



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 03:25 AM UTC

PDB ID : 2L6E / pdb_00002l6e
Title : NMR Structure of the monomeric mutant C-terminal domain of HIV-1 Capsid
in complex with stapled peptide Inhibitor
Authors : Bhattacharya, S.; Zhang, H.; Debnath, A.K.; Cowburn, D.
Deposited on : 2010-11-18

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
Mogul : 2022.3.0, CSD as543be (2022)
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

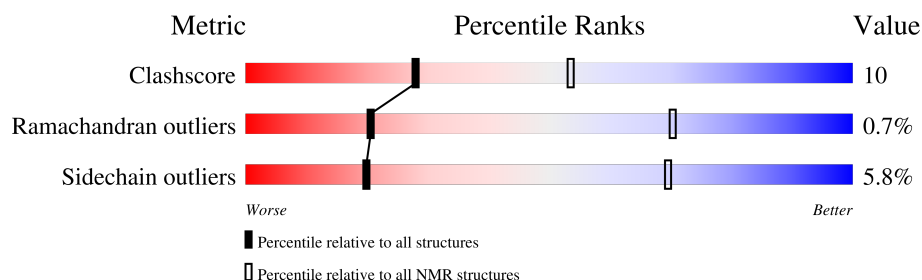
1 Overall quality at a glance

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	105	
2	B	14	

2 Ensemble composition and analysis

This entry contains 20 models. Model 7 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:150-A:218, B:2-B:3, B:5-B:7, B:9-B:10 (76)	0.58	7

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 1711 atoms, of which 874 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Capsid protein p24.

Mol	Chain	Residues	Atoms						Trace
1	A	94	Total	C	H	N	O	S	0
			1449	442	736	130	136	5	

There are 23 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	127	MET	-	initiating methionine	UNP P35963
A	128	GLY	-	expression tag	UNP P35963
A	129	SER	-	expression tag	UNP P35963
A	130	SER	-	expression tag	UNP P35963
A	131	HIS	-	expression tag	UNP P35963
A	132	HIS	-	expression tag	UNP P35963
A	133	HIS	-	expression tag	UNP P35963
A	134	HIS	-	expression tag	UNP P35963
A	135	HIS	-	expression tag	UNP P35963
A	136	HIS	-	expression tag	UNP P35963
A	137	SER	-	expression tag	UNP P35963
A	138	SER	-	expression tag	UNP P35963
A	139	GLY	-	expression tag	UNP P35963
A	140	LEU	-	expression tag	UNP P35963
A	141	VAL	-	expression tag	UNP P35963
A	142	PRO	-	expression tag	UNP P35963
A	143	ARG	-	expression tag	UNP P35963
A	144	GLY	-	expression tag	UNP P35963
A	145	SER	-	expression tag	UNP P35963
A	146	HIS	-	expression tag	UNP P35963
A	147	MET	-	expression tag	UNP P35963
A	184	ALA	TRP	engineered mutation	UNP P35963
A	185	ALA	MET	engineered mutation	UNP P35963

- Molecule 2 is a protein called NYAD-13 stapled peptide inhibitor.

Mol	Chain	Residues	Atoms						Trace
2	B	14	Total	C	H	N	O		0
			262	87	138	17	20		

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: Capsid protein p24

Chain A: 



- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B: 



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: Capsid protein p24

Chain A: 



- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B: 



