	2.31	1	3
1:A:383:ILE:CG2	1:A:434:VAL:HG13	0.56	2.30	6	1
1:A:383:ILE:CD1	1:A:434:VAL:HG22	0.56	2.28	10	2
1:A:386:VAL:HG23	1:A:419:GLU:HG3	0.55	1.75	3	1
1:A:452:LEU:C	1:A:452:LEU:HD13	0.55	2.26	12	2
1:A:423:LEU:O	1:A:423:LEU:HD23	0.55	2.00	13	1
1:A:386:VAL:HG13	1:A:419:GLU:HG3	0.55	1.77	15	1
1:A:428:THR:OG1	1:A:434:VAL:HG21	0.55	2.01	18	1
1:A:416:LEU:CG	1:A:449:LEU:HD13	0.54	2.32	10	1
1:A:386:VAL:HB	1:A:423:LEU:HD21	0.54	1.80	16	1
1:A:416:LEU:HD23	1:A:448:ILE:CD1	0.54	2.22	20	1
1:A:420:LEU:CG	1:A:445:ILE:HD12	0.54	2.31	9	1
1:A:389:LYS:HD3	1:A:393:LEU:HD12	0.54	1.78	10	2
1:A:420:LEU:HD12	1:A:421:LEU:N	0.53	2.17	2	1
1:A:443:CYS:O	1:A:447:ALA:HB2	0.52	2.02	20	8
1:A:449:LEU:HD12	1:A:449:LEU:C	0.52	2.28	15	1
1:A:397:VAL:CG2	1:A:448:ILE:HD11	0.52	2.34	2	1
1:A:382:LYS:HD3	1:A:426:VAL:HG23	0.52	1.82	9	1
1:A:400:PHE:HE1	1:A:408:ALA:HB3	0.52	1.63	19	1
1:A:409:TYR:CD2	1:A:452:LEU:HD23	0.52	2.39	6	1
1:A:379:SER:HB3	1:A:434:VAL:HG21	0.52	1.81	20	2
1:A:419:GLU:OE1	1:A:445:ILE:HG22	0.51	2.05	10	1
1:A:390:VAL:HG11	1:A:444:LYS:HG2	0.51	1.83	2	2
1:A:416:LEU:HD22	1:A:448:ILE:CG2	0.51	2.36	19	1
1:A:394:GLU:O	1:A:397:VAL:HG22	0.51	2.06	14	3
1:A:428:THR:HG23	1:A:434:VAL:CG1	0.51	2.34	17	1
1:A:397:VAL:HG11	1:A:448:ILE:CG2	0.51	2.34	19	1
1:A:412:LEU:HD22	1:A:452:LEU:HD11	0.51	1.83	6	1
1:A:420:LEU:C	1:A:420:LEU:HD23	0.51	2.31	10	4
1:A:379:SER:HB2	1:A:434:VAL:HG21	0.50	1.82	2	1
1:A:380:ILE:HD11	1:A:383:ILE:HD11	0.50	1.81	3	1
1:A:380:ILE:HD13	1:A:433:SER:OG	0.50	2.05	8	1
1:A:413:GLU:O	1:A:417:THR:HG23	0.50	2.07	18	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:416:LEU:CD1	1:A:452:LEU:HD12	0.50	2.37	9	1
1:A:397:VAL:HG13	1:A:412:LEU:CD2	0.50	2.35	20	1
1:A:431:GLN:HG2	1:A:434:VAL:HG23	0.50	1.81	6	1
1:A:428:THR:HG23	1:A:428:THR:O	0.50	2.06	6	2
1:A:393:LEU:HD11	1:A:415:MET:HE2	0.50	1.83	11	1
1:A:408:ALA:HA	1:A:411:LEU:HD12	0.50	1.84	9	1
1:A:383:ILE:HA	1:A:423:LEU:HD11	0.50	1.84	16	1
1:A:397:VAL:HG22	1:A:452:LEU:HD11	0.50	1.82	17	1
1:A:416:LEU:HD23	1:A:449:LEU:HD13	0.49	1.84	8	1
