



# Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 09:32 PM BST

PDB ID : 2JQ9  
Title : VPS4A MIT-CHMP1A complex  
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Deposited on : 2007-05-30

This is a Full wwPDB NMR Structure Validation Report for a publicly released PDB entry.  
We welcome your comments at [validation@mail.wwpdb.org](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)  
NmrClust : Kelley et al. (1996)  
MolProbity : 4.02b-467  
Mogul : unknown  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
RCI : v\_1n\_11\_5\_13\_A (Berjanski et al., 2005)  
PANAV : Wang et al. (2010)  
ShiftChecker : rb-20027457  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027457

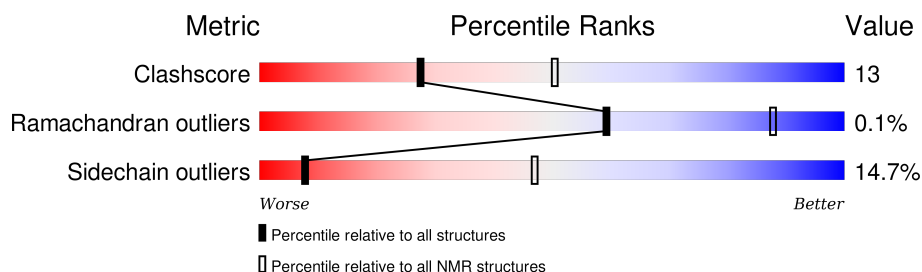
# 1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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  $\geq 3$ , 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	84	<div> <div style="width: 65%; background-color: green;"></div> <div style="width: 19%; background-color: yellow;"></div> <div style="width: 15%; background-color: grey;"></div> </div> <div>65% 19% 15%</div>
2	B	17	<div> <div style="width: 47%; background-color: green;"></div> <div style="width: 12%; background-color: yellow;"></div> <div style="width: 6%; background-color: orange;"></div> <div style="width: 12%; background-color: cyan;"></div> <div style="width: 24%; background-color: grey;"></div> </div> <div>47% 12% 6% 12% 24%</div>

## 2 Ensemble composition and analysis ⓘ

This entry contains 20 models. Model 10 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *lowest energy*.

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:75, B:115-B:125 (82)	0.29	10

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

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

NmrClust was unable to cluster the ensemble.

Error message: Inconsistent models

### 3 Entry composition [i](#)

There are 2 unique types of molecules in this entry. The entry contains 1412 atoms, of which 712 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Vacuolar protein sorting-associated protein 4A.

Mol	Chain	Residues	Atoms						Trace
1	A	71	Total	C	H	N	O	S	0
			1193	376	601	103	112	1	

- Molecule 2 is a protein called Chromatin-modifying protein 1a.

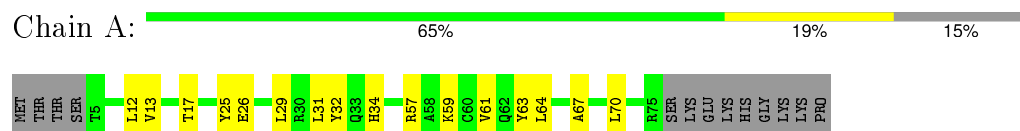
Mol	Chain	Residues	Atoms					Trace
2	B	13	Total	C	H	N	O	0
			219	63	111	24	21	

## 4 Residue-property plots [i](#)

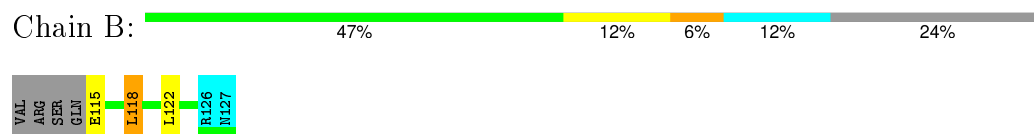
### 4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: Vacuolar protein sorting-associated protein 4A



