



Full wwPDB NMR Structure Validation Report ⓘ

Jun 4, 2023 – 03:11 PM EDT

PDB ID : 2LGC
BMRB ID : 6468
Title : Joint NMR and X-ray refinement reveals the structure of a novel dibenzo[a,d]cycloheptenone inhibitor/p38 MAP kinase complex in solution
Authors : Habeck, M.
Deposited on : 2011-07-25

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 : 4.02b-467
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
BMRB Restraints Analysis : v1.2
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.33

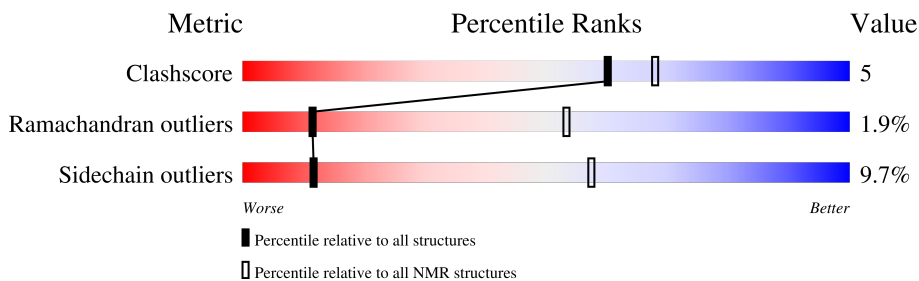
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 22%.

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	359	 82% 14% •

2 Ensemble composition and analysis

This entry contains 10 models. Model 4 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *best r-free*.

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:-4-A:354 (359)	0.10	4

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 1 clusters and 7 single-model clusters were found.

Cluster number	Models
1	4, 5, 9
Single-model clusters	1; 2; 3; 6; 7; 8; 10

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 3242 atoms, of which 344 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Mitogen-activated protein kinase 14.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	359	3242	1851	344	494	538	15	0

There are 6 discrepancies between the modelled and reference sequences:

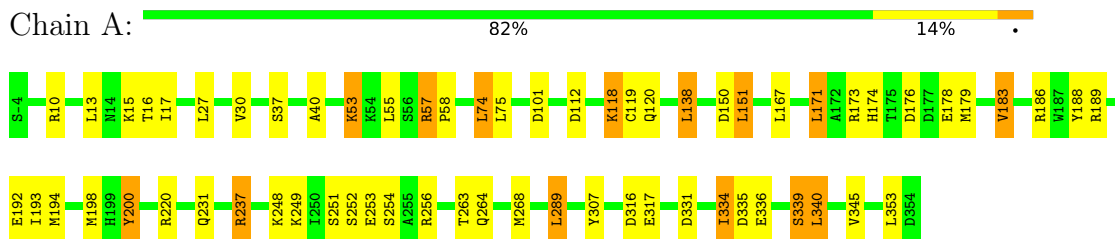
Chain	Residue	Modelled	Actual	Comment	Reference
A	-4	SER	-	expression tag	UNP Q16539
A	-3	HIS	-	expression tag	UNP Q16539
A	-2	MET	-	expression tag	UNP Q16539
A	-1	LEU	-	expression tag	UNP Q16539
A	0	GLU	-	expression tag	UNP Q16539
A	1	MET	-	expression tag	UNP Q16539

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: Mitogen-activated protein kinase 14