1:A:420:LEU:HD11	1:A:445:ILE:CG1	0.49	2.37	15	1
1:A:380:ILE:HD12	1:A:383:ILE:HD12	0.49	1.85	9	1
1:A:423:LEU:C	1:A:423:LEU:HD12	0.49	2.31	3	1
1:A:416:LEU:HD21	1:A:448:ILE:HG12	0.49	1.85	1	1
1:A:383:ILE:HG21	1:A:434:VAL:HG13	0.49	1.84	6	1
1:A:431:GLN:CG	1:A:434:VAL:HG23	0.49	2.38	6	1
1:A:383:ILE:HD13	1:A:423:LEU:CD1	0.48	2.39	11	1
1:A:394:GLU:CG	1:A:448:ILE:HD12	0.48	2.37	12	1
1:A:439:LYS:HA	1:A:442:VAL:CG2	0.48	2.38	20	5
1:A:401:VAL:HG13	1:A:402:GLY:N	0.48	2.23	9	15
1:A:423:LEU:HD11	1:A:441:ALA:HB1	0.48	1.84	12	1
1:A:412:LEU:CD1	1:A:452:LEU:HD11	0.47	2.34	15	3
1:A:393:LEU:HD23	1:A:412:LEU:CD2	0.47	2.39	4	2
1:A:420:LEU:CG	1:A:445:ILE:HG21	0.47	2.40	4	1
1:A:445:ILE:O	1:A:448:ILE:HG22	0.47	2.10	17	2
1:A:400:PHE:CE1	1:A:408:ALA:HB3	0.47	2.45	19	1
1:A:383:ILE:HD11	1:A:438:ARG:HB2	0.47	1.86	17	1
1:A:409:TYR:CZ	1:A:452:LEU:HD11	0.47	2.45	12	1
1:A:416:LEU:HD11	1:A:448:ILE:CG2	0.47	2.39	14	1
1:A:383:ILE:CG1	1:A:437:ALA:HB1	0.46	2.41	12	1
1:A:423:LEU:HD11	1:A:441:ALA:CB	0.46	2.41	12	2
1:A:383:ILE:HD11	1:A:426:VAL:HG11	0.46	1.87	7	2
1:A:416:LEU:HD11	1:A:448:ILE:HG21	0.46	1.88	7	1
1:A:439:LYS:HA	1:A:442:VAL:HG22	0.45	1.87	5	2
1:A:379:SER:CB	1:A:434:VAL:HG21	0.45	2.41	20	2
1:A:380:ILE:HD13	1:A:380:ILE:C	0.45	2.35	19	1
1:A:380:ILE:HG23	1:A:381:LYS:N	0.45	2.27	5	3
1:A:412:LEU:O	1:A:416:LEU:HD12	0.45	2.11	13	1
1:A:404:LYS:CG	1:A:409:TYR:CD2	0.45	3.00	1	1
1:A:442:VAL:HA	1:A:445:ILE:HD12	0.45	1.88	4	2
1:A:416:LEU:HD22	1:A:448:ILE:HD11	0.45	1.87	15	1
1:A:400:PHE:CZ	1:A:409:TYR:HB2	0.45	2.47	19	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:409:TYR:CE1	1:A:452:LEU:CD2	0.45	2.99	5	1
1:A:412:LEU:C	1:A:416:LEU:HD12	0.45	2.37	2	1
1:A:380:ILE:HD11	1:A:437:ALA:CB	0.44	2.41	9	1
1:A:434:VAL:HG12	1:A:438:ARG:HG3	0.44	1.88	18	1
1:A:389:LYS:HE2	1:A:393:LEU:HD12	0.44	1.89	9	1
1:A:400:PHE:CE1	1:A:409:TYR:HB2	0.44	2.48	6	3
1:A:420:LEU:HG	1:A:445:ILE:HD12	0.44	1.89	9	1
1:A:416:LEU:HD11	1:A:445:ILE:HB	0.44	1.88	20	1
1:A:393:LEU:HD21	1:A:415:MET:CG	0.44	2.43	2	1
1:A:389:LYS:CE	1:A:393:LEU:HD12	0.44	2.43	9	1