- Molecule 2: Chromatin-modifying protein 1a

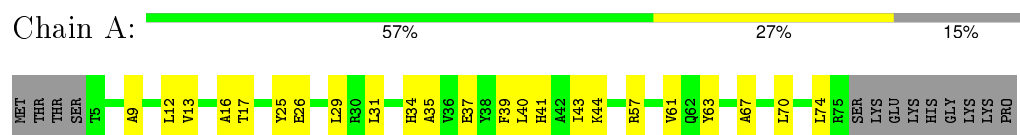


### 4.2 Scores per residue for each member of the ensemble

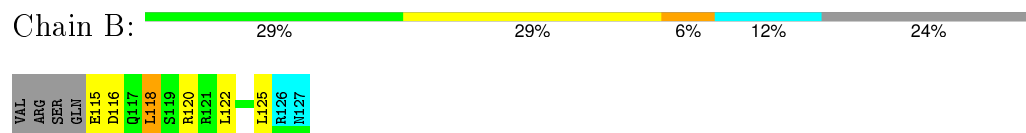
Colouring as in section 4.1 above.

#### 4.2.1 Score per residue for model 1

- Molecule 1: Vacuolar protein sorting-associated protein 4A

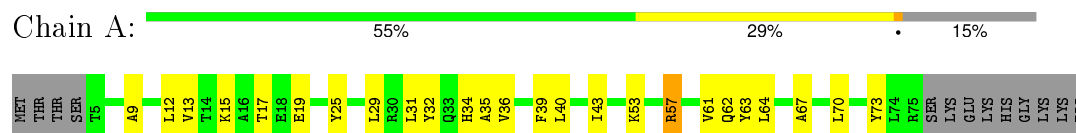


- Molecule 2: Chromatin-modifying protein 1a

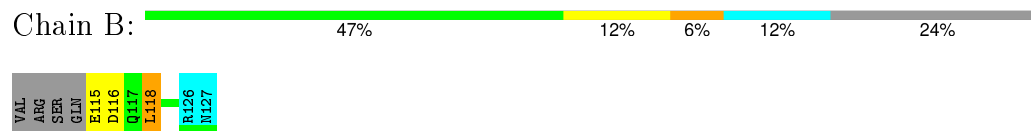


### 4.2.2 Score per residue for model 2

- Molecule 1: Vacuolar protein sorting-associated protein 4A

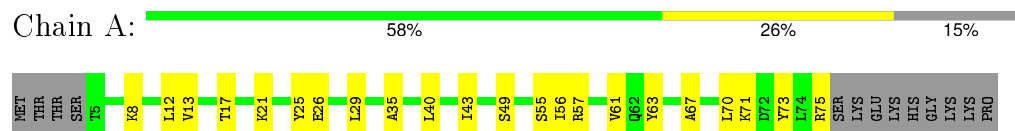


- Molecule 2: Chromatin-modifying protein 1a



### 4.2.3 Score per residue for model 3

- Molecule 1: Vacuolar protein sorting-associated protein 4A

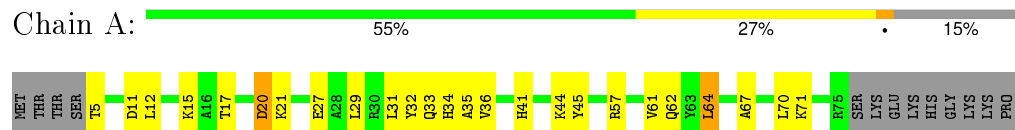


- Molecule 2: Chromatin-modifying protein 1a

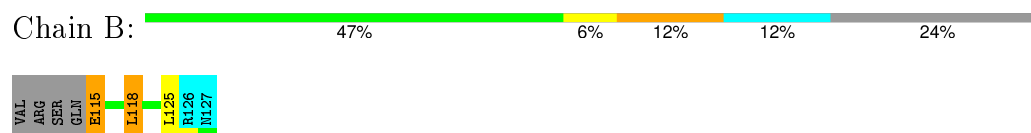


### 4.2.4 Score per residue for model 4

- Molecule 1: Vacuolar protein sorting-associated protein 4A

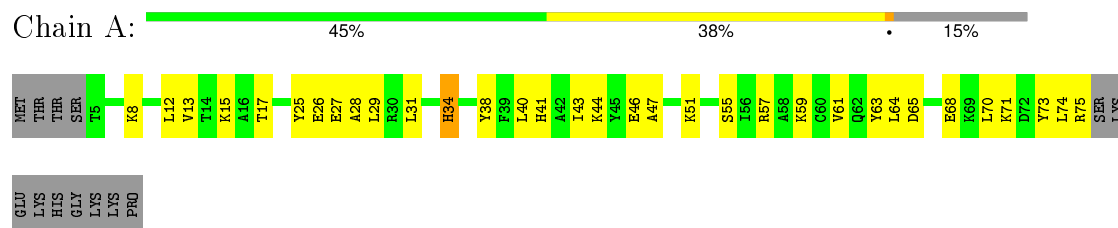


- Molecule 2: Chromatin-modifying protein 1a

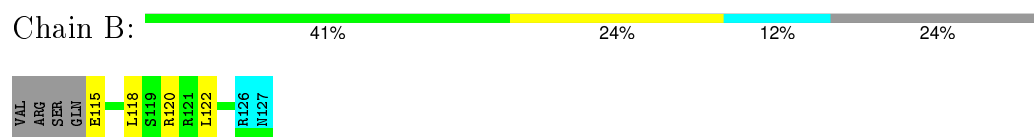


### 4.2.5 Score per residue for model 5

- Molecule 1: Vacuolar protein sorting-associated protein 4A

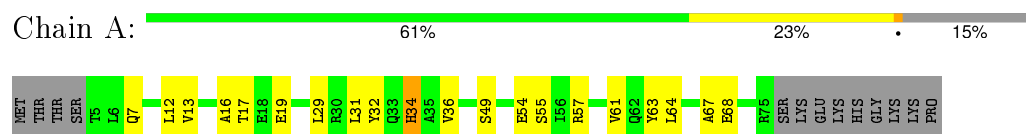


- Molecule 2: Chromatin-modifying protein 1a

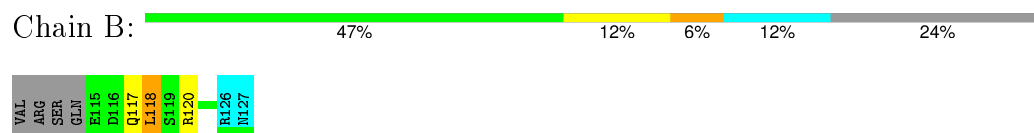


### 4.2.6 Score per residue for model 6

- Molecule 1: Vacuolar protein sorting-associated protein 4A

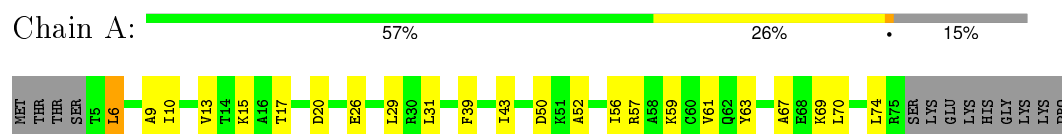


- Molecule 2: Chromatin-modifying protein 1a



### 4.2.7 Score per residue for model 7

- Molecule 1: Vacuolar protein sorting-associated protein 4A



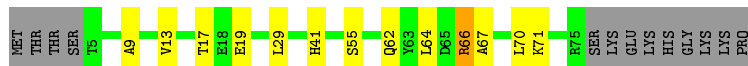
- Molecule 2: Chromatin-modifying protein 1a