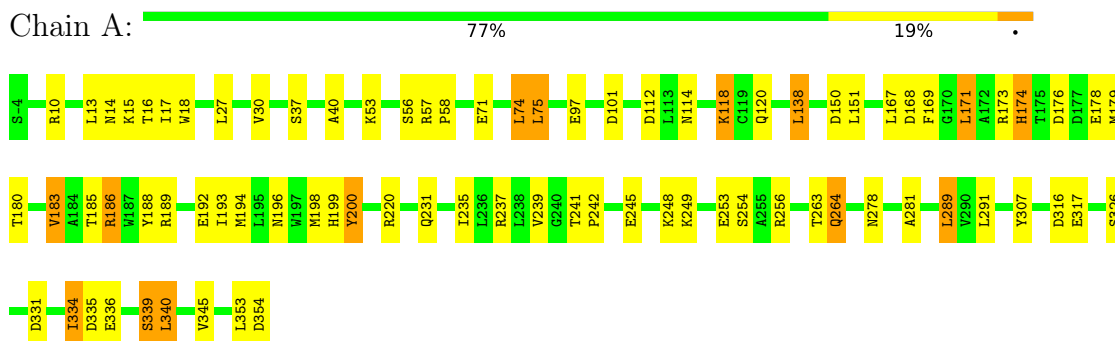


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

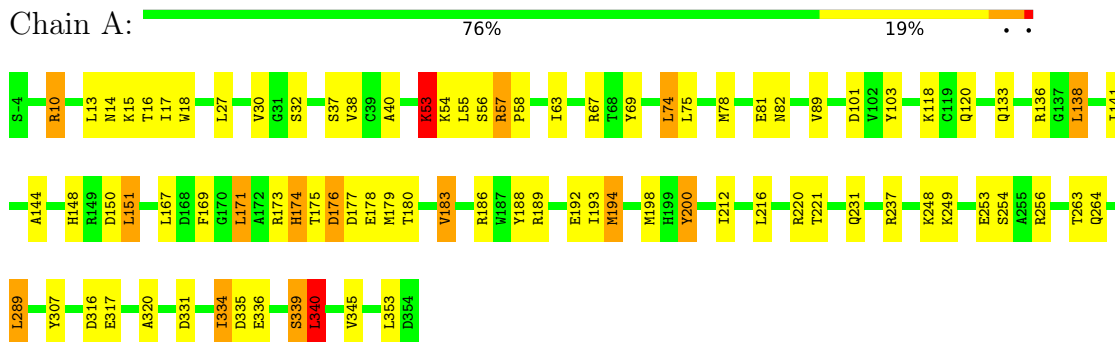
4.2.1 Score per residue for model 1

- Molecule 1: Mitogen-activated protein kinase 14



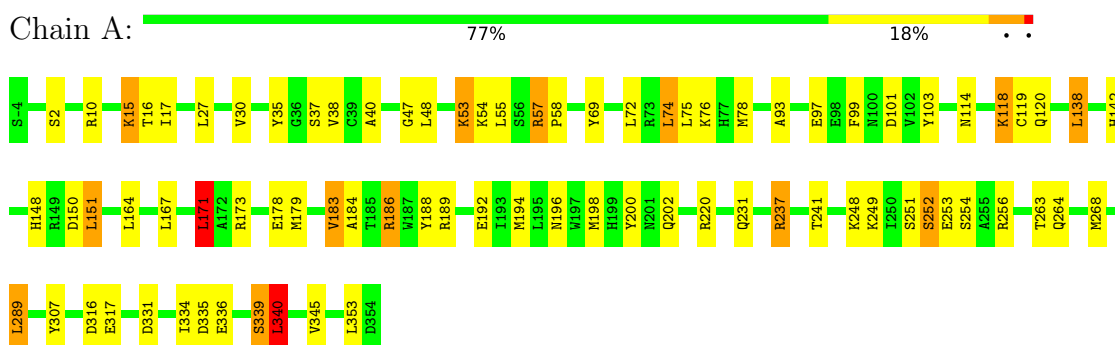
4.2.2 Score per residue for model 2

- Molecule 1: Mitogen-activated protein kinase 14



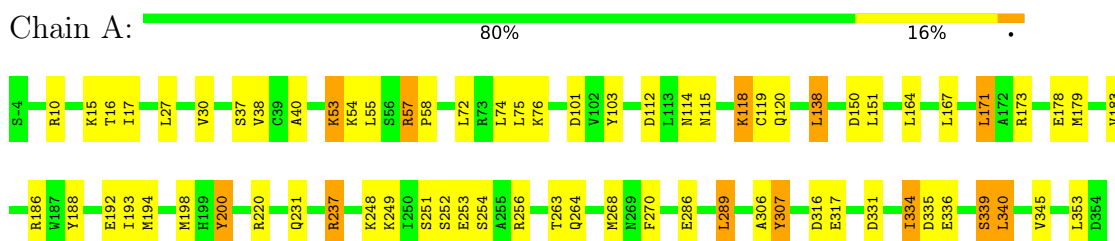
4.2.3 Score per residue for model 3

- Molecule 1: Mitogen-activated protein kinase 14



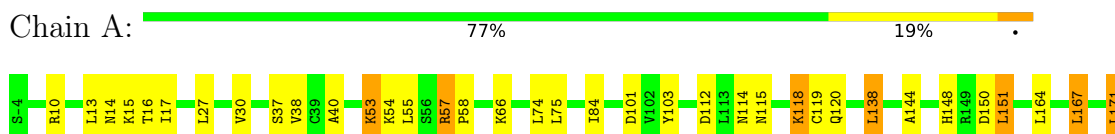
4.2.4 Score per residue for model 4 (medoid)

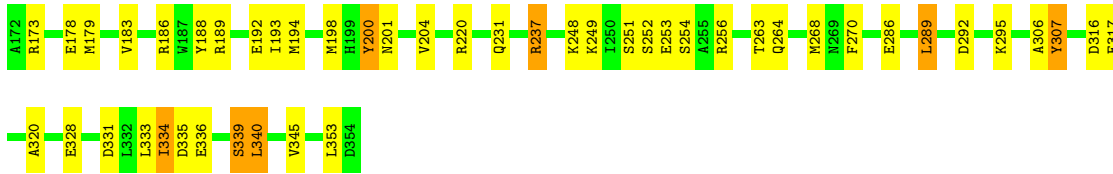
- Molecule 1: Mitogen-activated protein kinase 14



