



Full wwPDB NMR Structure Validation Report ⓘ

Mar 7, 2026 – 01:02 AM UTC

PDB ID : 1NMF / pdb_00001nmf
Title : MAJOR COLD-SHOCK PROTEIN, NMR, 20 STRUCTURES
Authors : Schnuchel, A.; Holak, T.A.
Deposited on : 1996-02-05

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

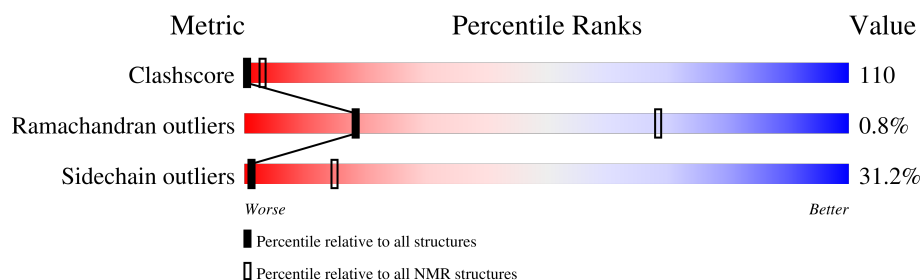
1 Overall quality at a glance

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	67	12% 55% 10% 22%

2 Ensemble composition and analysis

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:33, A:46-A:65 (52)	0.39	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 6 clusters and 1 single-model cluster was found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1014 atoms, of which 493 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called MAJOR COLD-SHOCK PROTEIN.

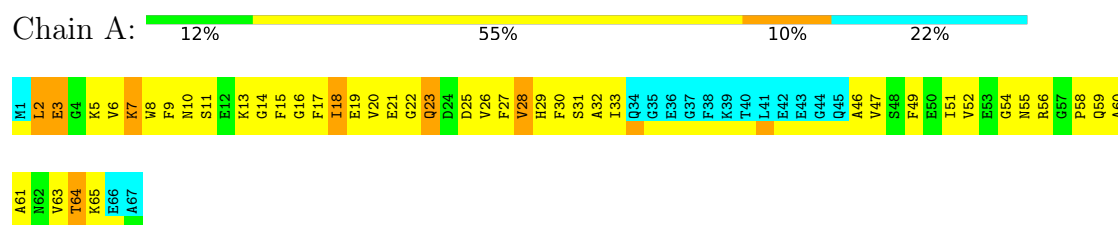
Mol	Chain	Residues	Atoms						Trace
1	A	67	Total	C	H	N	O	S	0
			1014	331	493	85	104	1	

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: MAJOR COLD-SHOCK PROTEIN

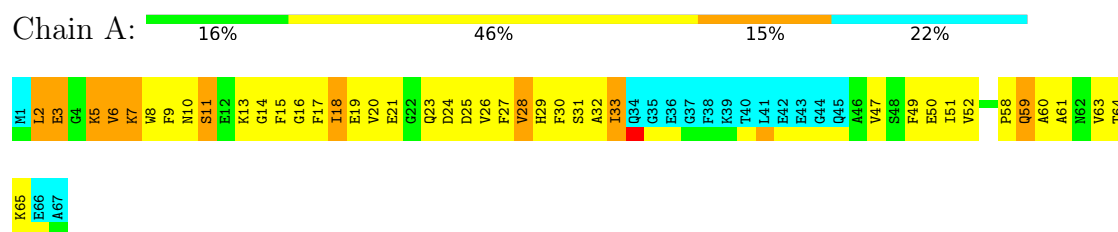


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

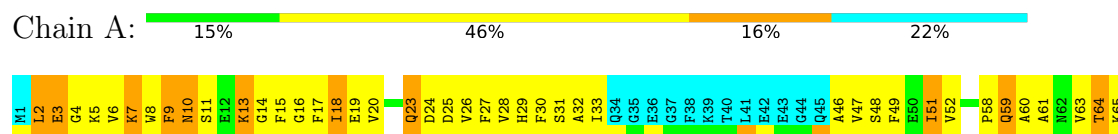
4.2.1 Score per residue for model 1

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



4.2.2 Score per residue for model 2

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



E66
A67

4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

Chain A: 12% 52% 13% 22%

M1 L2 L3 E3 G4 K5 V6 K7 W8 F9 F10 N10 N11 S11 E12 K13 G14 F15 G16 F17 F18 I18 E19 V20 E21 G22 Q23 D24 D25 V26 V27 F28 V29 H29 F30 F31 S31 A32 I33 Q34 Q35 E36 G37 F38 K39 T40 L41 E42 E43 E44 Q45 A46 V47 V48 F49 E50 I51 V52 E53 G54 N55 R56 R57 P58 Q59 A60

A61
A62
V63
T64
K65
E66
A67

4.2.4 Score per residue for model 4

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

Chain A: 10% 51% 16% 22%

M1 L2 L3 E3 G4 K5 V6 K7 W8 F9 F10 N10 N11 S11 E12 K13 G14 F15 G16 F17 F18 I18 E19 V20 E21 G22 Q23 D24 D25 V26 V27 F28 V29 H29 F30 F31 S31 A32 I33 Q34 Q35 E36 G37 F38 K39 T40 L41 E42 E43 E44 Q45 A46 V47 V48 F49 E50 I51 V52 E53 G54 N55 P58 Q59 A60 A61 N62

V63
T64
K65
E66
A67

4.2.5 Score per residue for model 5

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

Chain A: 10% 54% 13% 22%

M1 L2 L3 E3 G4 K5 V6 K7 W8 F9 F10 N10 N11 S11 E12 K13 G14 F15 G16 F17 F18 I18 E19 V20 E21 G22 Q23 D24 D25 V26 V27 F28 V29 H29 F30 F31 S31 A32 I33 Q34 Q35 E36 G37 F38 K39 T40 L41 E42 E43 E44 Q45 A46 V47 V48 F49 E50 I51 V52 E53 G54 N55 P58 Q59 A60 A61