#### 4.2.8 Score per residue for model 8

- Molecule 1: Vacuolar protein sorting-associated protein 4A



- Molecule 2: Chromatin-modifying protein 1a



#### 4.2.9 Score per residue for model 9

- Molecule 1: Vacuolar protein sorting-associated protein 4A

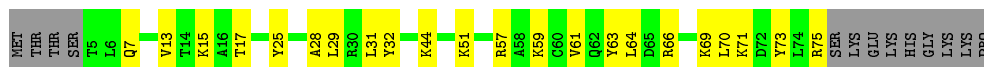


- Molecule 2: Chromatin-modifying protein 1a



#### 4.2.10 Score per residue for model 10 (medoid)

- Molecule 1: Vacuolar protein sorting-associated protein 4A



- Molecule 2: Chromatin-modifying protein 1a

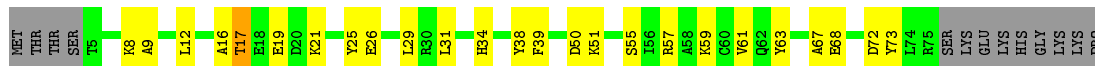






#### 4.2.11 Score per residue for model 11

- Molecule 1: Vacuolar protein sorting-associated protein 4A

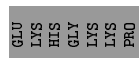


- Molecule 2: Chromatin-modifying protein 1a



#### 4.2.12 Score per residue for model 12

- Molecule 1: Vacuolar protein sorting-associated protein 4A

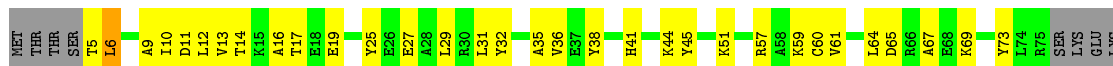


- Molecule 2: Chromatin-modifying protein 1a



#### 4.2.13 Score per residue for model 13

- Molecule 1: Vacuolar protein sorting-associated protein 4A



HIS  
GLY  
LYS  
GLN  
PRO

- Molecule 2: Chromatin-modifying protein 1a

Chain B: 

VAL  
ARG  
SER  
GLN  
E115  
L118  
L125  
R126  
N127

#### 4.2.14 Score per residue for model 14

- Molecule 1: Vacuolar protein sorting-associated protein 4A

Chain A: 

MET  
THR  
THR  
SER  
SER  
T5  
L6  
Q7  
K8  
A9  
I10  
V13  
T14  
K15  
A16  
T17  
E18  
E19  
D20  
Y25  
A28  
L29  
R30  
L31  
Y32  
Q33  
L40  
L43  
E54  
R57  
A58  
K59  
Q60  
V61  
Q62  
Y63  
L64  
L70  
K71  
R75  
SER  
LYS  
GLU  
LYS  
HIS  
GLY  
LYS  
LYS  
PRO

- Molecule 2: Chromatin-modifying protein 1a

Chain B: 

VAL  
ARG  
SER  
GLN  
E115  
L118  
L122  
L125  
R126  
N127

#### 4.2.15 Score per residue for model 15

- Molecule 1: Vacuolar protein sorting-associated protein 4A

Chain A: 

MET  
THR  
THR  
SER  
SER  
T5  
A9  
I10  
D11  
L12  
V13  
T14  
K15  
A16  
T17  
Y25  
E26  
L29  
R30  
L31  
Y32  
Q33  
R34  
E37  
K44  
S55  
T56  
R57  
V61  
L64  
A67  
E68  
K69  
L70  
L74  
R75  
SER  
LYS  
GLU  
LYS  
HIS  
GLY  
LYS  
LYS  
PRO

- Molecule 2: Chromatin-modifying protein 1a

Chain B: 

VAL  
ARG  
SER  
GLN  
E115  
D116  
Q117  
L118  
S119  
R120  
R121  
L122  
R126  
N127

#### 4.2.16 Score per residue for model 16

- Molecule 1: Vacuolar protein sorting-associated protein 4A

Chain A: 



- Molecule 2: Chromatin-modifying protein 1a

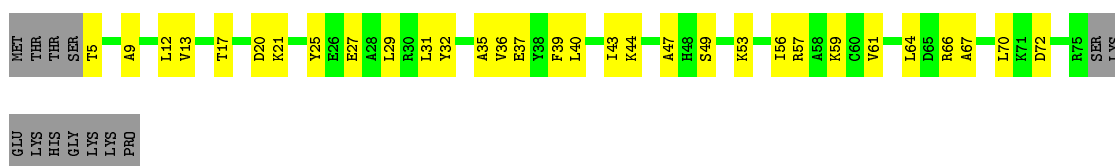
Chain B: 53% 12% 12% 24%



#### 4.2.17 Score per residue for model 17

- Molecule 1: Vacuolar protein sorting-associated protein 4A

Chain A: 48% 37% 15%



- Molecule 2: Chromatin-modifying protein 1a

Chain B: 35% 29% 12% 24%



#### 4.2.18 Score per residue for model 18

- Molecule 1: Vacuolar protein sorting-associated protein 4A

Chain A: 50% 35% 15%



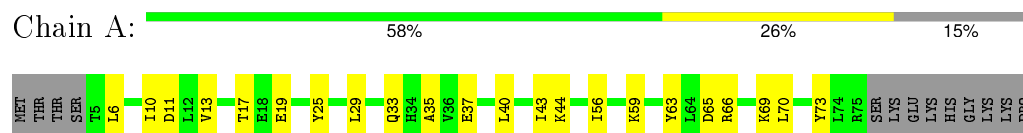
- Molecule 2: Chromatin-modifying protein 1a

Chain B: 47% 6% 12% 12% 24%



### 4.2.19 Score per residue for model 19

- Molecule 1: Vacuolar protein sorting-associated protein 4A

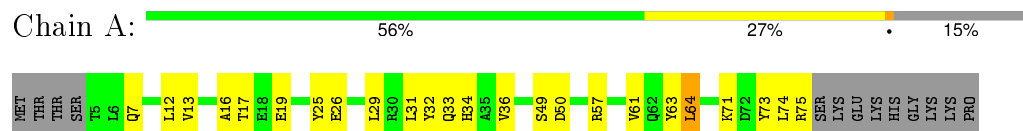


- Molecule 2: Chromatin-modifying protein 1a

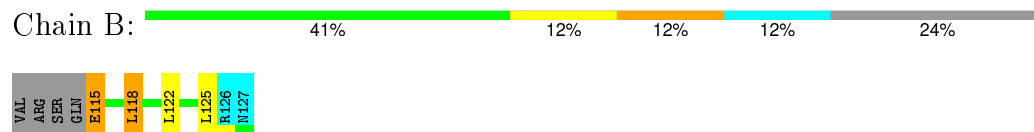


### 4.2.20 Score per residue for model 20

- Molecule 1: Vacuolar protein sorting-associated protein 4A



- Molecule 2: Chromatin-modifying protein 1a



## 5 Refinement protocol and experimental data overview ⓘ

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

Of the 200 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
CYANA	structure solution	2.1
CNS	refinement	1.2

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

## 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	592	601	597	17±4
2	B	88	92	91	3±1
All	All	13600	13860	13760	349

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 13.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:61:VAL:HG22	2:B:118:LEU:HD22	0.82	1.50	15	13
1:A:43:ILE:HD11	1:A:56:ILE:HG21	0.80	1.52	19	3
1:A:57:ARG:O	1:A:61:VAL:HG23	0.79	1.78	1	18
1:A:36:VAL:HG11	1:A:64:LEU:HD23	0.77	1.55	20	1
1:A:32:TYR:O	1:A:36:VAL:HG23	0.75	1.81	17	9
1:A:9:ALA:O	1:A:13:VAL:HG23	0.74	1.83	7	5
1:A:29:LEU:HD11	1:A:33:GLN:NE2	0.74	1.97	15	1
1:A:43:ILE:HD11	1:A:56:ILE:CG2	0.71	2.14	16	5
1:A:20:ASP:OD2	1:A:70:LEU:HD11	0.69	1.88	14	3
1:A:40:LEU:HA	1:A:43:ILE:HD12	0.69	1.65	5	7
1:A:13:VAL:HG21	1:A:63:TYR:CZ	0.68	2.23	10	9
1:A:33:GLN:OE1	2:B:125:LEU:HD23	0.68	1.89	18	2
1:A:29:LEU:O	1:A:29:LEU:HD13	0.68	1.88	7	6