4.2.5 Score per residue for model 5

- Molecule 1: Mitogen-activated protein kinase 14

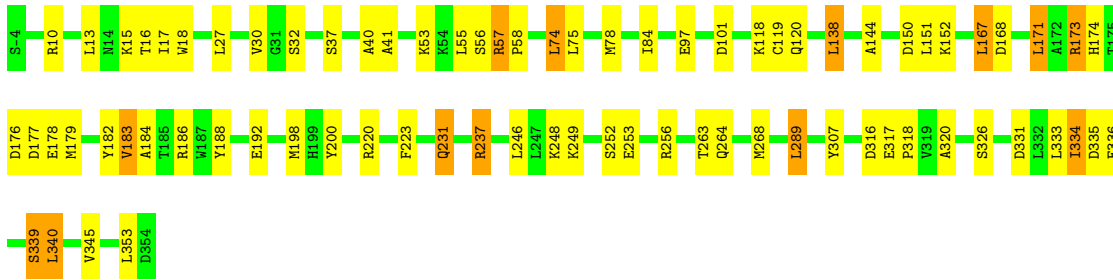




4.2.6 Score per residue for model 6

- Molecule 1: Mitogen-activated protein kinase 14

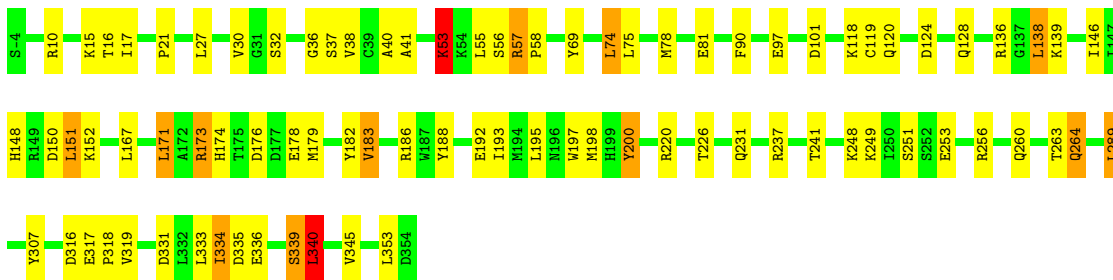
Chain A: 79% 18%



4.2.7 Score per residue for model 7

- Molecule 1: Mitogen-activated protein kinase 14

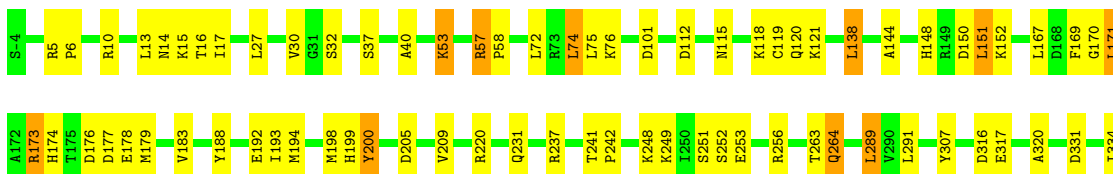
Chain A: 77% 19%



4.2.8 Score per residue for model 8

- Molecule 1: Mitogen-activated protein kinase 14

Chain A: 78% 19%

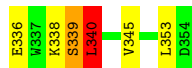
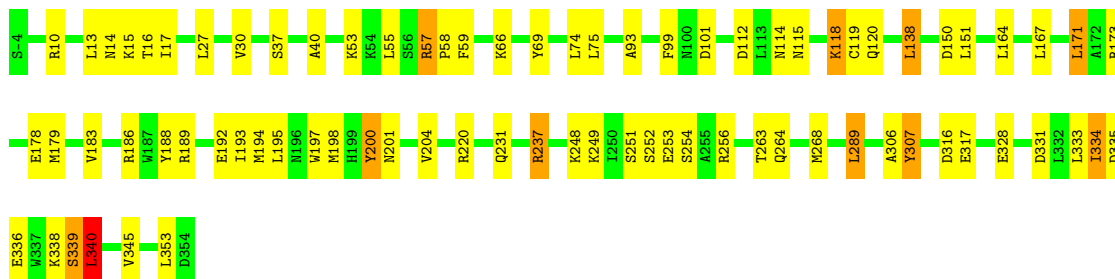




4.2.9 Score per residue for model 9

- Molecule 1: Mitogen-activated protein kinase 14

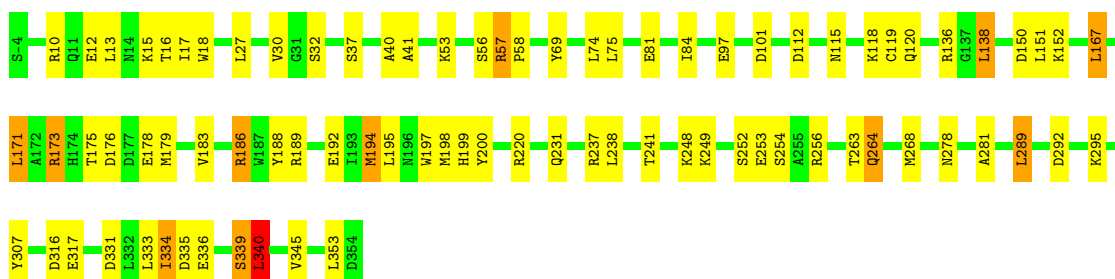
Chain A: 78% 19%



4.2.10 Score per residue for model 10

- Molecule 1: Mitogen-activated protein kinase 14

Chain A: 77% 20%



5 Refinement protocol and experimental data overview

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

Of the 3000 calculated structures, 10 were deposited, based on the following criterion: *lowest R-free*.

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

Software name	Classification	Version
ISD	refinement	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1112
Number of shifts mapped to atoms	1112
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	22%

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	1.08±0.00	7±0/2965 (0.2± 0.0%)	1.09±0.00	20±0/4023 (0.5± 0.0%)
All	All	1.08	70/29650 (0.2%)	1.09	202/40230 (0.5%)

All unique bond 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(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	15	LYS	CA-CB	-10.84	1.30	1.53	4	10
1	A	339	SER	CA-CB	7.89	1.64	1.52	6	10
1	A	53	LYS	CB-CG	-6.06	1.36	1.52	10	10
1	A	192	GLU	CB-CG	-5.35	1.42	1.52	7	10
1	A	307	TYR	CD2-CE2	-5.33	1.31	1.39	8	10
1	A	345	VAL	CB-CG1	5.22	1.63	1.52	6	10
1	A	188	TYR	CD1-CE1	5.08	1.47	1.39	7	1
1	A	188	TYR	CD2-CE2	5.07	1.47	1.39	8	9

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	10	ARG	NE-CZ-NH2	-15.02	112.79	120.30	7	10
1	A	10	ARG	NE-CZ-NH1	12.22	126.41	120.30	7	10
1	A	339	SER	N-CA-CB	8.19	122.78	110.50	7	10
1	A	15	LYS	N-CA-CB	7.91	124.84	110.60	7	10
1	A	74	LEU	CB-CG-CD2	-7.28	98.63	111.00	6	10
1	A	289	LEU	CB-CG-CD1	6.97	122.86	111.00	9	10
1	A	15	LYS	CA-CB-CG	-6.85	98.33	113.40	10	10
1	A	167	LEU	CB-CG-CD2	-6.75	99.52	111.00	9	10
1	A	10	ARG	CG-CD-NE	-6.34	98.50	111.80	2	10
1	A	150	ASP	CB-CG-OD1	6.25	123.93	118.30	6	10
1	A	150	ASP	CB-CA-C	6.25	122.89	110.40	4	10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	138	LEU	CB-CG-CD1	6.25	121.62	111.00	3	10
1	A	192	GLU	CB-CA-C	-5.91	98.59	110.40	5	10
1	A	101	ASP	CB-CG-OD1	5.80	123.52	118.30	4	10
1	A	15	LYS	CB-CA-C	-5.67	99.06	110.40	1	10
1	A	220	ARG	NE-CZ-NH2	-5.51	117.55	120.30	7	10
1	A	171	LEU	CA-CB-CG	5.38	127.67	115.30	7	10
1	A	167	LEU	CA-CB-CG	5.33	127.56	115.30	10	10
1	A	340	LEU	CB-CG-CD2	5.13	119.72	111.00	5	10
1	A	167	LEU	CB-CA-C	-5.05	100.60	110.20	6	10
1	A	340	LEU	CB-CG-CD1	5.01	119.52	111.00	9	2

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	2898	344	2884	27±3
All	All	28980	3440	28840	271

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 5.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:248:LYS:HA	1:A:256:ARG:HH21	0.92	1.23	7	10
1:A:16:THR:HG22	1:A:17:ILE:N	0.71	2.00	5	9
1:A:248:LYS:HA	1:A:256:ARG:NH2	0.69	2.03	7	3
1:A:114:ASN:O	1:A:118:LYS:HD2	0.66	1.90	3	5
1:A:334:ILE:O	1:A:336:GLU:N	0.64	2.31	1	10
1:A:16:THR:HG22	1:A:17:ILE:H	0.62	1.52	9	10
1:A:63:ILE:O	1:A:67:ARG:HG3	0.61	1.96	2	1
1:A:316:ASP:O	1:A:317:GLU:HG3	0.60	1.95	1	10
1:A:57:ARG:N	1:A:58:PRO:CD	0.60	2.65	8	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:148:HIS:CE1	1:A:151:LEU:H	0.58	2.17	2	5
1:A:186:ARG:HG2	1:A:194:MET:HE1	0.58	1.73	1	3
1:A:27:LEU:HA	1:A:40:ALA:O	0.57	2.00	1	10
1:A:81:GLU:HB2	1:A:136:ARG:HH12	0.56	1.60	7	3
1:A:72:LEU:O	1:A:76:LYS:HG3	0.56	2.01	3	3
1:A:112:ASP:H	1:A:115:ASN:ND2	0.56	1.98	8	5
1:A:189:ARG:HB3	1:A:194:MET:HE3	0.56	1.76	5	4
1:A:241:THR:OG1	1:A:264:GLN:HG3	0.56	2.01	1	4
1:A:170:GLY:HA2	1:A:173:ARG:HG2	0.54	1.78	8	1
1:A:152:LYS:NZ	1:A:173:ARG:HH21	0.54	2.00	7	4
1:A:248:LYS:CA	1:A:256:ARG:HH21	0.54	2.12	6	2
1:A:71:GLU:HG2	1:A:75:LEU:HD22	0.54	1.78	1	1
1:A:193:ILE:HG22	1:A:200:TYR:CD2	0.53	2.38	1	2
1:A:38:VAL:HG22	1:A:53:LYS:HB3	0.53	1.80	7	5
1:A:84:ILE:HG13	1:A:167:LEU:HD23	0.53	1.81	6	3
1:A:27:LEU:HG	1:A:41:ALA:HB2	0.52	1.82	7	3
1:A:237:ARG:O	1:A:268:MET:HG3	0.52	2.05	4	5
1:A:74:LEU:HD22	1:A:169:PHE:CE2	0.51	2.41	8	2
1:A:47:GLY:O	1:A:48:LEU:HD23	0.51	2.06	3	1
1:A:13:LEU:HD12	1:A:18:TRP:CG	0.50	2.41	10	2
1:A:53:LYS:NZ	1:A:174:HIS:HE1	0.50	2.04	2	1
1:A:54:LYS:HE3	1:A:103:TYR:OH	0.50	2.06	3	4
1:A:212:ILE:O	1:A:216:LEU:HG	0.50	2.06	2	1
1:A:168:ASP:OD2	1:A:174:HIS:NE2	0.50	2.44	6	2
1:A:16:THR:CG2	1:A:17:ILE:N	0.49	2.72	5	6
1:A:183:VAL:HG12	1:A:184:ALA:H	0.49	1.67	6	2
1:A:74:LEU:O	1:A:78:MET:HG2	0.49	2.08	3	3
1:A:186:ARG:HG2	1:A:194:MET:CE	0.49	2.36	4	3
1:A:334:ILE:C	1:A:336:GLU:H	0.48	2.11	1	9
1:A:334:ILE:C	1:A:336:GLU:N	0.48	2.67	10	10
1:A:97:GLU:H	1:A:97:GLU:CD	0.48	2.11	7	5
1:A:195:LEU:HB2	1:A:197:TRP:NE1	0.48	2.24	10	3
1:A:139:LYS:HE2	1:A:319:VAL:CG1	0.47	2.40	7	1
1:A:141:ILE:HD13	1:A:169:PHE:HE1	0.47	1.68	2	1
1:A:13:LEU:HB2	1:A:18:TRP:CD1	0.47	2.45	1	3
1:A:193:ILE:HG22	1:A:200:TYR:CD1	0.47	2.45	8	5