1:A:396:GLU:HB2	1:A:412:LEU:HD21	0.44	1.89	15	1
1:A:442:VAL:HG23	1:A:443:CYS:N	0.43	2.27	5	1
1:A:384:ILE:HG23	1:A:385:HIS:N	0.43	2.28	19	1
1:A:423:LEU:HD21	1:A:441:ALA:CB	0.43	2.43	14	1
1:A:393:LEU:HD21	1:A:412:LEU:O	0.43	2.13	15	1
1:A:416:LEU:CD2	1:A:448:ILE:HG21	0.43	2.44	16	1
1:A:409:TYR:HE1	1:A:452:LEU:HD22	0.43	1.72	4	4
1:A:394:GLU:O	1:A:397:VAL:HG12	0.43	2.13	6	3
1:A:428:THR:HG21	1:A:434:VAL:HB	0.43	1.89	5	1
1:A:383:ILE:HB	1:A:437:ALA:HB1	0.43	1.91	15	1
1:A:400:PHE:CD1	1:A:412:LEU:CD1	0.43	3.00	9	1
1:A:426:VAL:O	1:A:426:VAL:HG13	0.42	2.14	20	1
1:A:438:ARG:O	1:A:442:VAL:HG22	0.42	2.14	5	1
1:A:420:LEU:CD2	1:A:445:ILE:HG21	0.42	2.44	4	1
1:A:445:ILE:HG13	1:A:446:GLN:N	0.42	2.30	5	3
1:A:448:ILE:HG23	1:A:449:LEU:N	0.42	2.29	10	1
1:A:401:VAL:HG13	1:A:402:GLY:H	0.42	1.75	6	1
1:A:416:LEU:HB3	1:A:449:LEU:HD11	0.42	1.92	4	2
1:A:380:ILE:O	1:A:383:ILE:HG22	0.42	2.15	5	2
1:A:428:THR:CG2	1:A:431:GLN:CB	0.42	2.98	18	1
1:A:383:ILE:O	1:A:386:VAL:HG22	0.41	2.15	10	1
1:A:414:GLU:CG	1:A:415:MET:N	0.41	2.83	12	1
1:A:383:ILE:CD1	1:A:426:VAL:HG11	0.41	2.45	7	1
1:A:417:THR:HA	1:A:420:LEU:HD21	0.41	1.93	2	1
1:A:380:ILE:O	1:A:383:ILE:HG13	0.41	2.14	12	2
1:A:439:LYS:CA	1:A:442:VAL:HG22	0.41	2.45	5	1
1:A:393:LEU:HD11	1:A:415:MET:CB	0.41	2.41	14	1
1:A:400:PHE:CE1	1:A:401:VAL:HG12	0.41	2.50	14	1
1:A:380:ILE:HB	1:A:434:VAL:HG22	0.41	1.92	17	1
1:A:416:LEU:HD21	1:A:448:ILE:CG1	0.41	2.46	1	1
1:A:386:VAL:HG21	1:A:423:LEU:HB2	0.41	1.92	14	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:423:LEU:HD11	1:A:441:ALA:HB3	0.41	1.93	2	1
1:A:423:LEU:CD1	1:A:441:ALA:CB	0.41	2.98	2	1
1:A:423:LEU:HD23	1:A:423:LEU:C	0.41	2.40	2	1
1:A:416:LEU:CG	1:A:449:LEU:HD12	0.41	2.40	14	1
1:A:387:LEU:HG	1:A:441:ALA:HB2	0.41	1.92	17	1
1:A:404:LYS:HG3	1:A:409:TYR:CD2	0.41	2.51	1	1
1:A:389:LYS:CE	1:A:393:LEU:CD1	0.41	2.99	11	1
1:A:448:ILE:CD1	1:A:449:LEU:N	0.41	2.80	15	1
1:A:383:ILE:HD12	1:A:387:LEU:CD1	0.40	2.45	1	1
1:A:411:LEU:HD12	1:A:411:LEU:C	0.40	2.41	6	1
1:A:437:ALA:O	1:A:441:ALA:HB2	0.40	2.16	10	1