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:60:CYS:O	1:A:64:LEU:HD23	0.68	1.89	13	1
1:A:36:VAL:HG11	1:A:64:LEU:HD12	0.67	1.66	18	1
1:A:8:LYS:O	1:A:12:LEU:HD23	0.67	1.89	11	2
1:A:64:LEU:HD13	1:A:64:LEU:O	0.66	1.89	16	1
1:A:66:ARG:O	1:A:70:LEU:HD13	0.66	1.91	16	4
1:A:70:LEU:O	1:A:74:LEU:HD12	0.66	1.88	7	1
1:A:12:LEU:HD23	1:A:31:LEU:HD23	0.65	1.67	13	3
1:A:25:TYR:CD1	1:A:70:LEU:HD22	0.65	2.27	14	6
1:A:12:LEU:CB	1:A:35:ALA:HB2	0.65	2.22	17	4
1:A:29:LEU:CD2	1:A:67:ALA:HB1	0.63	2.23	17	12
1:A:6:LEU:HD23	1:A:10:ILE:HD11	0.63	1.69	13	1
1:A:12:LEU:HD22	1:A:34:HIS:CB	0.63	2.24	18	3
1:A:12:LEU:HD22	1:A:34:HIS:HB3	0.62	1.71	20	5
1:A:28:ALA:HB3	1:A:70:LEU:HD23	0.62	1.71	5	1
1:A:40:LEU:HD11	2:B:122:LEU:HD13	0.62	1.72	5	2
1:A:36:VAL:HG11	1:A:64:LEU:HD21	0.61	1.70	13	1
1:A:29:LEU:HD23	1:A:29:LEU:O	0.61	1.95	20	3
1:A:15:LYS:CB	1:A:31:LEU:HD22	0.61	2.26	18	1
1:A:28:ALA:HB3	1:A:70:LEU:CD2	0.60	2.26	5	2
1:A:43:ILE:HD11	1:A:56:ILE:HG22	0.60	1.73	16	3
1:A:12:LEU:HD22	1:A:34:HIS:HB2	0.60	1.73	12	4
1:A:17:THR:HG22	1:A:21:LYS:HE3	0.60	1.74	11	1
1:A:64:LEU:HD13	2:B:118:LEU:HB2	0.58	1.75	4	1
1:A:9:ALA:HB1	1:A:39:PHE:CE2	0.58	2.33	11	1
1:A:12:LEU:HB2	1:A:35:ALA:HB2	0.58	1.76	17	1
1:A:9:ALA:HB1	1:A:39:PHE:CE1	0.58	2.33	2	4
1:A:16:ALA:HB2	1:A:31:LEU:HB3	0.58	1.75	14	4
1:A:26:GLU:HG2	1:A:74:LEU:HD13	0.57	1.77	1	2
1:A:29:LEU:HD23	1:A:67:ALA:O	0.56	1.99	3	9
1:A:33:GLN:CD	2:B:125:LEU:HD13	0.55	2.22	9	1
1:A:64:LEU:HD23	2:B:122:LEU:CD2	0.55	2.32	16	1
1:A:29:LEU:HD13	1:A:29:LEU:O	0.55	2.01	4	2
1:A:52:ALA:O	1:A:56:ILE:HD12	0.54	2.02	9	5
1:A:15:LYS:HB3	1:A:31:LEU:HD13	0.54	1.79	2	6
1:A:67:ALA:HA	1:A:70:LEU:HD12	0.54	1.80	18	2
1:A:61:VAL:HG22	2:B:118:LEU:HB3	0.53	1.80	3	1
1:A:20:ASP:OD2	1:A:70:LEU:HD21	0.53	2.02	7	1
1:A:12:LEU:HB3	1:A:35:ALA:HB2	0.53	1.81	2	6
1:A:64:LEU:HD21	2:B:122:LEU:HG	0.53	1.81	10	3
1:A:33:GLN:CD	2:B:125:LEU:HD23	0.53	2.24	18	1
1:A:6:LEU:CD2	1:A:10:ILE:HD11	0.52	2.34	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:27:GLU:O	1:A:31:LEU:HD12	0.52	2.04	17	1
1:A:33:GLN:HG2	2:B:125:LEU:HD23	0.51	1.82	4	2
1:A:37:GLU:HB2	2:B:122:LEU:HD21	0.51	1.81	1	1
1:A:12:LEU:HD13	1:A:31:LEU:HD23	0.51	1.80	5	1
1:A:25:TYR:HA	1:A:70:LEU:HD23	0.51	1.81	12	1
1:A:26:GLU:CG	1:A:74:LEU:HD13	0.51	2.36	16	1
1:A:33:GLN:NE2	2:B:125:LEU:HD22	0.51	2.21	9	1
1:A:64:LEU:O	1:A:64:LEU:HD13	0.50	2.06	20	2
1:A:64:LEU:CD2	2:B:122:LEU:HD22	0.50	2.36	16	1
1:A:8:LYS:O	1:A:12:LEU:HD12	0.50	2.07	3	2
1:A:25:TYR:CE2	1:A:73:TYR:CE1	0.50	3.00	18	5
1:A:25:TYR:CE2	1:A:73:TYR:CE2	0.50	3.00	3	3
1:A:16:ALA:HB1	1:A:32:TYR:CE2	0.50	2.41	13	2
1:A:26:GLU:CA	1:A:74:LEU:HD11	0.50	2.37	5	2
1:A:34:HIS:CD2	1:A:38:TYR:CE2	0.50	3.00	11	2
1:A:40:LEU:HD21	2:B:118:LEU:HD11	0.50	1.83	1	2
1:A:12:LEU:O	1:A:31:LEU:HD12	0.50	2.06	12	1
1:A:26:GLU:HB3	1:A:74:LEU:HD13	0.49	1.84	12	1
1:A:25:TYR:CE1	1:A:73:TYR:CE1	0.49	3.00	16	2
1:A:25:TYR:CE2	1:A:73:TYR:CZ	0.49	3.00	20	3
1:A:25:TYR:CZ	1:A:73:TYR:CZ	0.49	3.00	16	2
1:A:29:LEU:HD21	1:A:67:ALA:HB1	0.49	1.83	12	6
1:A:25:TYR:CE1	1:A:73:TYR:CZ	0.49	3.00	10	1
1:A:41:HIS:CE1	1:A:45:TYR:CE1	0.48	3.00	16	2
1:A:29:LEU:HD13	1:A:29:LEU:C	0.48	2.29	19	6
1:A:13:VAL:HG11	1:A:63:TYR:CZ	0.48	2.44	16	2
1:A:29:LEU:C	1:A:29:LEU:HD13	0.47	2.29	17	8
1:A:64:LEU:HD21	2:B:122:LEU:CG	0.47	2.39	5	2
2:B:115:GLU:HA	2:B:118:LEU:HD21	0.47	1.87	14	13
1:A:25:TYR:HA	1:A:70:LEU:HD22	0.47	1.85	18	1
1:A:16:ALA:HB1	1:A:32:TYR:CD2	0.47	2.44	13	1
1:A:43:ILE:HG21	1:A:57:ARG:NH1	0.47	2.25	3	1
1:A:47:ALA:HB1	1:A:53:LYS:CG	0.47	2.40	17	1
1:A:41:HIS:CE1	1:A:45:TYR:CZ	0.47	3.02	13	1
1:A:36:VAL:HG11	1:A:64:LEU:CD2	0.47	2.39	13	1
1:A:25:TYR:O	1:A:70:LEU:HD23	0.46	2.10	10	1
1:A:29:LEU:HD11	1:A:71:LYS:HB2	0.46	1.88	14	3
1:A:33:GLN:HB3	2:B:125:LEU:HD23	0.46	1.88	19	1
1:A:9:ALA:HB1	1:A:39:PHE:CD1	0.46	2.45	2	2
1:A:15:LYS:HB3	1:A:31:LEU:HD22	0.46	1.88	18	1
1:A:25:TYR:HB2	1:A:74:LEU:HD11	0.46	1.88	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:VAL:HG21	1:A:63:TYR:CE1	0.45	2.47	10	2
1:A:13:VAL:N	1:A:35:ALA:HB2	0.45	2.27	19	2
1:A:25:TYR:CD2	1:A:73:TYR:CE1	0.45	3.04	20	2
1:A:36:VAL:HG12	2:B:122:LEU:CD1	0.45	2.41	17	1
1:A:13:VAL:HG21	1:A:63:TYR:CE2	0.45	2.46	20	1
1:A:37:GLU:HG2	2:B:122:LEU:HD21	0.45	1.89	19	1
1:A:6:LEU:HD23	1:A:10:ILE:CD1	0.45	2.39	13	1
1:A:20:ASP:OD1	1:A:70:LEU:HD11	0.44	2.11	4	1
1:A:13:VAL:CG2	1:A:63:TYR:CE1	0.44	3.01	10	2
1:A:9:ALA:HB1	1:A:39:PHE:CZ	0.44	2.48	17	2
1:A:13:VAL:CG1	1:A:63:TYR:CZ	0.44	3.00	18	1
1:A:29:LEU:HD22	1:A:67:ALA:HB1	0.43	1.91	9	2
1:A:40:LEU:CD1	2:B:122:LEU:HD13	0.43	2.44	14	2
1:A:56:ILE:HG23	1:A:59:LYS:HE2	0.43	1.88	17	1
1:A:9:ALA:HB2	1:A:38:TYR:HB3	0.43	1.90	13	1
1:A:29:LEU:O	1:A:29:LEU:HD23	0.43	2.14	16	1
1:A:33:GLN:NE2	2:B:125:LEU:HD13	0.43	2.27	9	1
1:A:29:LEU:C	1:A:29:LEU:HD23	0.42	2.35	16	1
1:A:64:LEU:HD12	2:B:118:LEU:HB2	0.42	1.89	12	1
1:A:37:GLU:CB	2:B:122:LEU:HD21	0.42	2.44	1	1
1:A:57:ARG:NE	1:A:61:VAL:HG21	0.42	2.28	12	1
1:A:6:LEU:O	1:A:10:ILE:HD12	0.42	2.14	14	2
1:A:9:ALA:CB	1:A:39:PHE:CE1	0.42	3.02	1	2
1:A:33:GLN:CG	2:B:125:LEU:HD23	0.42	2.44	18	1
1:A:26:GLU:N	1:A:74:LEU:HD11	0.42	2.29	15	2
1:A:16:ALA:HB2	1:A:31:LEU:CB	0.42	2.45	1	4
1:A:43:ILE:HG23	1:A:53:LYS:HG2	0.41	1.93	2	1
1:A:39:PHE:O	1:A:43:ILE:HD12	0.41	2.16	7	1
1:A:15:LYS:CB	1:A:31:LEU:HD13	0.41	2.46	7	2
1:A:13:VAL:HG13	1:A:32:TYR:HE1	0.41	1.76	13	1
1:A:59:LYS:O	1:A:63:TYR:CD2	0.41	2.74	16	9
1:A:64:LEU:HD13	1:A:64:LEU:C	0.40	2.36	16	1
1:A:15:LYS:HB2	1:A:31:LEU:HD22	0.40	1.90	18	1
1:A:28:ALA:O	1:A:32:TYR:CD2	0.40	2.74	14	2
1:A:41:HIS:O	1:A:45:TYR:CD2	0.40	2.75	4	1
1:A:64:LEU:HD21	2:B:122:LEU:HD12	0.40	1.91	5	1
1:A:6:LEU:CD1	1:A:10:ILE:HD11	0.40	2.46	7	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	69/84 (82%)	66±1 (96±1%)	3±1 (4±1%)	0±0 (0±1%)	59	88
2	B	10/17 (59%)	10±0 (100±0%)	0±0 (0±0%)	0±0 (0±0%)	100	100
All	All	1580/2020 (78%)	1519 (96%)	59 (4%)	2 (0%)	59	88

All 2 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	47	ALA	1
1	A	46	GLU	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	61/73 (84%)	53±2 (87±4%)	8±2 (13±4%)	9	50
2	B	9/15 (60%)	7±1 (75±10%)	2±1 (25±10%)	3	26
All	All	1400/1760 (80%)	1194 (85%)	206 (15%)	8	47

All 44 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	17	THR	19
2	B	118	LEU	16
1	A	19	GLU	10
1	A	44	LYS	10
1	A	64	LEU	9

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Mol	Chain	Res	Type	Models (Total)
2	B	115	GLU	8
1	A	75	ARG	7
2	B	120	ARG	6
1	A	51	LYS	6
1	A	5	THR	6
1	A	55	SER	6
1	A	72	ASP	5
1	A	69	LYS	5
1	A	62	GLN	5
1	A	11	ASP	5
1	A	21	LYS	5
2	B	117	GLN	5
1	A	71	LYS	5
1	A	49	SER	5
1	A	7	GLN	4
1	A	54	GLU	4
1	A	65	ASP	4
1	A	26	GLU	4
2	B	116	ASP	4
1	A	27	GLU	4
1	A	50	ASP	4
1	A	8	LYS	3
1	A	41	HIS	3
2	B	122	LEU	3
1	A	66	ARG	3
1	A	68	GLU	3
1	A	6	LEU	2
1	A	20	ASP	2
1	A	57	ARG	2
1	A	37	GLU	2
1	A	34	HIS	2
2	B	125	LEU	2
1	A	14	THR	2
1	A	33	GLN	1
1	A	46	GLU	1
1	A	59	LYS	1
1	A	30	ARG	1
2	B	121	ARG	1
1	A	15	LYS	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 carbohydrates 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