A62
V63
T64
K65
E66
A67

4.2.6 Score per residue for model 6

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

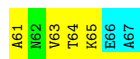
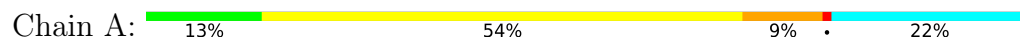
Chain A: 15% 46% 16% 22%

M1 L2 L3 E3 G4 K5 V6 K7 W8 F9 F10 N10 N11 S11 E12 K13 G14 F15 G16 F17 F18 I18 E19 V20 E21 G22 Q23 D24 D25 V26 V27 F28 V29 H29 F30 F31 S31 A32 I33 Q34 Q35 E36 G37 F38 K39 T40 L41 E42 E43 E44 Q45 A46 V47 V48 F49 E50 I51 V52 E53 G54 N55 P58 Q59 A60 A61



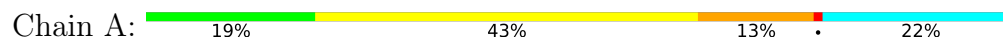
4.2.7 Score per residue for model 7

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



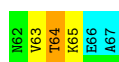
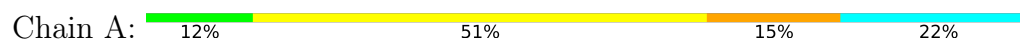
4.2.8 Score per residue for model 8

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



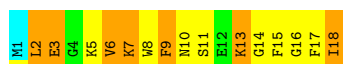
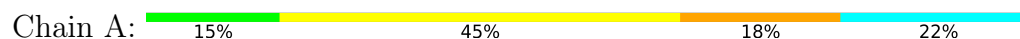
4.2.9 Score per residue for model 9

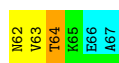
- Molecule 1: MAJOR COLD-SHOCK PROTEIN



4.2.10 Score per residue for model 10

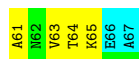
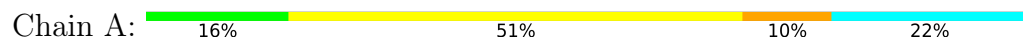
- Molecule 1: MAJOR COLD-SHOCK PROTEIN





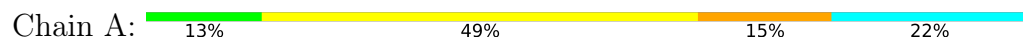
4.2.11 Score per residue for model 11

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



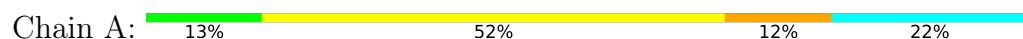
4.2.12 Score per residue for model 12

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



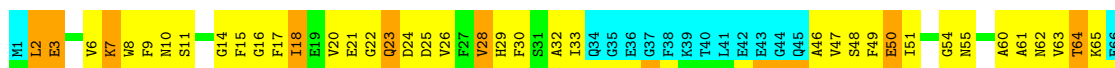
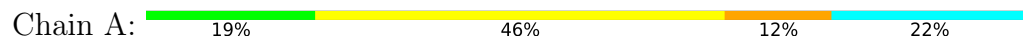
4.2.13 Score per residue for model 13

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



4.2.14 Score per residue for model 14

- Molecule 1: MAJOR COLD-SHOCK PROTEIN



A67

4.2.15 Score per residue for model 15

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

Chain A: 15% 52% 10% 22%

H62
V63
T64
K65
E66
A67

4.2.16 Score per residue for model 16

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

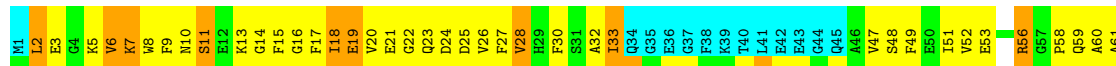
Chain A: 15% 46% 16% 22%

H62
V63
T64
K65
E66
A67

4.2.17 Score per residue for model 17

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

Chain A: 16% 46% 15% 22%

H62
V63
T64
K65
E66
A67

4.2.18 Score per residue for model 18

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

Chain A: 16% 52% 9% 22%





4.2.19 Score per residue for model 19

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

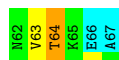
Chain A: 10% 54% 13% 22%



4.2.20 Score per residue for model 20

- Molecule 1: MAJOR COLD-SHOCK PROTEIN

Chain A: 16% 43% 16% 22%



5 Refinement protocol and experimental data overview ⓘ

Of the ? calculated structures, 20 were deposited, based on the following criterion: ?.

The authors did not provide any information on software used for structure solution, optimization or refinement.

No chemical shift data was provided.

6 Model quality [i](#)

6.1 Standard geometry [i](#)

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	1.49±0.01	0±0/416 (0.0± 0.0%)	1.42±0.01	2±1/561 (0.3± 0.1%)
All	All	1.49	0/8320 (0.0%)	1.42	37/11220 (0.3%)

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	7	LYS	N-CA-C	-8.70	103.17	113.88	20	20
1	A	22	GLY	N-CA-C	-5.71	108.29	115.08	10	13
1	A	49	PHE	CA-CB-CG	-5.18	108.62	113.80	5	3
1	A	30	PHE	CA-CB-CG	-5.15	108.65	113.80	9	1

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	406	388	388	87±7
All	All	8120	7760	7760	1746

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 110.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:2:LEU:HD11	1:A:49:PHE:CE1	1.10	1.82	14	19
1:A:26:VAL:HG22	1:A:51:ILE:HD11	1.08	1.11	2	3
1:A:26:VAL:HG21	1:A:49:PHE:CZ	0.98	1.93	9	16
1:A:26:VAL:HG22	1:A:51:ILE:CD1	0.94	1.91	19	3
1:A:18:ILE:HD12	1:A:28:VAL:CG1	0.94	1.92	3	15
1:A:26:VAL:HG21	1:A:49:PHE:CE1	0.93	1.98	19	15
1:A:18:ILE:HD12	1:A:28:VAL:HG12	0.91	1.43	1	9
1:A:51:ILE:HD13	1:A:59:GLN:C	0.91	1.91	19	3
1:A:49:PHE:CB	1:A:63:VAL:HG22	0.91	1.96	1	20
1:A:9:PHE:CE1	1:A:28:VAL:HG21	0.90	2.01	4	5
1:A:2:LEU:HD22	1:A:49:PHE:CE1	0.90	2.02	11	1
1:A:28:VAL:HB	1:A:33:ILE:HD11	0.89	1.44	14	8
1:A:18:ILE:CD1	1:A:28:VAL:HG11	0.87	2.00	19	12
1:A:2:LEU:C	1:A:2:LEU:HD13	0.86	1.94	8	19
1:A:16:GLY:O	1:A:28:VAL:HG22	0.86	1.70	6	10
1:A:26:VAL:CG2	1:A:51:ILE:HD11	0.84	2.01	9	19
1:A:18:ILE:HD12	1:A:28:VAL:HG21	0.84	1.47	8	6
1:A:33:ILE:HD13	1:A:63:VAL:CG1	0.83	2.02	9	2
1:A:18:ILE:HD12	1:A:28:VAL:HG11	0.83	1.47	6	10
1:A:2:LEU:HD13	1:A:2:LEU:O	0.83	1.72	8	19
1:A:18:ILE:HD11	1:A:47:VAL:HG21	0.83	1.51	2	13
1:A:26:VAL:HG23	1:A:51:ILE:HD11	0.82	1.48	9	14
1:A:2:LEU:HD12	1:A:49:PHE:O	0.82	1.74	2	19
1:A:3:GLU:OE2	1:A:46:ALA:HB1	0.82	1.75	12	7
1:A:33:ILE:HD13	1:A:63:VAL:HB	0.81	1.50	15	2
1:A:60:ALA:HB1	1:A:63:VAL:CG2	0.81	2.06	10	20
1:A:33:ILE:HD13	1:A:63:VAL:CB	0.80	2.06	15	2
1:A:18:ILE:CD1	1:A:47:VAL:HG21	0.79	2.08	2	14
1:A:29:HIS:O	1:A:33:ILE:HD12	0.78	1.78	19	6
1:A:3:GLU:CD	1:A:46:ALA:HB1	0.78	2.04	19	5
1:A:2:LEU:HD22	1:A:3:GLU:O	0.78	1.78	6	17
1:A:26:VAL:HG12	1:A:28:VAL:HG13	0.77	1.56	10	8
1:A:28:VAL:CB	1:A:33:ILE:HD11	0.76	2.11	12	9
1:A:51:ILE:CD1	1:A:60:ALA:HB2	0.76	2.11	10	1
1:A:2:LEU:HD11	1:A:49:PHE:CD1	0.75	2.15	10	18
1:A:49:PHE:HB3	1:A:63:VAL:HG22	0.75	1.59	1	20
1:A:60:ALA:HB1	1:A:63:VAL:HG22	0.74	1.59	16	20
1:A:32:ALA:HB1	1:A:61:ALA:O	0.73	1.83	2	20
1:A:8:TRP:CH2	1:A:17:PHE:CD1	0.72	2.78	14	19
1:A:8:TRP:CZ2	1:A:17:PHE:CG	0.71	2.78	6	20
1:A:33:ILE:HG23	1:A:63:VAL:CG1	0.71	2.14	6	3
1:A:16:GLY:C	1:A:28:VAL:HG22	0.71	2.10	15	8