1:A:66:LYS:HE2	1:A:328:GLU:OE1	0.47	2.10	5	2
1:A:256:ARG:O	1:A:260:GLN:HG3	0.46	2.10	7	1
1:A:333:LEU:O	1:A:336:GLU:HB2	0.45	2.11	6	5
1:A:189:ARG:HB3	1:A:194:MET:CE	0.45	2.42	10	2
1:A:164:LEU:C	1:A:164:LEU:HD23	0.45	2.32	4	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:PRO:HD3	1:A:90:PHE:CE1	0.45	2.46	7	1
1:A:27:LEU:N	1:A:27:LEU:HD12	0.45	2.27	1	3
1:A:59:PHE:CD2	1:A:338:LYS:HD2	0.45	2.46	9	1
1:A:93:ALA:HB2	1:A:99:PHE:HA	0.45	1.89	3	2
1:A:112:ASP:H	1:A:115:ASN:HD22	0.45	1.52	5	4
1:A:13:LEU:O	1:A:14:ASN:HB2	0.45	2.11	5	3
1:A:201:ASN:O	1:A:204:VAL:HG22	0.44	2.12	9	2
1:A:74:LEU:HD21	1:A:146:ILE:HD13	0.44	1.89	7	1
1:A:5:ARG:HG3	1:A:6:PRO:HD2	0.44	1.88	8	1
1:A:242:PRO:HB3	1:A:291:LEU:HD23	0.44	1.89	8	2
1:A:223:PHE:HB2	1:A:231:GLN:NE2	0.44	2.27	6	1
1:A:144:ALA:HB2	1:A:320:ALA:CB	0.44	2.42	5	4
1:A:292:ASP:HB3	1:A:295:LYS:HB2	0.44	1.90	10	2
1:A:270:PHE:CD2	1:A:286:GLU:HG3	0.43	2.48	5	2
1:A:69:TYR:CE1	1:A:340:LEU:HB3	0.43	2.48	7	5
1:A:112:ASP:OD1	1:A:112:ASP:C	0.43	2.57	9	3
1:A:317:GLU:N	1:A:318:PRO:CD	0.43	2.82	7	2
1:A:142:HIS:HB3	1:A:202:GLN:NE2	0.42	2.29	3	1
1:A:74:LEU:HD13	1:A:169:PHE:HD2	0.42	1.74	1	1
1:A:278:ASN:O	1:A:281:ALA:HB3	0.42	2.15	10	2
1:A:252:SER:O	1:A:256:ARG:HB2	0.42	2.15	3	1
1:A:124:ASP:OD2	1:A:128:GLN:NE2	0.42	2.52	7	1
1:A:112:ASP:OD1	1:A:114:ASN:HB2	0.42	2.15	1	1
1:A:78:MET:HA	1:A:78:MET:HE2	0.42	1.92	7	1
1:A:205:ASP:O	1:A:209:VAL:HG23	0.42	2.14	8	1
1:A:151:LEU:HD12	1:A:151:LEU:HA	0.41	1.80	7	1
1:A:238:LEU:HA	1:A:268:MET:HG3	0.41	1.92	10	1
1:A:185:THR:O	1:A:189:ARG:NH2	0.41	2.54	1	1
1:A:36:GLY:N	1:A:174:HIS:CE1	0.41	2.88	7	1
1:A:152:LYS:NZ	1:A:173:ARG:NH2	0.41	2.68	7	1
1:A:306:ALA:O	1:A:307:TYR:C	0.41	2.59	5	3
1:A:182:TYR:OH	1:A:226:THR:HG22	0.41	2.16	7	1
1:A:235:ILE:O	1:A:239:VAL:HG22	0.40	2.15	1	1
1:A:171:LEU:CD2	1:A:171:LEU:N	0.40	2.84	3	1
1:A:82:ASN:ND2	1:A:133:GLN:HB3	0.40	2.32	2	1
1:A:12:GLU:HA	1:A:16:THR:O	0.40	2.16	10	1
1:A:57:ARG:N	1:A:58:PRO:HD3	0.40	2.31	2	1
1:A:164:LEU:HD23	1:A:164:LEU:C	0.40	2.36	3	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	357/359 (99%)	331±2 (93±1%)	20±2 (6±1%)	7±1 (2±0%)	11	53
All	All	3570/3590 (99%)	3306 (93%)	197 (6%)	67 (2%)	11	53

All 12 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	151	LEU	10
1	A	183	VAL	10
1	A	200	TYR	10
1	A	335	ASP	9
1	A	57	ARG	9
1	A	334	ILE	8
1	A	174	HIS	3
1	A	177	ASP	3
1	A	196	ASN	2
1	A	176	ASP	1
1	A	2	SER	1
1	A	35	TYR	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	319/319 (100%)	288±3 (90±1%)	31±3 (10±1%)	12	57
All	All	3190/3190 (100%)	2882 (90%)	308 (10%)	12	57

All 49 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	30	VAL	10
1	A	37	SER	10
1	A	75	LEU	10
1	A	118	LYS	10
1	A	120	GLN	10
1	A	138	LEU	10
1	A	171	LEU	10
1	A	173	ARG	10
1	A	178	GLU	10
1	A	179	MET	10
1	A	198	MET	10
1	A	231	GLN	10
1	A	237	ARG	10
1	A	249	LYS	10
1	A	253	GLU	10
1	A	263	THR	10
1	A	264	GLN	10
1	A	289	LEU	10
1	A	331	ASP	10
1	A	339	SER	10
1	A	340	LEU	10
1	A	353	LEU	10
1	A	119	CYS	8
1	A	186	ARG	7
1	A	254	SER	7
1	A	55	LEU	7
1	A	252	SER	7
1	A	176	ASP	6
1	A	251	SER	6
1	A	56	SER	5
1	A	32	SER	5
1	A	183	VAL	3
1	A	199	HIS	3
1	A	53	LYS	3
1	A	194	MET	3
1	A	14	ASN	2
1	A	180	THR	2
1	A	326	SER	2
1	A	175	THR	2
1	A	245	GLU	1
1	A	354	ASP	1
1	A	10	ARG	1
1	A	89	VAL	1

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Mol	Chain	Res	Type	Models (Total)
1	A	221	THR	1
1	A	15	LYS	1
1	A	241	THR	1
1	A	182	TYR	1
1	A	246	LEU	1
1	A	121	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 monosaccharides 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 i

The completeness of assignment taking into account all chemical shift lists is 22% for the well-defined parts and 22% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping i

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1112
Number of shifts mapped to atoms	1112
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	1

7.1.2 Chemical shift referencing i

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	232	0.47 ± 0.16	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	219	1.03 ± 0.12	Should be checked
$^{13}\text{C}'$	227	0.18 ± 0.11	None needed (< 0.5 ppm)
^{15}N	217	1.11 ± 0.30	Should be applied

7.1.3 Completeness of resonance assignments i

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 22%, i.e. 1112 atoms were assigned a chemical shift out of a possible 5021. 0 out of 66 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	893/1776 (50%)	217/716 (30%)	459/718 (64%)	217/342 (63%)
Sidechain	219/2847 (8%)	0/1857 (0%)	219/886 (25%)	0/104 (0%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	0/398 (0%)	0/207 (0%)	0/191 (0%)	0/0 (—%)
Overall	1112/5021 (22%)	217/2780 (8%)	678/1795 (38%)	217/446 (49%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 22%, i.e. 1112 atoms were assigned a chemical shift out of a possible 5021. 0 out of 66 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	893/1776 (50%)	217/716 (30%)	459/718 (64%)	217/342 (63%)
Sidechain	219/2847 (8%)	0/1857 (0%)	219/886 (25%)	0/104 (0%)
Aromatic	0/398 (0%)	0/207 (0%)	0/191 (0%)	0/0 (—%)
Overall	1112/5021 (22%)	217/2780 (8%)	678/1795 (38%)	217/446 (49%)

7.1.4 Statistically unusual chemical shifts [i](#)

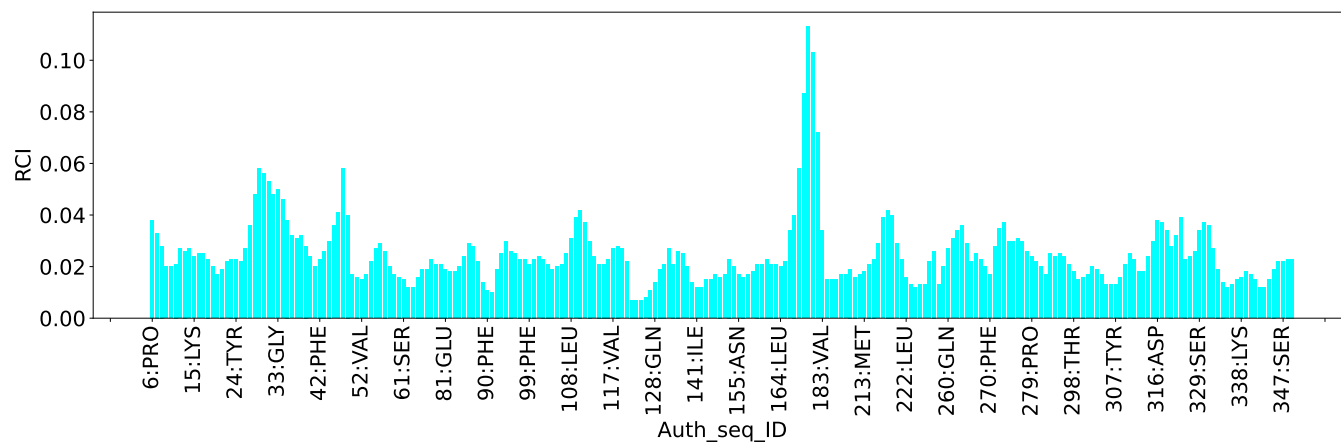
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	91	THR	C	184.43	166.08 – 183.07	5.8

7.1.5 Random Coil Index (RCI) plots [i](#)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition. If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:



8 NMR restraints analysis

No restraints data found

9 Distance violation analysis

No distance restraints data found

10 Dihedral-angle violation analysis

No dihedral-angle restraints found