4.2.2 Score per residue for model 2

- Molecule 1: Capsid protein p24

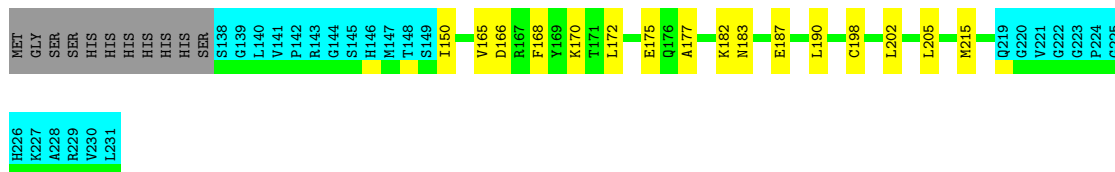


- Molecule 2: NYAD-13 stapled peptide inhibitor



4.2.3 Score per residue for model 3

- Molecule 1: Capsid protein p24



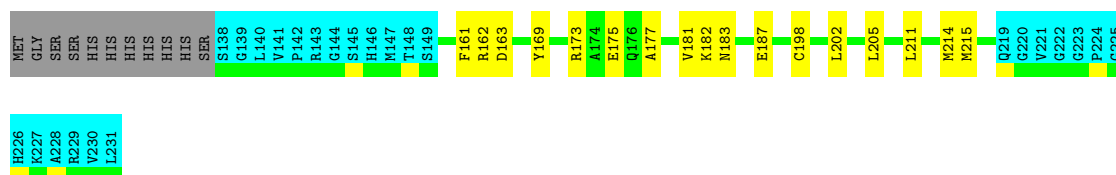
- Molecule 2: NYAD-13 stapled peptide inhibitor



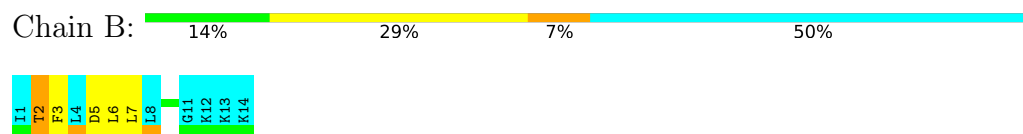
4.2.4 Score per residue for model 4

- Molecule 1: Capsid protein p24



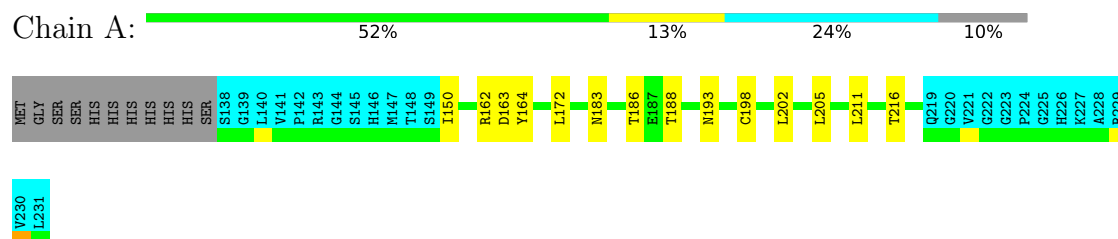


- Molecule 2: NYAD-13 stapled peptide inhibitor

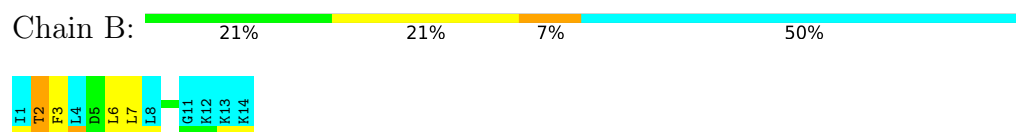


4.2.5 Score per residue for model 5

- Molecule 1: Capsid protein p24

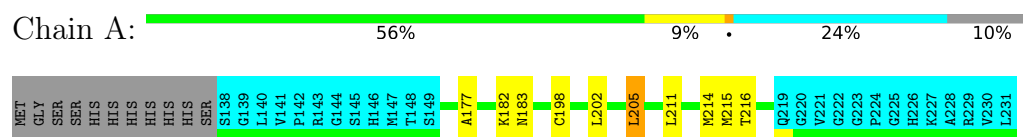


- Molecule 2: NYAD-13 stapled peptide inhibitor

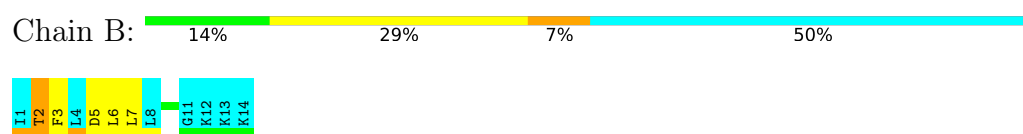


4.2.6 Score per residue for model 6

- Molecule 1: Capsid protein p24

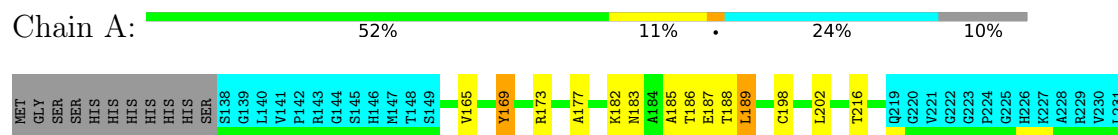


- Molecule 2: NYAD-13 stapled peptide inhibitor

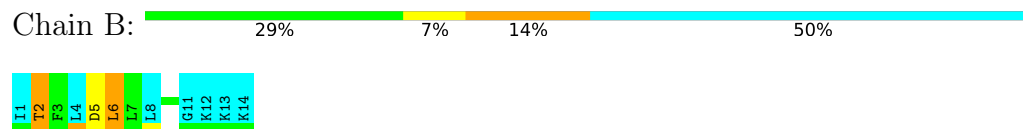


4.2.7 Score per residue for model 7 (medoid)

- Molecule 1: Capsid protein p24

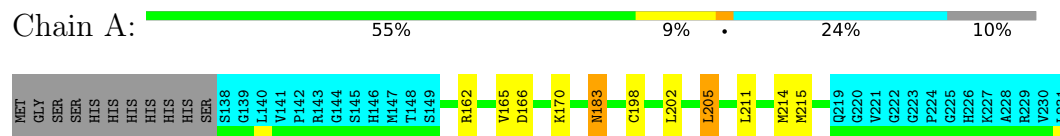


- Molecule 2: NYAD-13 stapled peptide inhibitor

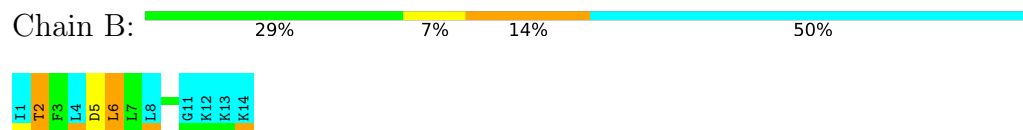


4.2.8 Score per residue for model 8

- Molecule 1: Capsid protein p24

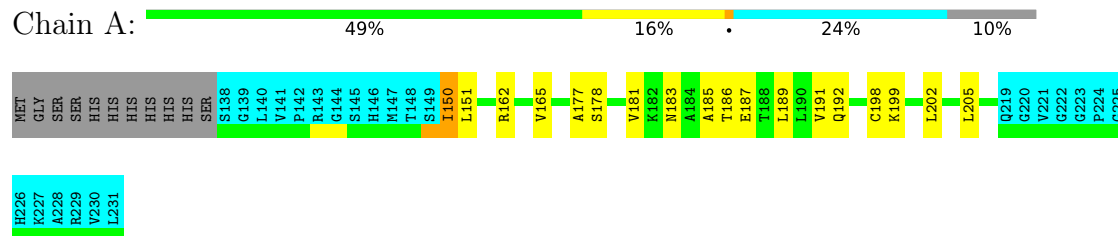


- Molecule 2: NYAD-13 stapled peptide inhibitor



4.2.9 Score per residue for model 9

- Molecule 1: Capsid protein p24



- Molecule 2: NYAD-13 stapled peptide inhibitor

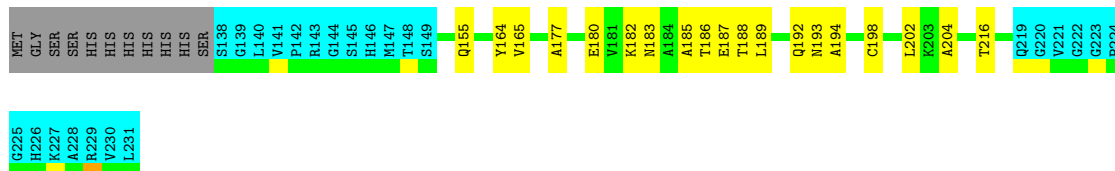




4.2.10 Score per residue for model 10

- Molecule 1: Capsid protein p24

Chain A:



- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B:



4.2.11 Score per residue for model 11

- Molecule 1: Capsid protein p24

Chain A:



- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B:



4.2.12 Score per residue for model 12

- Molecule 1: Capsid protein p24

Chain A:



V230
L231

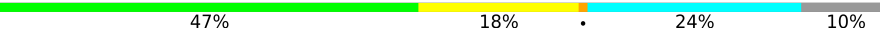
- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B: 

I1 I2 F3 L4 D5 L6 L7 L8 G11 G12 K13 K14

4.2.13 Score per residue for model 13

- Molecule 1: Capsid protein p24

Chain A: 

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER S138 G139 L140 V141 P142 R143 G144 S145 H146 M147 T148 S149 I150 L151 D152 R162 D163 Y164 V165 D166 Y169 K170 T171 L172 R173 A177 K182 N183 A184 A185 L189 N193 C198 L202 L211 M215 T216 Q219
G220 V221 G222 P224 G225 H226 K227 A228 R229 V230 L231

G220 V221 G222 P224 G225 H226 K227 A228 R229 V230 L231

- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B: 

I1 I2 F3 L4 D5 L6 L7 L8 G11 G12 K13 K14

4.2.14 Score per residue for model 14

- Molecule 1: Capsid protein p24

Chain A: 

MET GLY SER SER HIS HIS HIS HIS HIS HIS SER S138 G139 L140 V141 P142 R143 G144 S145 H146 M147 T148 S149 R167 K170 T171 L172 E175 T186 E187 V191 C198 K199 L202 A209 T210 L211 M214 M215 Q219 G220 V221 G222 G223 P224 G225 H226 K227 A228 R229

V230
L231

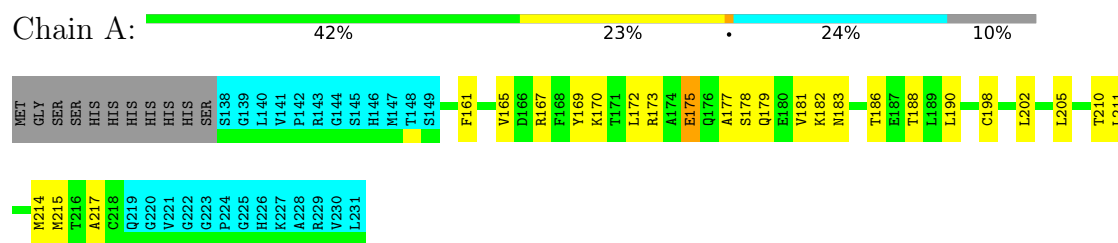
- Molecule 2: NYAD-13 stapled peptide inhibitor

Chain B: 

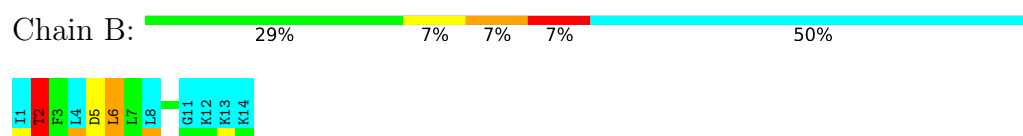
I1 I2 F3 L4 D5 L6 L7 L8 G11 G12 K13 K14

4.2.15 Score per residue for model 15

- Molecule 1: Capsid protein p24

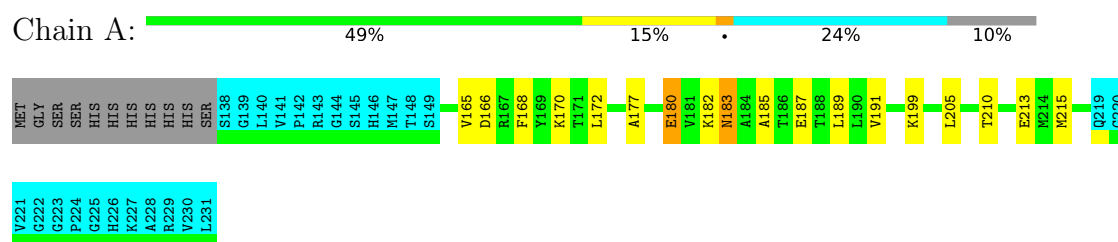


- Molecule 2: NYAD-13 stapled peptide inhibitor

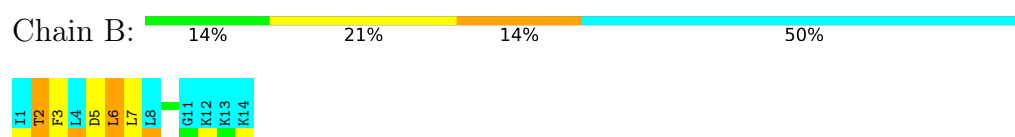


4.2.16 Score per residue for model 16

- Molecule 1: Capsid protein p24

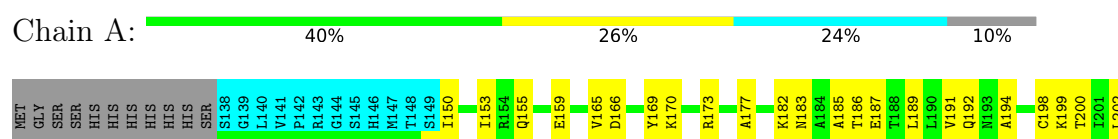


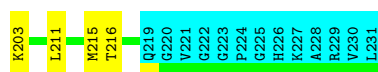
- Molecule 2: NYAD-13 stapled peptide inhibitor



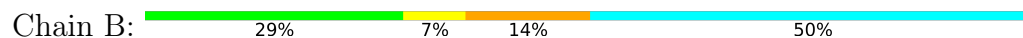
4.2.17 Score per residue for model 17

- Molecule 1: Capsid protein p24



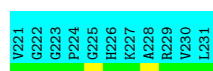


- Molecule 2: NYAD-13 stapled peptide inhibitor

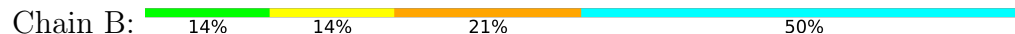


4.2.18 Score per residue for model 18

- Molecule 1: Capsid protein p24

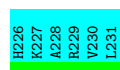


- Molecule 2: NYAD-13 stapled peptide inhibitor



4.2.19 Score per residue for model 19

- Molecule 1: Capsid protein p24

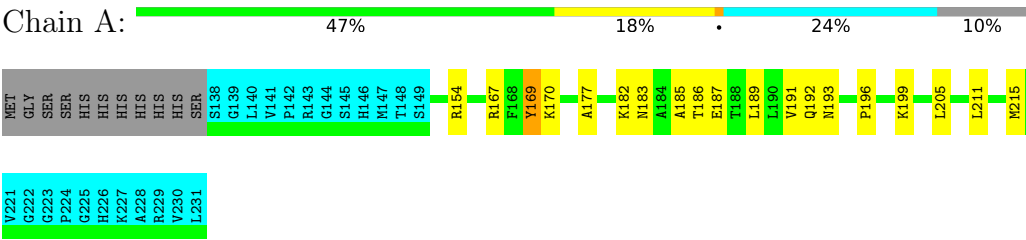


- Molecule 2: NYAD-13 stapled peptide inhibitor

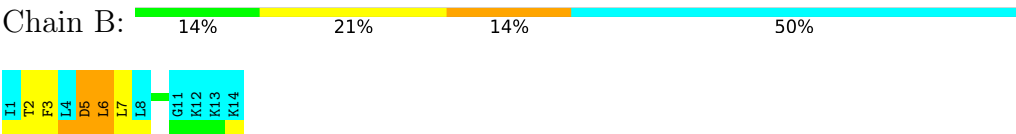


4.2.20 Score per residue for model 20

- Molecule 1: Capsid protein p24



- Molecule 2: NYAD-13 stapled peptide inhibitor



5 Refinement protocol and experimental data overview ⓘ

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

Of the 1000 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
ARIA	refinement	2.2

No chemical shift data was provided.