1:A:388:GLU:O	1:A:392:TYR:CD2	0.40	2.74	14	1
1:A:416:LEU:CD2	1:A:448:ILE:HG23	0.40	2.46	17	1
1:A:445:ILE:O	1:A:449:LEU:HD13	0.40	2.16	18	1
1:A:380:ILE:HD11	1:A:437:ALA:HB2	0.40	1.92	9	1
1:A:379:SER:HB2	1:A:426:VAL:HG22	0.40	1.93	10	1
1:A:380:ILE:CD1	1:A:437:ALA:CB	0.40	2.99	9	1
1:A:380:ILE:HG13	1:A:383:ILE:HD11	0.40	1.93	20	1
1:A:427:GLU:O	1:A:428:THR:CG2	0.40	2.69	14	1
1:A:442:VAL:HG12	1:A:446:GLN:NE2	0.40	2.31	17	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	77/99 (78%)	70±2 (90±3%)	7±2 (9±3%)	0±0 (1±1%)	26	74
All	All	1540/1980 (78%)	1393 (90%)	139 (9%)	8 (1%)	26	74

All 4 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	430	GLY	5
1	A	380	ILE	1

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Mol	Chain	Res	Type	Models (Total)
1	A	431	GLN	1
1	A	428	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	70/91 (77%)	53±3 (76±4%)	17±3 (24±4%)	2	26
All	All	1400/1820 (77%)	1066 (76%)	334 (24%)	2	26

All 58 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	393	LEU	19
1	A	389	LYS	17
1	A	449	LEU	14
1	A	382	LYS	12
1	A	381	LYS	11
1	A	380	ILE	10
1	A	407	LYS	10
1	A	454	LYS	10
1	A	420	LEU	10
1	A	388	GLU	9
1	A	416	LEU	9
1	A	444	LYS	9
1	A	451	LYS	9
1	A	404	LYS	8
1	A	435	ARG	8
1	A	455	LYS	8
1	A	403	LYS	7
1	A	450	GLU	7
1	A	418	LYS	7
1	A	419	GLU	7
1	A	433	SER	7
1	A	453	GLU	7
1	A	439	LYS	7

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Mol	Chain	Res	Type	Models (Total)
1	A	413	GLU	6
1	A	431	GLN	6
1	A	383	ILE	5
1	A	398	GLU	5
1	A	438	ARG	5
1	A	379	SER	5
1	A	452	LEU	5
1	A	427	GLU	5
1	A	436	GLN	5
1	A	387	LEU	5
1	A	395	GLN	5
1	A	421	LEU	4
1	A	405	THR	4
1	A	411	LEU	4
1	A	391	GLN	4
1	A	422	GLU	3
1	A	446	GLN	3
1	A	414	GLU	3
1	A	417	THR	3
1	A	425	SER	3
1	A	415	MET	3
1	A	385	HIS	3
1	A	443	CYS	2
1	A	423	LEU	2
1	A	410	TRP	2
1	A	440	GLU	2
1	A	448	ILE	2
1	A	432	ASP	1
1	A	424	ASP	1
1	A	434	VAL	1
1	A	396	GLU	1
1	A	394	GLU	1
1	A	399	GLU	1
1	A	428	THR	1
1	A	445	ILE	1

6.3.3 RNA ⓘ

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 [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided