



Full wwPDB NMR Structure Validation Report ⓘ

Dec 13, 2023 – 09:30 PM EST

PDB ID : 2JMJ
Title : NMR solution structure of the PHD domain from the yeast YNG1 protein in complex with H3(1-9)K4me3 peptide
Authors : Ilin, S.; Taverna, S.D.; Rogers, R.S.; Tanny, J.C.; Lavender, H.; Li, H.; Baker, L.; Boyle, J.; Blair, L.P.; Chait, B.T.; Patel, D.J.; Aitchison, J.D.; Tackett, A.J.; Allis, C.D.
Deposited on : 2006-11-15

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:

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
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) : 2.36

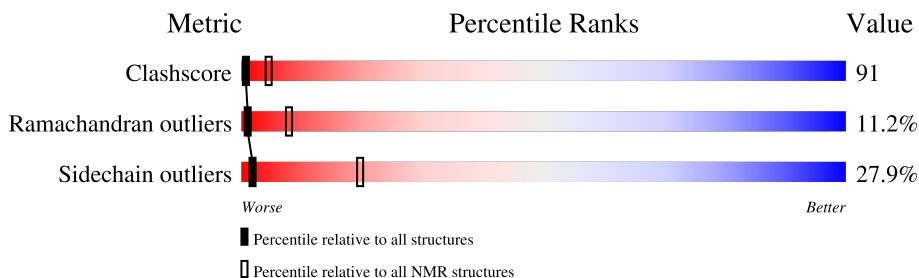
1 Overall quality at a glance

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	158937	12864
Ramachandran outliers	154571	11451
Sidechain outliers	154315	11428

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

Mol	Chain	Length	Quality of chain
1	A	90	
2	P	9	

2 Ensemble composition and analysis

This entry contains 20 models. Model 19 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:25-A:78, P:1-P:3 (57)	0.41	19

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. No single-model clusters were found.

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

3 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 1094 atoms, of which 536 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Protein YNG1.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	60	924	304	444	82	86	8	0

There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	GLY	-	cloning artifact	UNP Q08465
A	2	PRO	-	cloning artifact	UNP Q08465
A	3	LEU	-	cloning artifact	UNP Q08465
A	4	GLY	-	cloning artifact	UNP Q08465
A	5	SER	-	cloning artifact	UNP Q08465
A	6	HIS	-	cloning artifact	UNP Q08465
A	7	MET	-	cloning artifact	UNP Q08465
A	8	ALA	-	cloning artifact	UNP Q08465
A	9	SER	-	cloning artifact	UNP Q08465
A	10	GLU	-	cloning artifact	UNP Q08465
A	11	PHE	-	cloning artifact	UNP Q08465

- Molecule 2 is a protein called Histone H3.

Mol	Chain	Residues	Atoms					Trace
			Total	C	H	N	O	
2	P	9	168	46	92	18	12	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
P	4	M3L	LYS	modified residue	UNP P61830

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

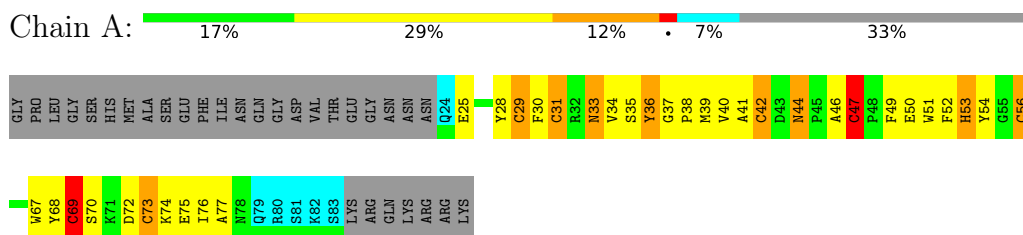
Mol	Chain	Residues	Atoms	
			Total	Zn
3	A	2	2	2

4 Residue-property plots

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: Protein YNG1



- Molecule 2: Histone H3

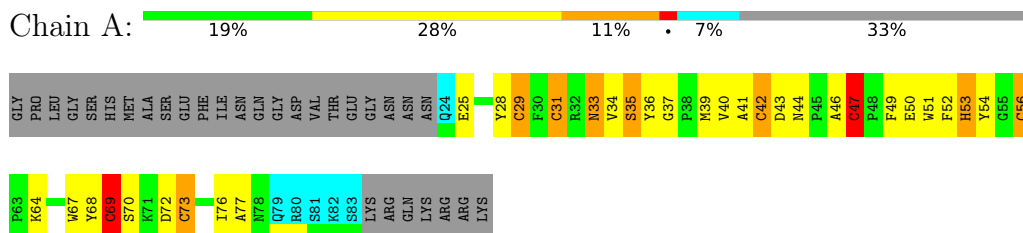


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

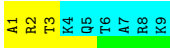
4.2.1 Score per residue for model 1

- Molecule 1: Protein YNG1



- Molecule 2: Histone H3


Chain P:  33% 67%

 A1 R2 T3 K4 Q5 T6 A7 R8 K9

4.2.2 Score per residue for model 2

- Molecule 1: Protein YNG1

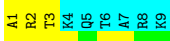
Chain A:  20% 26% 12% 7% 33%

 GLY PRO LEU GLY SER HIS MET ALA SER GLU PHE ILE ASN GLN GLY ASP VAL THR GLU GLY ASN ASN ASN Q24 Y28 C29 F30 C31 R32 N33 V34 S35 Y36 G37 P38 K39 V40 A41 C42 D43 N44 P45 A46 C47 P48 F49 E50 W51 F52 H53 Y54 G55 C56 V57 G58 L59 A62 P63

 K64 W67 Y68 C69 K71 D72 C73 K74 A77 Q79 R80 S81 K82 S83 LYS ARG GLN ARG ASN ARG LYS

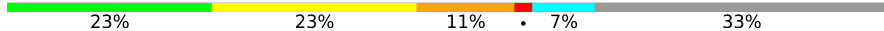
- Molecule 2: Histone H3

Chain P:  33% 67%


 A1 R2 T3 K4 Q5 T6 A7 R8 K9

4.2.3 Score per residue for model 3

- Molecule 1: Protein YNG1

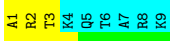
Chain A:  23% 23% 11% 7% 33%

 GLY PRO LEU GLY SER HIS MET ALA SER GLU PHE ILE ASN GLN GLY ASP VAL THR GLU GLY ASN ASN ASN Q24 E25 E26 Y27 Y28 C29 F30 C31 R32 N33 V34 S35 Y36 M39 V40 A41 C42 D43 N44 C47 E50 W51 F52 H53 Y54 G55 C56 V57 G58 L59 A62 W67

 Y68 C69 S70 K71 D72 C73 K74 E75 N78 Q79 R80 S81 K82 S83 LYS ARG GLN LYS ARG LYS

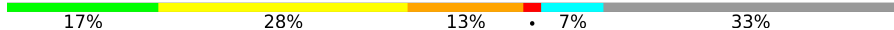
- Molecule 2: Histone H3

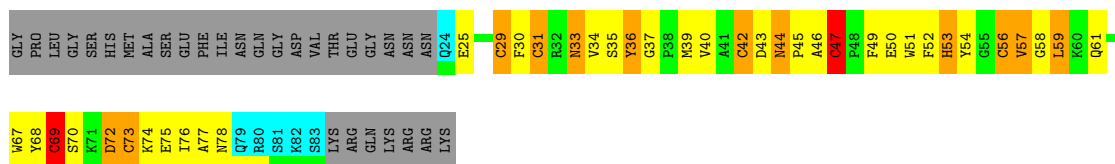
Chain P:  33% 67%

 A1 R2 T3 K4 Q5 T6 A7 R8 K9

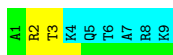
4.2.4 Score per residue for model 4

- Molecule 1: Protein YNG1

Chain A:  17% 28% 13% 7% 33%



- Molecule 2: Histone H3



4.2.5 Score per residue for model 5

- Molecule 1: Protein YNG1

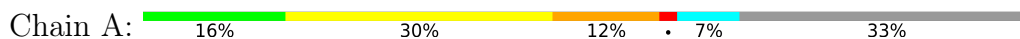


- Molecule 2: Histone H3

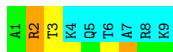


4.2.6 Score per residue for model 6

- Molecule 1: Protein YNG1

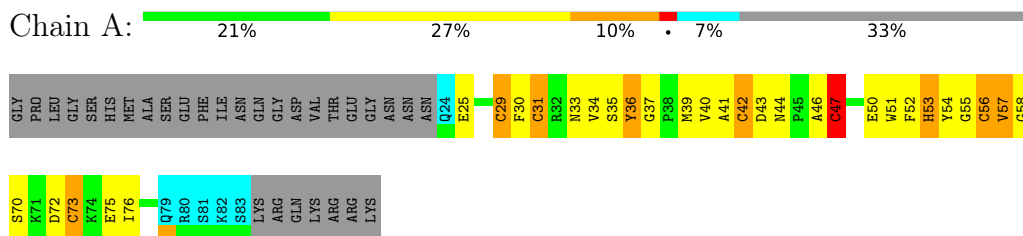


- Molecule 2: Histone H3



4.2.7 Score per residue for model 7

- Molecule 1: Protein YNG1

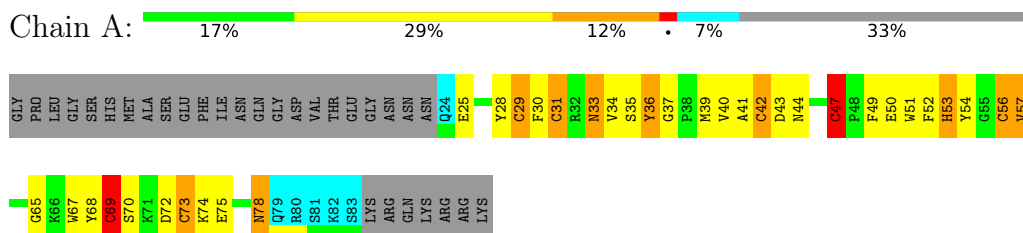


- Molecule 2: Histone H3



4.2.8 Score per residue for model 8

- Molecule 1: Protein YNG1

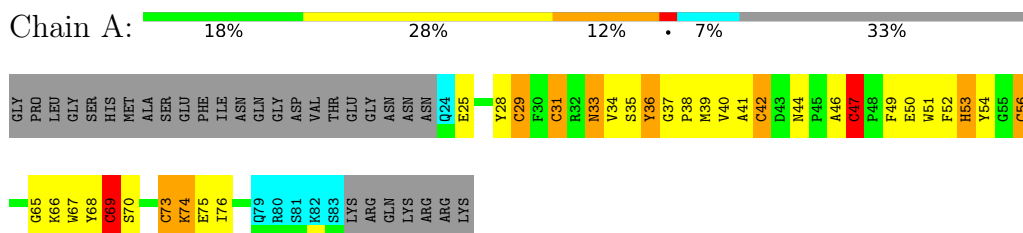


- Molecule 2: Histone H3



4.2.9 Score per residue for model 9

- Molecule 1: Protein YNG1



- Molecule 2: Histone H3

Chain P: 33% 67%

A1 R2 T3 K4 O5 T6 A7 R8 R9

4.2.10 Score per residue for model 10

- Molecule 1: Protein YNG1

Chain A: 14% 29% 14% 7% 33%

GLY PRO LEU GLY SER HIS MET ALA SER GLU PHE ILE ASN GLN GLY ASP VAL THR GLU GLY ASN ASN ASN E24 E25 Y28 C29 F30 C31 R32 N33 V34 S35 Y36 G37 P38 M39 V40 A41 C42 D43 N44 P45 A46 C47 E50 W51 F52 H53 Y54 G55 C56 V57 G58 L59 R60 A62

P63 A64 G65 F66 W67 Y68 C69 S70 K71 D72 C73 K74 F75 I76 A77 H78 Q79 R80 S81 K82 S83 LYS ARG LYS ARG LYS

- Molecule 2: Histone H3

Chain P: 11% 22% 67%

A1 R2 T3 K4 O5 T6 A7 R8 R9

4.2.11 Score per residue for model 11

- Molecule 1: Protein YNG1

Chain A: 28% 20% 10% 7% 33%

GLY PRO LEU GLY SER HIS MET ALA SER GLU PHE ILE ASN GLN GLY ASP VAL THR GLU GLY ASN ASN ASN E24 E25 C29 F30 C31 R32 N33 V34 S35 Y36 M39 V40 A41 C42 D43 N44 C47 P48 F49 E50 W51 F52 H53 Y54 G55 C56 V57 G58 L59 W67 Y68 C69 S70

C73 K74 E75 Q79 R80 S81 K82 S83 LYS ARG GLN LYS ARG ARG LYS

- Molecule 2: Histone H3

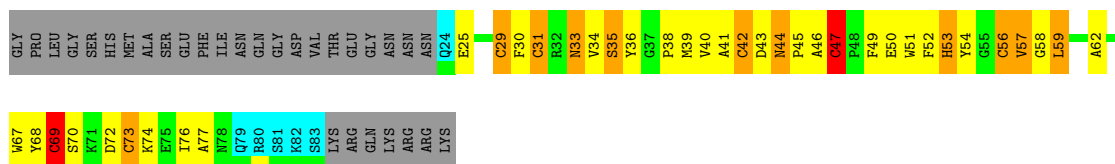
Chain P: 33% 67%

A1 R2 T3 K4 O5 T6 A7 R8 R9

4.2.12 Score per residue for model 12

- Molecule 1: Protein YNG1

Chain A: 18% 28% 12% 7% 33%

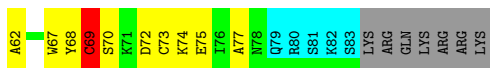
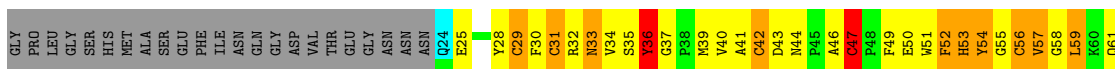


- Molecule 2: Histone H3

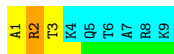


4.2.13 Score per residue for model 13

- Molecule 1: Protein YNG1

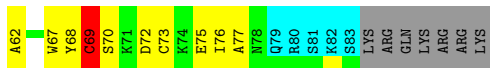
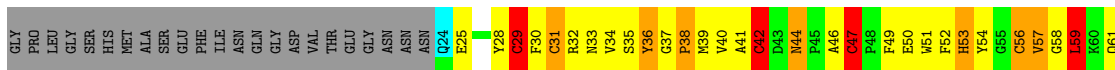
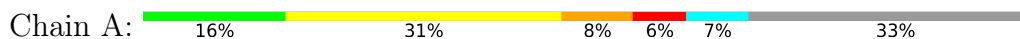


- Molecule 2: Histone H3

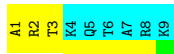


4.2.14 Score per residue for model 14

- Molecule 1: Protein YNG1



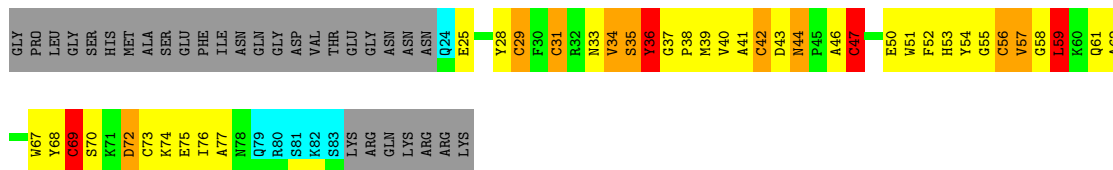
- Molecule 2: Histone H3



4.2.15 Score per residue for model 15

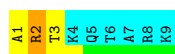
- Molecule 1: Protein YNG1

Chain A: 



- Molecule 2: Histone H3

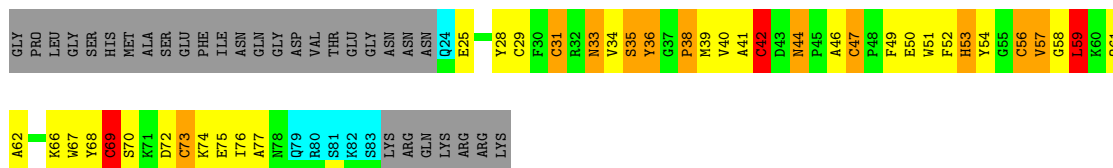
Chain P: 



4.2.16 Score per residue for model 16

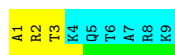
- Molecule 1: Protein YNG1

Chain A: 



- Molecule 2: Histone H3

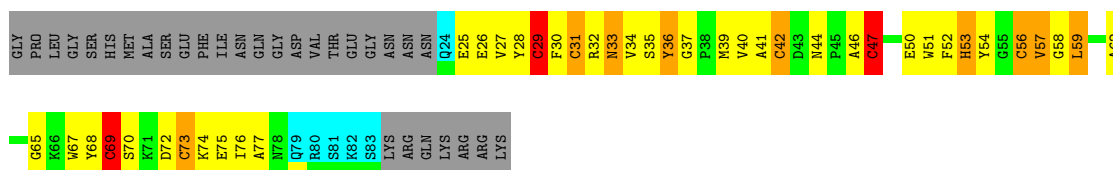
Chain P: 



4.2.17 Score per residue for model 17

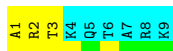
- Molecule 1: Protein YNG1

Chain A: 



- Molecule 2: Histone H3

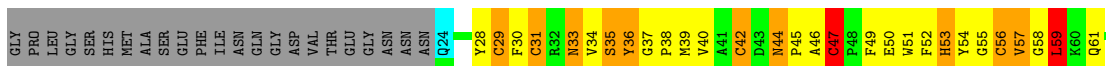
Chain P:



4.2.18 Score per residue for model 18

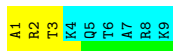
- Molecule 1: Protein YNG1

Chain A:



- Molecule 2: Histone H3

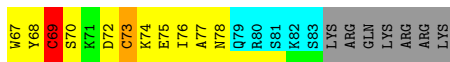
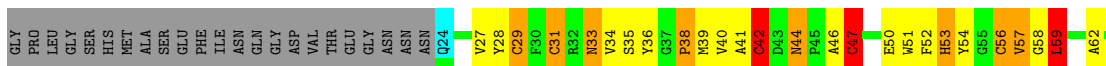
Chain P:



4.2.19 Score per residue for model 19 (medoid)

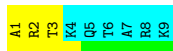
- Molecule 1: Protein YNG1

Chain A:



- Molecule 2: Histone H3

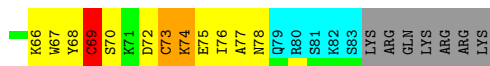
Chain P:



4.2.20 Score per residue for model 20

- Molecule 1: Protein YNG1

Chain A:



- Molecule 2: Histone H3



5 Refinement protocol and experimental data overview

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

Of the 100 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
X-PLOR NIH	structure solution	
X-PLOR NIH	refinement	

No chemical shift data was provided.

6 Model quality i

6.1 Standard geometry i

Bond lengths and bond angles in the following residue types are not validated in this section: M3L, ZN

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	430	392	398	79±6
2	P	23	27	27	4±2
3	A	2	0	0	1±0
All	All	9100	8380	8490	1598

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 91.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:47:CYS:SG	1:A:69:CYS:SG	1.47	1.48	17	7
1:A:42:CYS:CB	1:A:69:CYS:SG	1.22	2.27	18	20
1:A:69:CYS:SG	1:A:73:CYS:CB	1.22	2.28	9	20
1:A:42:CYS:SG	1:A:69:CYS:CB	1.12	2.38	15	20
1:A:31:CYS:CB	1:A:56:CYS:SG	1.10	2.38	5	20
1:A:42:CYS:SG	1:A:47:CYS:CB	1.10	2.40	18	20
1:A:29:CYS:CB	1:A:56:CYS:SG	1.04	2.44	16	20
1:A:42:CYS:CB	1:A:47:CYS:SG	1.04	2.44	18	20
1:A:29:CYS:SG	1:A:56:CYS:CB	1.01	2.48	14	20
1:A:42:CYS:CB	1:A:47:CYS:HG	0.99	1.69	4	6

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:CYS:SG	1:A:56:CYS:SG	0.98	0.98	13	20
1:A:31:CYS:SG	1:A:56:CYS:CB	0.98	2.52	5	18
1:A:42:CYS:SG	1:A:73:CYS:SG	0.97	0.97	13	20
1:A:29:CYS:CB	1:A:56:CYS:HG	0.96	1.71	15	2
1:A:29:CYS:SG	1:A:31:CYS:CB	0.96	2.53	15	20
1:A:40:VAL:HG23	2:P:3:THR:HG22	0.92	1.40	5	18
1:A:42:CYS:SG	1:A:47:CYS:SG	0.92	0.95	12	20
1:A:69:CYS:CB	1:A:73:CYS:SG	0.88	2.62	7	20
1:A:29:CYS:CB	1:A:31:CYS:SG	0.86	2.63	2	8
1:A:59:LEU:HD12	1:A:59:LEU:N	0.85	1.87	13	20
1:A:36:TYR:CD1	1:A:36:TYR:N	0.83	2.41	15	6
1:A:29:CYS:CB	1:A:31:CYS:HG	0.83	1.86	18	8
1:A:47:CYS:SG	1:A:73:CYS:CB	0.83	2.67	20	14
1:A:29:CYS:HG	1:A:53:HIS:CE1	0.82	1.93	16	3
1:A:57:VAL:HG23	1:A:58:GLY:N	0.81	1.90	13	19
1:A:39:MET:SD	1:A:53:HIS:CB	0.81	2.68	7	5
1:A:35:SER:CB	1:A:39:MET:SD	0.79	2.71	4	13
1:A:54:TYR:OH	1:A:62:ALA:HB2	0.78	1.79	9	4
1:A:54:TYR:CD2	1:A:59:LEU:HD13	0.78	2.13	4	1
1:A:52:PHE:CE1	1:A:69:CYS:HB3	0.77	2.15	8	20
1:A:39:MET:SD	1:A:53:HIS:CG	0.77	2.77	12	2
1:A:25:GLU:HB3	1:A:34:VAL:HG21	0.76	1.55	15	15
1:A:39:MET:O	2:P:3:THR:HG23	0.76	1.79	4	1
1:A:40:VAL:HG11	1:A:67:TRP:CD1	0.76	2.15	9	20
2:P:1:ALA:O	2:P:3:THR:HG23	0.76	1.80	5	17
1:A:29:CYS:HG	1:A:56:CYS:CB	0.75	1.89	14	2
1:A:42:CYS:HG	1:A:47:CYS:CB	0.75	1.87	2	4
1:A:35:SER:HB2	1:A:39:MET:SD	0.74	2.21	4	14
1:A:25:GLU:CG	1:A:34:VAL:HG21	0.74	2.12	17	2
1:A:51:TRP:C	1:A:52:PHE:CD1	0.73	2.62	15	20
1:A:36:TYR:CE1	1:A:53:HIS:CG	0.72	2.77	13	3
1:A:53:HIS:O	1:A:57:VAL:HG22	0.71	1.85	5	14
1:A:39:MET:SD	1:A:53:HIS:HB3	0.71	2.26	15	3
1:A:53:HIS:CE1	1:A:56:CYS:N	0.70	2.59	15	4
1:A:53:HIS:N	1:A:53:HIS:CD2	0.70	2.59	4	5
1:A:39:MET:SD	1:A:53:HIS:HB2	0.69	2.28	7	2
1:A:33:ASN:ND2	1:A:53:HIS:CE1	0.69	2.61	6	11
1:A:34:VAL:HG12	1:A:35:SER:N	0.69	2.02	7	15
1:A:36:TYR:CE2	1:A:53:HIS:CE1	0.69	2.81	15	1
1:A:39:MET:SD	1:A:53:HIS:CD2	0.69	2.85	12	3
1:A:62:ALA:CB	2:P:3:THR:HG21	0.68	2.18	20	9

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:42:CYS:CB	1:A:47:CYS:CB	0.68	2.72	16	20
1:A:44:ASN:OD1	1:A:47:CYS:N	0.67	2.27	16	3
1:A:34:VAL:CG1	1:A:35:SER:N	0.67	2.57	18	20
1:A:59:LEU:N	1:A:59:LEU:CD1	0.67	2.56	13	18
1:A:44:ASN:ND2	1:A:46:ALA:H	0.67	1.87	4	9
1:A:44:ASN:HD22	1:A:77:ALA:HB2	0.67	1.50	16	2
1:A:59:LEU:HD23	1:A:67:TRP:CD2	0.67	2.25	10	20
1:A:53:HIS:CD2	1:A:55:GLY:H	0.67	2.08	15	3
1:A:35:SER:OG	1:A:39:MET:SD	0.66	2.54	1	11
2:P:2:ARG:H	2:P:2:ARG:CD	0.66	2.04	13	2
1:A:25:GLU:HG3	1:A:34:VAL:HG21	0.66	1.66	17	2
1:A:44:ASN:ND2	1:A:77:ALA:HB2	0.65	2.06	16	2
1:A:39:MET:SD	1:A:53:HIS:HA	0.65	2.32	12	3
1:A:29:CYS:SG	1:A:36:TYR:OH	0.64	2.54	15	1
1:A:62:ALA:HB1	2:P:3:THR:HG21	0.64	1.68	6	2
1:A:39:MET:SD	1:A:53:HIS:CA	0.64	2.86	2	5
1:A:54:TYR:CG	1:A:59:LEU:HD13	0.64	2.28	4	13
1:A:29:CYS:SG	1:A:29:CYS:O	0.64	2.56	20	3
1:A:42:CYS:HG	3:A:201:ZN:ZN	0.63	0.39	11	9
1:A:46:ALA:CB	1:A:76:ILE:HG22	0.63	2.23	16	10
1:A:52:PHE:CD1	1:A:52:PHE:N	0.62	2.65	13	20
1:A:57:VAL:HG23	1:A:58:GLY:H	0.62	1.54	13	3
1:A:36:TYR:CZ	1:A:53:HIS:ND1	0.62	2.67	15	1
1:A:53:HIS:CD2	1:A:53:HIS:N	0.62	2.67	2	1
1:A:44:ASN:HD22	1:A:47:CYS:N	0.61	1.93	1	1
1:A:42:CYS:HG	1:A:47:CYS:HG	0.61	0.87	7	3
1:A:29:CYS:SG	1:A:53:HIS:CE1	0.61	2.94	16	4
1:A:52:PHE:CE1	1:A:69:CYS:CB	0.61	2.84	6	20
1:A:57:VAL:CG2	1:A:59:LEU:HD11	0.61	2.26	14	17
1:A:42:CYS:CA	1:A:69:CYS:SG	0.60	2.89	8	20
1:A:56:CYS:HG	3:A:401:ZN:ZN	0.60	0.36	2	2
1:A:29:CYS:SG	1:A:31:CYS:N	0.60	2.75	7	17
1:A:44:ASN:HD22	1:A:46:ALA:H	0.59	1.40	12	2
1:A:67:TRP:NE1	1:A:68:TYR:O	0.59	2.36	18	19
1:A:42:CYS:CB	1:A:69:CYS:CB	0.58	2.80	18	20
1:A:67:TRP:CG	1:A:68:TYR:N	0.58	2.70	8	20
1:A:38:PRO:CB	1:A:54:TYR:CD2	0.58	2.86	20	5
1:A:39:MET:SD	1:A:53:HIS:HD2	0.58	2.21	2	1
1:A:35:SER:O	1:A:36:TYR:C	0.58	2.42	13	4
1:A:36:TYR:CD1	1:A:53:HIS:HB3	0.58	2.33	15	1
1:A:68:TYR:O	1:A:70:SER:N	0.58	2.36	4	20

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:54:TYR:CD1	1:A:54:TYR:N	0.58	2.72	6	14
1:A:44:ASN:ND2	1:A:47:CYS:H	0.57	1.97	8	8
1:A:42:CYS:HB3	1:A:47:CYS:CB	0.57	2.30	16	20
1:A:36:TYR:CZ	1:A:53:HIS:CE1	0.57	2.93	18	2
1:A:40:VAL:HG22	1:A:41:ALA:N	0.57	2.15	1	11
1:A:62:ALA:HB2	2:P:3:THR:HG21	0.57	1.77	12	4
1:A:44:ASN:ND2	1:A:47:CYS:N	0.56	2.53	6	6
1:A:53:HIS:NE2	1:A:55:GLY:HA3	0.56	2.15	18	4
1:A:34:VAL:O	1:A:36:TYR:CD1	0.56	2.59	6	3
1:A:44:ASN:HD21	1:A:46:ALA:HB3	0.56	1.61	17	3
1:A:53:HIS:CD2	1:A:53:HIS:H	0.55	2.19	1	5
1:A:57:VAL:CG2	1:A:58:GLY:N	0.55	2.62	13	10
1:A:44:ASN:ND2	1:A:77:ALA:HA	0.55	2.17	14	5
1:A:29:CYS:HA	1:A:52:PHE:CD2	0.55	2.37	20	4
1:A:46:ALA:O	1:A:47:CYS:C	0.54	2.45	17	10
1:A:38:PRO:HB2	1:A:54:TYR:CD2	0.54	2.38	20	7
1:A:36:TYR:CE1	1:A:53:HIS:HB3	0.54	2.38	15	1
1:A:53:HIS:ND1	1:A:53:HIS:N	0.54	2.56	3	6
1:A:40:VAL:CG2	2:P:3:THR:HG22	0.54	2.28	17	10
1:A:57:VAL:HG11	1:A:69:CYS:O	0.54	2.02	13	10
1:A:33:ASN:ND2	1:A:36:TYR:OH	0.53	2.42	13	8
1:A:44:ASN:OD1	1:A:77:ALA:N	0.53	2.41	2	2
1:A:53:HIS:CE1	1:A:55:GLY:HA3	0.53	2.37	13	1
1:A:53:HIS:CE1	1:A:55:GLY:CA	0.53	2.91	13	1
1:A:29:CYS:C	1:A:31:CYS:H	0.53	2.07	7	15
1:A:53:HIS:ND1	1:A:56:CYS:HB2	0.53	2.18	15	2
1:A:42:CYS:CB	1:A:47:CYS:HB3	0.53	2.34	16	20
1:A:36:TYR:CD1	1:A:53:HIS:CG	0.53	2.97	15	1
1:A:33:ASN:HD22	1:A:53:HIS:CE1	0.52	2.21	10	2
1:A:38:PRO:HB3	1:A:54:TYR:CD2	0.52	2.39	16	4
1:A:70:SER:H	1:A:73:CYS:CB	0.52	2.18	5	14
1:A:44:ASN:OD1	1:A:44:ASN:C	0.52	2.48	16	2
1:A:42:CYS:HB3	1:A:47:CYS:HB3	0.52	1.82	5	20
1:A:49:PHE:HB2	1:A:52:PHE:CZ	0.52	2.39	1	13
1:A:35:SER:HA	1:A:53:HIS:CD2	0.52	2.40	3	8
1:A:34:VAL:CG1	1:A:35:SER:H	0.52	2.16	15	3
1:A:68:TYR:CB	1:A:74:LYS:HB3	0.52	2.35	15	5
1:A:25:GLU:HG2	1:A:34:VAL:HG21	0.51	1.80	17	2
1:A:29:CYS:CB	1:A:56:CYS:CB	0.51	2.85	14	1
1:A:33:ASN:HD22	1:A:33:ASN:C	0.51	2.09	8	4
1:A:25:GLU:CB	1:A:34:VAL:HG21	0.51	2.36	9	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:SER:H	1:A:73:CYS:HB3	0.51	1.66	13	7
1:A:53:HIS:N	1:A:53:HIS:ND1	0.51	2.57	19	2
1:A:42:CYS:HG	1:A:69:CYS:HG	0.51	0.51	19	2
1:A:44:ASN:HD22	1:A:45:PRO:N	0.51	2.04	2	2
1:A:31:CYS:SG	1:A:36:TYR:OH	0.51	2.57	15	1
1:A:50:GLU:O	1:A:51:TRP:CG	0.51	2.64	7	20
1:A:73:CYS:HA	1:A:76:ILE:HD12	0.51	1.80	6	9
1:A:57:VAL:HG23	1:A:59:LEU:CD1	0.51	2.36	14	7
1:A:57:VAL:HG23	1:A:59:LEU:HD11	0.51	1.83	20	2
1:A:36:TYR:CD1	1:A:53:HIS:CB	0.50	2.95	15	1
1:A:38:PRO:HB2	1:A:54:TYR:CG	0.50	2.42	10	1
1:A:41:ALA:HB3	2:P:2:ARG:CD	0.50	2.37	7	3
1:A:44:ASN:HD22	1:A:46:ALA:N	0.50	2.05	12	1
1:A:44:ASN:ND2	1:A:77:ALA:CA	0.49	2.75	4	4
1:A:31:CYS:SG	1:A:53:HIS:CE1	0.49	3.06	16	1
1:A:44:ASN:CG	1:A:77:ALA:HB2	0.49	2.28	13	2
1:A:44:ASN:HB3	1:A:47:CYS:SG	0.49	2.47	8	9
1:A:46:ALA:HB3	1:A:76:ILE:HG22	0.48	1.85	6	4
1:A:34:VAL:O	1:A:36:TYR:CE1	0.48	2.66	6	3
1:A:57:VAL:CG2	1:A:59:LEU:CD1	0.48	2.92	13	1
1:A:36:TYR:CE1	1:A:53:HIS:ND1	0.48	2.81	13	4
1:A:44:ASN:OD1	1:A:46:ALA:N	0.48	2.47	10	2
1:A:59:LEU:HD12	1:A:59:LEU:H	0.48	1.64	4	1
1:A:28:TYR:HB2	1:A:39:MET:HE1	0.48	1.86	6	1
1:A:44:ASN:HD22	1:A:77:ALA:CB	0.48	2.19	16	2
1:A:74:LYS:CG	1:A:75:GLU:N	0.47	2.76	11	6
1:A:72:ASP:O	1:A:75:GLU:N	0.47	2.46	20	10
1:A:52:PHE:CD1	1:A:69:CYS:HB3	0.47	2.45	20	8
1:A:39:MET:SD	1:A:52:PHE:C	0.47	2.92	2	1
1:A:44:ASN:OD1	1:A:73:CYS:O	0.47	2.32	2	2
1:A:44:ASN:ND2	1:A:45:PRO:HD2	0.47	2.25	2	1
1:A:42:CYS:CB	1:A:69:CYS:HB3	0.47	2.39	15	16
1:A:36:TYR:OH	1:A:53:HIS:CE1	0.47	2.67	18	1
1:A:44:ASN:ND2	1:A:46:ALA:HB3	0.47	2.25	17	2
1:A:72:ASP:O	1:A:74:LYS:N	0.47	2.48	10	6
1:A:29:CYS:C	1:A:31:CYS:N	0.47	2.67	13	14
1:A:59:LEU:CD2	1:A:67:TRP:CD2	0.47	2.98	4	14
1:A:54:TYR:CD1	1:A:59:LEU:CD1	0.47	2.98	15	1
1:A:44:ASN:C	1:A:46:ALA:H	0.46	2.14	12	1
1:A:29:CYS:O	1:A:31:CYS:N	0.46	2.49	13	4
1:A:30:PHE:C	1:A:32:ARG:H	0.46	2.12	6	3

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:51:TRP:N	1:A:52:PHE:CE1	0.46	2.84	8	2
1:A:53:HIS:CD2	1:A:55:GLY:N	0.46	2.81	15	1
1:A:53:HIS:N	1:A:53:HIS:HD2	0.46	2.05	4	3
1:A:59:LEU:HD13	1:A:59:LEU:O	0.46	2.10	3	7
2:P:2:ARG:CD	2:P:2:ARG:N	0.46	2.79	6	2
1:A:35:SER:HA	1:A:39:MET:SD	0.46	2.51	17	3
2:P:2:ARG:H	2:P:2:ARG:HD2	0.46	1.71	6	1
1:A:35:SER:O	1:A:35:SER:OG	0.46	2.30	18	1
1:A:31:CYS:HB2	1:A:33:ASN:ND2	0.46	2.25	13	1
1:A:67:TRP:CE2	1:A:68:TYR:O	0.45	2.69	2	9
1:A:52:PHE:CZ	1:A:69:CYS:HB2	0.45	2.46	9	1
1:A:54:TYR:N	1:A:54:TYR:CD1	0.45	2.84	12	6
1:A:30:PHE:O	1:A:30:PHE:CG	0.45	2.69	14	1
1:A:41:ALA:HB3	2:P:2:ARG:HD2	0.45	1.89	20	2
1:A:27:VAL:HG12	1:A:28:TYR:N	0.45	2.27	17	2
1:A:38:PRO:O	1:A:54:TYR:N	0.45	2.48	12	1
1:A:39:MET:HG2	1:A:53:HIS:HA	0.45	1.86	14	1
1:A:28:TYR:HB2	1:A:53:HIS:NE2	0.45	2.27	1	2
1:A:40:VAL:CG2	1:A:41:ALA:N	0.45	2.79	1	5
1:A:34:VAL:C	1:A:53:HIS:HE2	0.45	2.16	8	4
1:A:70:SER:N	1:A:73:CYS:HB2	0.45	2.26	1	12
1:A:72:ASP:C	1:A:74:LYS:N	0.45	2.70	16	4
1:A:72:ASP:O	1:A:73:CYS:C	0.44	2.55	18	8
1:A:29:CYS:SG	1:A:53:HIS:ND1	0.44	2.90	10	1
1:A:28:TYR:HB3	1:A:51:TRP:O	0.44	2.12	20	7
1:A:35:SER:CA	1:A:39:MET:SD	0.44	3.06	17	2
1:A:70:SER:H	1:A:73:CYS:HB2	0.44	1.72	20	3
1:A:36:TYR:CE2	1:A:53:HIS:CB	0.44	3.01	6	3
1:A:31:CYS:HB2	1:A:33:ASN:OD1	0.44	2.13	2	1
1:A:68:TYR:CG	1:A:74:LYS:CB	0.44	3.00	13	4
1:A:67:TRP:CD1	1:A:68:TYR:N	0.44	2.86	1	1
1:A:59:LEU:HD23	1:A:67:TRP:CG	0.44	2.48	3	4
1:A:53:HIS:ND1	1:A:56:CYS:CB	0.44	2.81	15	1
1:A:39:MET:SD	1:A:53:HIS:N	0.44	2.90	2	1
1:A:39:MET:HE3	1:A:52:PHE:C	0.44	2.33	6	3
1:A:46:ALA:O	1:A:47:CYS:O	0.43	2.36	16	1
1:A:34:VAL:O	1:A:53:HIS:NE2	0.43	2.51	8	2
1:A:68:TYR:CG	1:A:74:LYS:HA	0.43	2.48	12	2
1:A:53:HIS:CE1	1:A:56:CYS:HG	0.43	2.31	10	1
1:A:31:CYS:O	1:A:32:ARG:CG	0.43	2.66	13	1
1:A:44:ASN:HD22	1:A:47:CYS:H	0.43	1.56	1	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:43:ASP:HB2	2:P:1:ALA:CB	0.43	2.42	10	1
1:A:68:TYR:O	1:A:69:CYS:C	0.43	2.57	7	6
1:A:53:HIS:CE1	1:A:56:CYS:SG	0.43	3.11	16	1
1:A:44:ASN:OD1	1:A:77:ALA:CA	0.43	2.66	1	1
1:A:27:VAL:CG1	1:A:28:TYR:N	0.43	2.82	3	2
1:A:53:HIS:ND1	1:A:56:CYS:N	0.43	2.66	18	3
1:A:68:TYR:CD1	1:A:74:LYS:HA	0.43	2.48	13	3
1:A:57:VAL:CG2	1:A:58:GLY:H	0.43	2.23	4	1
1:A:44:ASN:ND2	1:A:45:PRO:CD	0.43	2.81	12	1
1:A:44:ASN:ND2	1:A:44:ASN:C	0.42	2.72	19	4
1:A:42:CYS:HG	1:A:69:CYS:CB	0.42	2.14	8	1
1:A:30:PHE:C	1:A:32:ARG:N	0.42	2.73	17	3
1:A:42:CYS:HA	1:A:69:CYS:SG	0.42	2.53	1	6
1:A:54:TYR:CG	1:A:59:LEU:CD1	0.42	2.99	4	1
1:A:44:ASN:ND2	1:A:77:ALA:N	0.42	2.67	10	1
1:A:61:GLN:CG	1:A:62:ALA:N	0.42	2.83	6	1
1:A:49:PHE:CB	1:A:52:PHE:CZ	0.42	3.03	12	1
1:A:68:TYR:CD2	1:A:74:LYS:HB2	0.42	2.50	13	1
1:A:36:TYR:HH	1:A:56:CYS:HG	0.42	1.51	15	1
1:A:61:GLN:HG3	1:A:62:ALA:N	0.42	2.30	6	1
1:A:39:MET:CE	1:A:52:PHE:N	0.42	2.83	14	1
1:A:60:LYS:C	1:A:62:ALA:H	0.42	2.17	10	1
1:A:47:CYS:HG	3:A:201:ZN:ZN	0.41	0.83	3	1
1:A:39:MET:HE2	1:A:52:PHE:C	0.41	2.35	10	1
1:A:59:LEU:O	1:A:59:LEU:CD1	0.41	2.68	6	1
1:A:37:GLY:O	1:A:38:PRO:C	0.41	2.58	20	1
1:A:41:ALA:N	2:P:2:ARG:O	0.41	2.52	20	1
1:A:44:ASN:O	1:A:46:ALA:N	0.41	2.52	4	3
2:P:2:ARG:H	2:P:2:ARG:HD3	0.41	1.76	13	1
1:A:35:SER:OG	1:A:39:MET:HG3	0.41	2.16	7	2
1:A:53:HIS:O	1:A:56:CYS:N	0.41	2.52	18	1
1:A:30:PHE:CD1	1:A:30:PHE:N	0.41	2.85	5	1
1:A:36:TYR:CZ	1:A:53:HIS:CD2	0.41	3.09	8	1
1:A:40:VAL:O	1:A:52:PHE:N	0.41	2.51	9	1
1:A:28:TYR:CD2	1:A:35:SER:HB2	0.41	2.51	13	1
1:A:33:ASN:OD1	1:A:33:ASN:N	0.41	2.53	15	1
1:A:33:ASN:C	1:A:33:ASN:HD22	0.40	2.18	6	1
1:A:72:ASP:O	1:A:76:ILE:N	0.40	2.46	6	1
1:A:26:GLU:N	1:A:34:VAL:HG22	0.40	2.31	17	1
1:A:70:SER:N	1:A:73:CYS:CB	0.40	2.84	2	2
1:A:29:CYS:HB3	1:A:53:HIS:ND1	0.40	2.32	17	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:38:PRO:O	1:A:53:HIS:HA	0.40	2.16	18	1
1:A:40:VAL:HG21	1:A:67:TRP:HB3	0.40	1.93	20	1
1:A:33:ASN:ND2	1:A:36:TYR:CE2	0.40	2.90	15	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	54/90 (60%)	33±2 (62±3%)	14±2 (26±3%)	6±2 (12±4%)	1	7
2	P	2/9 (22%)	2±0 (88±22%)	0±0 (12±22%)	0±0 (0±0%)	100	100
All	All	1120/1980 (57%)	704 (63%)	290 (26%)	126 (11%)	1	8

All 21 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	CYS	20
1	A	57	VAL	20
1	A	69	CYS	20
1	A	37	GLY	12
1	A	61	GLN	7
1	A	30	PHE	6
1	A	73	CYS	5
1	A	65	GLY	5
1	A	59	LEU	5
1	A	62	ALA	4
1	A	42	CYS	4
1	A	38	PRO	4
1	A	36	TYR	3
1	A	29	CYS	3
1	A	45	PRO	2
1	A	64	LYS	1
1	A	46	ALA	1
1	A	63	PRO	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	54	TYR	1
1	A	34	VAL	1
1	A	35	SER	1

6.3.2 Protein sidechains [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	46/77 (60%)	34±1 (73±3%)	12±1 (27±3%)	2 21
2	P	2/6 (33%)	1±0 (50±0%)	1±0 (50±0%)	0 1
All	All	960/1660 (58%)	692 (72%)	268 (28%)	2 19

All 26 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	42	CYS	20
1	A	56	CYS	20
1	A	59	LEU	20
1	A	69	CYS	20
2	P	2	ARG	20
1	A	29	CYS	19
1	A	31	CYS	19
1	A	33	ASN	19
1	A	47	CYS	19
1	A	53	HIS	19
1	A	36	TYR	19
1	A	73	CYS	11
1	A	44	ASN	11
1	A	43	ASP	8
1	A	35	SER	6
1	A	64	LYS	3
1	A	72	ASP	3
1	A	66	LYS	3
1	A	74	LYS	2
1	A	61	GLN	1
1	A	60	LYS	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	78	ASN	1
1	A	32	ARG	1
1	A	39	MET	1
1	A	52	PHE	1
1	A	49	PHE	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](#)

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds for which Mogul statistics could be retrieved, the number of bonds that are observed in the model and the number of bonds that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length is the number of standard deviations the observed value is removed from the expected value. A bond length with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond lengths.

Mol	Type	Chain	Res	Link	Bond lengths		
					Counts	RMSZ	#Z>2
2	M3L	P	4	2	10,11,12	0.52±0.10	0±0 (0±0%)

In the following table, the Counts columns list the number of angles for which Mogul statistics could be retrieved, the number of angles that are observed in the model and the number of angles that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond angle is the number of standard deviations the observed value is removed from the expected value. A bond angle with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the average root-mean-square of all Z scores of the bond angles.

Mol	Type	Chain	Res	Link	Bond angles		
					Counts	RMSZ	#Z>2
2	M3L	P	4	2	9,14,16	0.58±0.06	0±0 (0±0%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	M3L	P	4	2	-	0±0,9,10,12	-

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

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