6 Model quality ⓘ

6.1 Standard geometry ⓘ

Bond lengths and bond angles in the following residue types are not validated in this section: MK8

There are no covalent bond-length or bond-angle outliers.

There are no bond-length outliers.

There are no bond-angle outliers.

There are no chirality outliers.

There are no planarity outliers.

6.2 Too-close contacts ⓘ

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in each chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes averaged over the ensemble.

Mol	Chain	Non-H	H(model)	H(added)	Clashes
1	A	539	556	546	11±3
2	B	66	61	60	4±2
All	All	12100	12340	12120	232

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 10.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:167:ARG:HA	1:A:170:LYS:HE2	0.83	1.48	20	3
1:A:186:THR:HA	1:A:189:LEU:HD11	0.75	1.59	7	2
1:A:166:ASP:O	1:A:170:LYS:HG2	0.70	1.86	16	2
1:A:183:ASN:O	1:A:187:GLU:HG3	0.66	1.88	17	8
1:A:185:ALA:O	1:A:189:LEU:HG	0.66	1.89	16	8
1:A:177:ALA:HB1	1:A:181:VAL:CG1	0.66	2.20	9	3
1:A:165:VAL:HG13	2:B:6:LEU:HD11	0.65	1.69	2	14
1:A:186:THR:HA	1:A:189:LEU:CD1	0.64	2.21	7	4
1:A:182:LYS:HE2	1:A:182:LYS:HA	0.61	1.71	6	1
2:B:6:LEU:H	2:B:6:LEU:HD13	0.61	1.56	13	2
1:A:183:ASN:HB3	2:B:2:THR:OG1	0.60	1.96	15	3