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:VAL:HG13	1:A:23:GLN:HB2	0.69	1.63	15	17
1:A:8:TRP:O	1:A:8:TRP:CE3	0.69	2.45	11	20
1:A:26:VAL:HG13	1:A:60:ALA:H	0.68	1.49	5	3
1:A:20:VAL:HG13	1:A:23:GLN:CB	0.68	2.19	16	14
1:A:8:TRP:CZ2	1:A:17:PHE:CD1	0.68	2.82	17	19
1:A:49:PHE:CE1	1:A:51:ILE:CG1	0.67	2.77	10	1
1:A:2:LEU:C	1:A:2:LEU:HD23	0.67	2.13	11	1
1:A:28:VAL:HG11	1:A:63:VAL:HG21	0.67	1.66	16	1
1:A:2:LEU:HD11	1:A:49:PHE:HE1	0.67	1.47	10	1
1:A:2:LEU:C	1:A:2:LEU:CD1	0.66	2.69	8	19
1:A:18:ILE:HD12	1:A:28:VAL:CG2	0.65	2.19	8	4
1:A:16:GLY:O	1:A:28:VAL:HG13	0.65	1.92	17	9
1:A:15:PHE:CD1	1:A:15:PHE:N	0.65	2.63	11	1
1:A:26:VAL:HG21	1:A:51:ILE:CD1	0.64	2.22	10	3
1:A:16:GLY:O	1:A:28:VAL:HG23	0.64	1.92	10	5
1:A:33:ILE:HD13	1:A:63:VAL:HG11	0.64	1.68	9	1
1:A:9:PHE:CE1	1:A:28:VAL:CG2	0.64	2.81	3	5
1:A:49:PHE:CE1	1:A:51:ILE:HG12	0.64	2.28	10	4
1:A:8:TRP:CE3	1:A:8:TRP:C	0.64	2.76	4	20
1:A:26:VAL:CG2	1:A:51:ILE:CD1	0.64	2.76	18	19
1:A:29:HIS:NE2	1:A:30:PHE:CE2	0.63	2.66	5	2
1:A:29:HIS:NE2	1:A:30:PHE:CE1	0.63	2.67	8	3
1:A:26:VAL:HG21	1:A:51:ILE:HD11	0.63	1.71	7	8
1:A:33:ILE:HG22	1:A:33:ILE:O	0.63	1.92	1	2
1:A:9:PHE:HE1	1:A:28:VAL:HG21	0.63	1.53	3	3
1:A:17:PHE:CZ	1:A:27:PHE:CD2	0.63	2.87	10	5
1:A:9:PHE:C	1:A:9:PHE:CD1	0.62	2.76	19	1
1:A:33:ILE:HD12	1:A:33:ILE:N	0.62	2.09	10	4
1:A:3:GLU:OE1	1:A:46:ALA:HB1	0.62	1.93	19	1
1:A:17:PHE:CZ	1:A:27:PHE:CE2	0.62	2.88	8	11
1:A:33:ILE:CD1	1:A:33:ILE:N	0.62	2.62	1	2
1:A:33:ILE:CD1	1:A:63:VAL:HG11	0.62	2.24	9	2
1:A:60:ALA:CB	1:A:63:VAL:CG2	0.62	2.78	10	17
1:A:2:LEU:CD2	1:A:49:PHE:CE1	0.62	2.79	11	1
1:A:26:VAL:CG2	1:A:51:ILE:CG1	0.61	2.78	11	19
1:A:29:HIS:NE2	1:A:30:PHE:CZ	0.61	2.67	2	2
1:A:8:TRP:CZ3	1:A:10:ASN:CG	0.61	2.78	12	9
1:A:49:PHE:HB3	1:A:63:VAL:HG13	0.61	1.73	4	20
1:A:17:PHE:CE1	1:A:27:PHE:CE2	0.61	2.89	11	3
1:A:20:VAL:CG1	1:A:23:GLN:CB	0.60	2.79	16	14
1:A:26:VAL:CG1	1:A:60:ALA:HB3	0.60	2.26	16	14

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:ASN:CG	1:A:10:ASN:O	0.60	2.45	19	1
1:A:2:LEU:CD1	1:A:49:PHE:CD1	0.60	2.84	10	13
1:A:49:PHE:CD1	1:A:51:ILE:HD11	0.60	2.32	10	1
1:A:49:PHE:CD1	1:A:51:ILE:CD1	0.60	2.85	10	1
1:A:8:TRP:CZ3	1:A:10:ASN:OD1	0.59	2.55	17	3
1:A:26:VAL:CG1	1:A:60:ALA:CB	0.59	2.80	2	15
1:A:49:PHE:CD1	1:A:49:PHE:C	0.59	2.80	11	20
1:A:26:VAL:CG2	1:A:49:PHE:CZ	0.59	2.81	9	3
1:A:51:ILE:HD13	1:A:59:GLN:CA	0.59	2.28	4	3
1:A:18:ILE:CG2	1:A:19:GLU:N	0.59	2.65	8	13
1:A:28:VAL:HB	1:A:33:ILE:HD13	0.59	1.75	13	2
1:A:51:ILE:HD11	1:A:60:ALA:HB2	0.59	1.74	10	1
1:A:2:LEU:HD22	1:A:3:GLU:N	0.59	2.13	8	17
1:A:32:ALA:CB	1:A:61:ALA:O	0.58	2.51	13	19
1:A:14:GLY:O	1:A:29:HIS:CD2	0.58	2.56	16	3
1:A:33:ILE:HG23	1:A:63:VAL:HB	0.58	1.74	13	1
1:A:33:ILE:N	1:A:33:ILE:CD1	0.58	2.66	10	4
1:A:26:VAL:HG22	1:A:51:ILE:CG1	0.58	2.29	19	13
1:A:14:GLY:O	1:A:29:HIS:CE1	0.58	2.57	18	7
1:A:65:LYS:CD	1:A:65:LYS:N	0.58	2.65	6	1
1:A:8:TRP:CE2	1:A:17:PHE:HB2	0.58	2.34	17	20
1:A:6:VAL:CG1	1:A:8:TRP:N	0.58	2.67	4	11
1:A:18:ILE:O	1:A:25:ASP:HA	0.57	1.99	19	20
1:A:30:PHE:O	1:A:30:PHE:CD2	0.57	2.57	6	9
1:A:33:ILE:N	1:A:33:ILE:HD12	0.57	2.15	1	2
1:A:30:PHE:C	1:A:30:PHE:CD1	0.57	2.81	12	1
1:A:49:PHE:CE1	1:A:51:ILE:HD11	0.57	2.35	10	1
1:A:6:VAL:HG13	1:A:8:TRP:N	0.57	2.14	20	18
1:A:10:ASN:OD1	1:A:13:LYS:CB	0.57	2.53	19	2
1:A:13:LYS:N	1:A:13:LYS:CD	0.57	2.67	7	4
1:A:26:VAL:HG13	1:A:60:ALA:CB	0.56	2.30	20	11
1:A:26:VAL:O	1:A:28:VAL:HG12	0.56	2.00	20	7
1:A:18:ILE:CD1	1:A:28:VAL:HG21	0.56	2.27	8	1
1:A:2:LEU:CD1	1:A:49:PHE:CE1	0.56	2.79	10	3
1:A:18:ILE:CD1	1:A:28:VAL:CG1	0.56	2.82	14	7
1:A:28:VAL:HG23	1:A:33:ILE:CD1	0.56	2.30	7	1
1:A:26:VAL:CG1	1:A:28:VAL:HG13	0.56	2.27	10	3
1:A:51:ILE:CD1	1:A:60:ALA:CB	0.56	2.83	10	1
1:A:49:PHE:CE1	1:A:51:ILE:HG13	0.56	2.35	16	16
1:A:9:PHE:CD1	1:A:16:GLY:HA3	0.56	2.35	9	10
1:A:10:ASN:C	1:A:15:PHE:O	0.56	2.49	17	18

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:VAL:HG12	1:A:63:VAL:HG21	0.56	1.77	2	1
1:A:10:ASN:O	1:A:10:ASN:OD1	0.56	2.24	19	1
1:A:6:VAL:HG22	1:A:9:PHE:CD1	0.56	2.36	5	2
1:A:8:TRP:CE3	1:A:10:ASN:OD1	0.55	2.59	14	2
1:A:29:HIS:O	1:A:33:ILE:CD1	0.55	2.55	13	3
1:A:26:VAL:HG11	1:A:60:ALA:CB	0.55	2.32	18	10
1:A:49:PHE:HB3	1:A:63:VAL:CG2	0.55	2.29	17	20
1:A:28:VAL:O	1:A:28:VAL:CG2	0.55	2.55	7	2
1:A:29:HIS:CE1	1:A:30:PHE:CE1	0.54	2.96	11	2
1:A:33:ILE:CG1	1:A:63:VAL:HB	0.54	2.33	13	5
1:A:28:VAL:CG2	1:A:33:ILE:HD11	0.54	2.32	19	3
1:A:20:VAL:CG1	1:A:23:GLN:HB2	0.54	2.32	15	17
1:A:8:TRP:CZ3	1:A:10:ASN:ND2	0.54	2.76	18	3
1:A:8:TRP:O	1:A:8:TRP:CD2	0.54	2.60	5	20
1:A:8:TRP:CE3	1:A:10:ASN:ND2	0.54	2.76	18	1
1:A:49:PHE:HB2	1:A:63:VAL:HG22	0.54	1.79	4	9
1:A:26:VAL:HG22	1:A:51:ILE:HG12	0.54	1.80	18	16
1:A:14:GLY:C	1:A:29:HIS:NE2	0.53	2.67	16	1
1:A:10:ASN:ND2	1:A:15:PHE:O	0.53	2.42	19	1
1:A:16:GLY:O	1:A:28:VAL:CG2	0.53	2.57	5	10
1:A:10:ASN:O	1:A:11:SER:C	0.53	2.52	18	19
1:A:10:ASN:HB2	1:A:15:PHE:CD1	0.53	2.39	18	1
1:A:14:GLY:C	1:A:15:PHE:CD2	0.53	2.86	1	2
1:A:33:ILE:O	1:A:33:ILE:CG2	0.53	2.56	1	2
1:A:26:VAL:HG21	1:A:51:ILE:CG1	0.53	2.34	7	4
1:A:2:LEU:CD2	1:A:3:GLU:O	0.53	2.55	16	9
1:A:20:VAL:CG1	1:A:23:GLN:HB3	0.52	2.35	20	5
1:A:23:GLN:NE2	1:A:51:ILE:HG21	0.52	2.19	14	1
1:A:10:ASN:OD1	1:A:13:LYS:C	0.52	2.52	19	1
1:A:26:VAL:CG2	1:A:51:ILE:HG12	0.52	2.35	5	4
1:A:33:ILE:HG23	1:A:63:VAL:CB	0.52	2.35	13	2
1:A:17:PHE:HA	1:A:28:VAL:HG13	0.52	1.82	7	1
1:A:13:LYS:O	1:A:15:PHE:CE2	0.52	2.63	12	1
1:A:10:ASN:HB2	1:A:15:PHE:O	0.52	2.05	4	11
1:A:29:HIS:N	1:A:33:ILE:CD1	0.52	2.72	13	1
1:A:63:VAL:HG12	1:A:64:THR:N	0.52	2.20	13	13
1:A:5:LYS:O	1:A:6:VAL:C	0.52	2.53	7	16
1:A:8:TRP:CZ2	1:A:17:PHE:HB2	0.52	2.40	13	20
1:A:14:GLY:O	1:A:29:HIS:NE2	0.51	2.43	16	3
1:A:10:ASN:OD1	1:A:14:GLY:N	0.51	2.43	19	1
1:A:16:GLY:CA	1:A:28:VAL:HG22	0.51	2.35	17	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:58:PRO:O	1:A:59:GLN:CG	0.51	2.58	16	2
1:A:9:PHE:CZ	1:A:28:VAL:CG2	0.51	2.93	7	3
1:A:28:VAL:HB	1:A:33:ILE:CD1	0.51	2.35	6	10
1:A:26:VAL:HG13	1:A:60:ALA:HB3	0.51	1.81	16	5
1:A:22:GLY:O	1:A:23:GLN:NE2	0.51	2.43	10	1
1:A:51:ILE:HD13	1:A:60:ALA:HA	0.51	1.83	10	1
1:A:15:PHE:CE1	1:A:17:PHE:CE1	0.51	2.98	19	1
1:A:10:ASN:OD1	1:A:13:LYS:CD	0.51	2.59	16	1
1:A:10:ASN:CB	1:A:15:PHE:O	0.51	2.58	4	5
1:A:18:ILE:O	1:A:26:VAL:N	0.51	2.44	10	7
1:A:8:TRP:CZ3	1:A:16:GLY:HA2	0.50	2.41	19	7
1:A:50:GLU:O	1:A:50:GLU:CG	0.50	2.59	8	2
1:A:49:PHE:CE1	1:A:51:ILE:CD1	0.50	2.94	10	1
1:A:26:VAL:HG12	1:A:28:VAL:CG1	0.50	2.32	18	1
1:A:28:VAL:CB	1:A:33:ILE:CD1	0.50	2.88	7	2
1:A:15:PHE:C	1:A:15:PHE:CD1	0.50	2.90	4	3
1:A:13:LYS:N	1:A:13:LYS:HD2	0.50	2.21	7	4
1:A:2:LEU:C	1:A:2:LEU:CD2	0.50	2.82	11	1
1:A:33:ILE:HG23	1:A:63:VAL:HG12	0.50	1.82	6	1
1:A:3:GLU:OE1	1:A:4:GLY:N	0.49	2.45	9	1
1:A:18:ILE:O	1:A:25:ASP:CA	0.49	2.59	20	15
1:A:28:VAL:CG1	1:A:63:VAL:HG21	0.49	2.37	16	2
1:A:9:PHE:CZ	1:A:28:VAL:HG23	0.49	2.43	14	1
1:A:33:ILE:CD1	1:A:63:VAL:CG1	0.49	2.88	15	1
1:A:29:HIS:CE1	1:A:30:PHE:CE2	0.49	3.00	5	1
1:A:52:VAL:O	1:A:58:PRO:HA	0.49	2.08	9	19
1:A:10:ASN:OD1	1:A:13:LYS:HB2	0.49	2.08	19	3
1:A:26:VAL:O	1:A:28:VAL:CG1	0.49	2.60	6	3
1:A:28:VAL:CG2	1:A:33:ILE:CD1	0.49	2.91	7	2
1:A:3:GLU:OE1	1:A:3:GLU:C	0.49	2.56	8	1
1:A:26:VAL:O	1:A:27:PHE:C	0.48	2.56	17	3
1:A:27:PHE:C	1:A:27:PHE:CD1	0.48	2.90	19	1
1:A:18:ILE:CD1	1:A:47:VAL:CG2	0.48	2.86	2	2
1:A:3:GLU:OE2	1:A:47:VAL:N	0.48	2.46	1	1
1:A:26:VAL:CG1	1:A:60:ALA:HB2	0.48	2.39	2	7
1:A:2:LEU:HG	1:A:3:GLU:N	0.48	2.22	11	1
1:A:10:ASN:OD1	1:A:13:LYS:CG	0.48	2.61	2	1
1:A:18:ILE:N	1:A:28:VAL:CG1	0.48	2.77	7	1
1:A:10:ASN:OD1	1:A:13:LYS:CE	0.48	2.62	11	1
1:A:10:ASN:CB	1:A:15:PHE:CE1	0.48	2.97	18	1
1:A:26:VAL:CG2	1:A:51:ILE:HG13	0.48	2.39	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:51:ILE:CD1	1:A:60:ALA:CA	0.48	2.90	10	1
1:A:18:ILE:CG1	1:A:28:VAL:HG11	0.48	2.39	14	2
1:A:15:PHE:CD1	1:A:15:PHE:C	0.48	2.92	18	1
1:A:25:ASP:CG	1:A:25:ASP:O	0.48	2.56	11	2
1:A:10:ASN:ND2	1:A:13:LYS:CB	0.47	2.77	5	1
1:A:26:VAL:HG12	1:A:26:VAL:O	0.47	2.08	13	1
1:A:14:GLY:O	1:A:15:PHE:CB	0.47	2.59	15	6
1:A:13:LYS:HB3	1:A:15:PHE:CZ	0.47	2.43	10	1
1:A:10:ASN:ND2	1:A:13:LYS:HB2	0.47	2.24	5	1
1:A:28:VAL:HG12	1:A:33:ILE:HD11	0.47	1.85	2	2
1:A:2:LEU:CD2	1:A:49:PHE:CZ	0.47	2.96	11	1
1:A:19:GLU:CG	1:A:25:ASP:OD1	0.47	2.62	6	1
1:A:53:GLU:N	1:A:53:GLU:CD	0.47	2.72	12	2
1:A:32:ALA:O	1:A:63:VAL:O	0.47	2.33	10	5
1:A:26:VAL:HG11	1:A:60:ALA:HB2	0.47	1.85	18	3
1:A:25:ASP:O	1:A:25:ASP:OD1	0.47	2.33	7	4
1:A:58:PRO:O	1:A:59:GLN:HG3	0.47	2.10	16	2
1:A:65:LYS:N	1:A:65:LYS:HD3	0.47	2.25	6	1
1:A:2:LEU:CG	1:A:3:GLU:N	0.47	2.77	11	1
1:A:6:VAL:CG1	1:A:7:LYS:N	0.47	2.78	20	1
1:A:58:PRO:O	1:A:59:GLN:OE1	0.46	2.33	3	1
1:A:56:ARG:NH1	1:A:56:ARG:CG	0.46	2.78	11	4
1:A:47:VAL:HG21	1:A:63:VAL:HG11	0.46	1.85	20	1
1:A:29:HIS:O	1:A:30:PHE:C	0.46	2.58	2	1
1:A:27:PHE:CB	1:A:59:GLN:CD	0.46	2.89	1	1
1:A:19:GLU:OE1	1:A:25:ASP:OD1	0.46	2.34	16	1
1:A:8:TRP:C	1:A:8:TRP:CD2	0.46	2.94	17	19
1:A:54:GLY:O	1:A:55:ASN:C	0.46	2.57	5	16
1:A:56:ARG:NH1	1:A:56:ARG:HG3	0.46	2.24	10	2
1:A:33:ILE:O	1:A:33:ILE:HG22	0.46	2.10	12	1
1:A:19:GLU:OE1	1:A:25:ASP:CG	0.46	2.59	16	1
1:A:49:PHE:HB3	1:A:63:VAL:CG1	0.45	2.40	4	5
1:A:26:VAL:HG21	1:A:51:ILE:HG13	0.45	1.87	10	1
1:A:30:PHE:CD1	1:A:30:PHE:O	0.45	2.69	14	2
1:A:51:ILE:CD1	1:A:59:GLN:CA	0.45	2.94	4	2
1:A:9:PHE:HA	1:A:16:GLY:CA	0.45	2.42	19	1
1:A:18:ILE:HG22	1:A:19:GLU:N	0.45	2.25	2	4
1:A:49:PHE:HB3	1:A:63:VAL:CB	0.45	2.42	17	6
1:A:28:VAL:HB	1:A:33:ILE:CG1	0.45	2.41	19	1
1:A:4:GLY:O	1:A:46:ALA:HA	0.45	2.11	2	2
1:A:28:VAL:CG1	1:A:33:ILE:HG12	0.45	2.42	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:10:ASN:CA	1:A:15:PHE:O	0.45	2.65	4	4
1:A:33:ILE:HG13	1:A:63:VAL:HB	0.45	1.89	1	3
1:A:25:ASP:O	1:A:25:ASP:OD2	0.45	2.35	10	1
1:A:49:PHE:HB3	1:A:63:VAL:HA	0.44	1.89	19	16
1:A:10:ASN:HB3	1:A:13:LYS:CG	0.44	2.42	3	1
1:A:17:PHE:CE1	1:A:27:PHE:CE1	0.44	3.05	12	1
1:A:47:VAL:CG2	1:A:63:VAL:HG11	0.44	2.42	20	1
1:A:18:ILE:O	1:A:25:ASP:OD1	0.44	2.34	9	2
1:A:14:GLY:C	1:A:29:HIS:CD2	0.44	2.95	16	1
1:A:2:LEU:CD1	1:A:49:PHE:O	0.44	2.60	5	5
1:A:3:GLU:HG2	1:A:47:VAL:O	0.44	2.13	15	2
1:A:10:ASN:O	1:A:15:PHE:N	0.44	2.50	19	1
1:A:29:HIS:O	1:A:31:SER:N	0.44	2.50	2	1
1:A:49:PHE:CD1	1:A:60:ALA:HB2	0.44	2.47	11	2
1:A:6:VAL:CG2	1:A:9:PHE:CD1	0.44	3.01	5	1
1:A:15:PHE:CD1	1:A:17:PHE:CE1	0.44	3.05	19	1
1:A:28:VAL:CG1	1:A:33:ILE:HD11	0.44	2.43	11	2
1:A:27:PHE:HB3	1:A:59:GLN:CD	0.44	2.37	19	1
1:A:62:ASN:OD1	1:A:62:ASN:N	0.44	2.51	19	1
1:A:7:LYS:CG	1:A:19:GLU:HB2	0.44	2.43	20	1
1:A:27:PHE:CB	1:A:59:GLN:HG2	0.44	2.41	13	4
1:A:3:GLU:OE1	1:A:47:VAL:O	0.44	2.36	7	1
1:A:28:VAL:CA	1:A:33:ILE:HD11	0.44	2.42	7	1
1:A:6:VAL:HG13	1:A:8:TRP:H	0.44	1.73	20	2
1:A:10:ASN:CG	1:A:13:LYS:HB2	0.44	2.38	6	5
1:A:47:VAL:HB	1:A:64:THR:O	0.44	2.13	9	4
1:A:25:ASP:O	1:A:25:ASP:CG	0.44	2.61	14	2
1:A:2:LEU:HD21	1:A:3:GLU:O	0.44	2.13	11	1
1:A:3:GLU:OE1	1:A:4:GLY:O	0.43	2.36	7	1
1:A:14:GLY:C	1:A:15:PHE:CG	0.43	2.94	15	1
1:A:62:ASN:OD1	1:A:62:ASN:O	0.43	2.37	13	2
1:A:12:GLU:O	1:A:12:GLU:OE2	0.43	2.36	4	1
1:A:33:ILE:CD1	1:A:63:VAL:HB	0.43	2.44	18	1
1:A:9:PHE:CE1	1:A:11:SER:HA	0.43	2.49	19	1
1:A:14:GLY:C	1:A:15:PHE:CD1	0.43	2.97	7	1
1:A:14:GLY:O	1:A:29:HIS:ND1	0.43	2.52	8	1
1:A:26:VAL:O	1:A:26:VAL:HG12	0.43	2.14	20	1
1:A:51:ILE:CD1	1:A:59:GLN:C	0.43	2.81	2	1
1:A:33:ILE:HA	1:A:63:VAL:O	0.43	2.14	14	6
1:A:14:GLY:O	1:A:15:PHE:HB3	0.43	2.13	15	8
1:A:28:VAL:O	1:A:28:VAL:HG22	0.43	2.13	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:63:VAL:HG12	1:A:64:THR:H	0.42	1.74	4	2
1:A:9:PHE:CD1	1:A:16:GLY:CA	0.42	3.02	20	1
1:A:18:ILE:HB	1:A:26:VAL:O	0.42	2.15	1	3
1:A:29:HIS:CD2	1:A:30:PHE:CE2	0.42	3.07	2	1
1:A:7:LYS:CG	1:A:19:GLU:OE1	0.42	2.68	8	1
1:A:24:ASP:OD1	1:A:24:ASP:N	0.42	2.49	14	1
1:A:18:ILE:HD11	1:A:47:VAL:CG2	0.42	2.45	16	1
1:A:8:TRP:CZ2	1:A:17:PHE:CB	0.42	3.03	17	10
1:A:58:PRO:C	1:A:59:GLN:HG2	0.42	2.39	3	1
1:A:33:ILE:CG2	1:A:63:VAL:HB	0.42	2.45	13	1
1:A:10:ASN:HB3	1:A:13:LYS:HB2	0.42	1.91	4	1
1:A:3:GLU:CD	1:A:47:VAL:O	0.42	2.63	7	1
1:A:7:LYS:HG2	1:A:19:GLU:CD	0.42	2.40	7	1
1:A:28:VAL:HA	1:A:33:ILE:HD11	0.42	1.91	17	1
1:A:30:PHE:CD1	1:A:30:PHE:C	0.42	2.97	17	1
1:A:8:TRP:CZ3	1:A:10:ASN:HB2	0.42	2.50	2	2
1:A:26:VAL:CG2	1:A:51:ILE:HD12	0.42	2.45	10	1
1:A:18:ILE:CG2	1:A:26:VAL:HB	0.42	2.45	20	2
1:A:29:HIS:CD2	1:A:30:PHE:CZ	0.42	3.08	2	1
1:A:27:PHE:HB3	1:A:59:GLN:HG2	0.42	1.92	8	1
1:A:47:VAL:HB	1:A:63:VAL:HG12	0.42	1.90	9	1
1:A:10:ASN:OD1	1:A:13:LYS:HD3	0.42	2.15	16	1
1:A:16:GLY:O	1:A:28:VAL:CG1	0.42	2.67	17	1
1:A:25:ASP:OD1	1:A:25:ASP:N	0.41	2.52	4	1
1:A:29:HIS:C	1:A:31:SER:N	0.41	2.78	2	1
1:A:47:VAL:CB	1:A:64:THR:O	0.41	2.68	9	1
1:A:27:PHE:HB2	1:A:59:GLN:NE2	0.41	2.31	9	1
1:A:26:VAL:HG12	1:A:27:PHE:O	0.41	2.14	7	1
1:A:3:GLU:HA	1:A:47:VAL:O	0.41	2.16	14	1
1:A:49:PHE:CD2	1:A:63:VAL:HG13	0.41	2.51	19	1
1:A:49:PHE:HD2	1:A:63:VAL:HG13	0.41	1.75	19	1
1:A:33:ILE:HG13	1:A:63:VAL:CG1	0.41	2.45	10	1
1:A:4:GLY:C	1:A:5:LYS:HG2	0.41	2.40	9	1
1:A:2:LEU:O	1:A:48:SER:HA	0.41	2.16	16	1
1:A:4:GLY:C	1:A:5:LYS:HG3	0.41	2.40	4	1
1:A:47:VAL:CG2	1:A:63:VAL:CG1	0.41	2.98	20	1
1:A:3:GLU:HG3	1:A:47:VAL:O	0.41	2.15	14	2
1:A:13:LYS:N	1:A:13:LYS:HD3	0.41	2.31	10	1
1:A:29:HIS:CD2	1:A:30:PHE:N	0.41	2.88	15	1
1:A:29:HIS:CD2	1:A:30:PHE:CD1	0.41	3.09	16	1
1:A:51:ILE:HG23	1:A:59:GLN:N	0.41	2.31	16	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:VAL:HB	1:A:33:ILE:HG12	0.40	1.93	2	1
1:A:19:GLU:O	1:A:19:GLU:HG3	0.40	2.15	7	1
1:A:22:GLY:C	1:A:23:GLN:NE2	0.40	2.79	10	1
1:A:19:GLU:CB	1:A:25:ASP:OD1	0.40	2.69	3	1
1:A:7:LYS:CG	1:A:19:GLU:HB3	0.40	2.47	7	1
1:A:7:LYS:HG3	1:A:19:GLU:OE1	0.40	2.16	8	1
1:A:63:VAL:CG1	1:A:64:THR:N	0.40	2.85	1	1
1:A:47:VAL:HB	1:A:63:VAL:CG1	0.40	2.47	8	1
1:A:3:GLU:CG	1:A:47:VAL:O	0.40	2.69	14	1
1:A:33:ILE:HG12	1:A:63:VAL:HB	0.40	1.93	17	1
1:A:27:PHE:CB	1:A:59:GLN:OE1	0.40	2.69	20	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	52/67 (78%)	40±1 (78±2%)	11±1 (21±1%)	0±0 (1±1%)	18	68
All	All	1040/1340 (78%)	809 (78%)	223 (21%)	8 (1%)	18	68

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	6	VAL	8

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	42/53 (79%)	29±2 (69±4%)	13±2 (31±4%)	1	15

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	840/1060 (79%)	578 (69%)	262 (31%)	1 15

All 32 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	2	LEU	20
1	A	18	ILE	20
1	A	64	THR	19
1	A	7	LYS	18
1	A	3	GLU	17
1	A	13	LYS	13
1	A	21	GLU	13
1	A	65	LYS	13
1	A	23	GLN	13
1	A	28	VAL	11
1	A	59	GLN	11
1	A	11	SER	9
1	A	24	ASP	9
1	A	56	ARG	9
1	A	48	SER	8
1	A	50	GLU	7
1	A	53	GLU	7
1	A	9	PHE	5
1	A	31	SER	5
1	A	62	ASN	5
1	A	19	GLU	5
1	A	10	ASN	4
1	A	55	ASN	4
1	A	5	LYS	3
1	A	51	ILE	3
1	A	26	VAL	3
1	A	33	ILE	2
1	A	15	PHE	2
1	A	25	ASP	1
1	A	30	PHE	1
1	A	29	HIS	1
1	A	52	VAL	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