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:211:LEU:HB2	2:B:5:ASP:OD1	0.59	1.98	20	1
2:B:6:LEU:HD22	2:B:7:LEU:N	0.58	2.14	13	2
1:A:183:ASN:ND2	2:B:3:PHE:HB3	0.58	2.13	6	3
1:A:187:GLU:CD	2:B:2:THR:HG22	0.58	2.24	7	4
1:A:189:LEU:HA	1:A:192:GLN:HB3	0.57	1.76	10	5
1:A:198:CYS:O	1:A:202:LEU:HG	0.57	2.00	8	18
1:A:183:ASN:HD22	2:B:3:PHE:HB3	0.57	1.59	6	3
1:A:183:ASN:OD1	2:B:3:PHE:HB3	0.57	1.98	19	3
1:A:191:VAL:O	1:A:199:LYS:HE2	0.56	2.00	16	6
2:B:3:PHE:CZ	2:B:7:LEU:HD21	0.56	2.35	19	1
2:B:3:PHE:HA	2:B:6:LEU:HD11	0.56	1.77	13	2
1:A:178:SER:O	1:A:181:VAL:HG12	0.55	2.01	15	2
1:A:167:ARG:CA	1:A:170:LYS:HE2	0.54	2.30	20	1
1:A:169:TYR:HB2	2:B:6:LEU:HD12	0.54	1.79	11	2
1:A:177:ALA:HB1	1:A:181:VAL:HG11	0.53	1.80	9	3
1:A:183:ASN:HA	1:A:186:THR:HG22	0.52	1.81	10	2
1:A:183:ASN:HB2	2:B:2:THR:OG1	0.52	2.04	1	1
1:A:211:LEU:O	1:A:215:MET:HG2	0.52	2.04	1	8
1:A:166:ASP:O	1:A:170:LYS:HG3	0.52	2.04	2	2
1:A:177:ALA:O	1:A:182:LYS:HE3	0.52	2.05	17	6
2:B:3:PHE:CD1	2:B:6:LEU:HD21	0.52	2.40	13	2
1:A:172:LEU:O	1:A:175:GLU:HB2	0.51	2.06	15	1
1:A:180:GLU:HA	1:A:183:ASN:ND2	0.51	2.20	1	3
1:A:169:TYR:CZ	1:A:173:ARG:HD3	0.50	2.42	17	2
1:A:211:LEU:HD22	2:B:6:LEU:HD22	0.50	1.83	8	1
1:A:169:TYR:HB2	2:B:6:LEU:CD1	0.50	2.36	11	1
1:A:164:TYR:OH	1:A:193:ASN:HB2	0.49	2.08	5	4
1:A:172:LEU:HD21	1:A:186:THR:OG1	0.49	2.07	14	3
1:A:177:ALA:HB3	1:A:182:LYS:HE3	0.48	1.86	6	1
1:A:177:ALA:CB	1:A:182:LYS:HE2	0.47	2.39	2	1
1:A:211:LEU:HB2	2:B:5:ASP:OD2	0.47	2.09	18	1
1:A:169:TYR:CE1	1:A:173:ARG:HD2	0.47	2.44	13	1
1:A:211:LEU:O	1:A:215:MET:HG3	0.47	2.10	4	5
1:A:211:LEU:HD22	2:B:6:LEU:HB3	0.47	1.86	13	2
1:A:168:PHE:CE1	1:A:186:THR:HG23	0.47	2.44	2	2
1:A:191:VAL:O	1:A:199:LYS:HD3	0.47	2.10	9	1
1:A:183:ASN:HA	2:B:3:PHE:H	0.47	1.70	16	1
1:A:187:GLU:HG2	2:B:2:THR:HG22	0.46	1.86	17	8
1:A:161:PHE:CD2	1:A:215:MET:HA	0.46	2.45	15	2
1:A:169:TYR:O	1:A:173:ARG:HG3	0.46	2.11	4	3
1:A:186:THR:OG1	2:B:3:PHE:HB2	0.46	2.10	5	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:169:TYR:CD1	2:B:6:LEU:HD23	0.46	2.45	13	2
1:A:211:LEU:HB2	2:B:5:ASP:HB3	0.46	1.87	13	1
1:A:153:ILE:HG23	1:A:167:ARG:HG3	0.46	1.86	18	1
1:A:196:PRO:HA	1:A:199:LYS:HB3	0.46	1.87	20	1
1:A:209:ALA:HB3	1:A:214:MET:HE1	0.46	1.86	14	2
1:A:168:PHE:HE1	1:A:172:LEU:HD11	0.46	1.70	2	1
2:B:3:PHE:CE1	2:B:7:LEU:HD21	0.46	2.46	19	1
1:A:177:ALA:HB3	1:A:182:LYS:CG	0.46	2.41	13	2
1:A:189:LEU:HD12	1:A:190:LEU:N	0.45	2.26	18	1
1:A:183:ASN:HD22	1:A:183:ASN:N	0.45	2.09	8	1
1:A:154:ARG:HG2	1:A:155:GLN:N	0.45	2.26	19	1
1:A:168:PHE:CE1	1:A:172:LEU:HD11	0.45	2.47	3	3
1:A:177:ALA:O	1:A:182:LYS:HE2	0.45	2.12	4	2
1:A:162:ARG:HG3	1:A:163:ASP:N	0.45	2.27	4	2
1:A:165:VAL:CG1	2:B:6:LEU:HD11	0.44	2.43	18	3
1:A:183:ASN:O	1:A:186:THR:HG22	0.44	2.13	15	1
1:A:177:ALA:HB3	1:A:182:LYS:HE2	0.43	1.89	2	1
1:A:177:ALA:HB3	1:A:182:LYS:HG3	0.43	1.89	4	2
1:A:187:GLU:HG2	2:B:2:THR:HA	0.43	1.89	14	1
1:A:166:ASP:O	1:A:170:LYS:HE3	0.43	2.14	3	2
1:A:180:GLU:H	1:A:180:GLU:CD	0.43	2.21	16	1
1:A:175:GLU:HB3	1:A:182:LYS:HE3	0.43	1.90	2	1
1:A:186:THR:HB	2:B:2:THR:HA	0.43	1.90	12	1
1:A:183:ASN:HB3	2:B:2:THR:HB	0.43	1.89	7	1
1:A:203:LYS:NZ	1:A:203:LYS:HB3	0.43	2.28	1	1
1:A:210:THR:O	1:A:214:MET:HG2	0.43	2.14	15	1
1:A:177:ALA:HB3	1:A:182:LYS:HG2	0.43	1.90	2	1
1:A:198:CYS:SG	1:A:218:CYS:SG	0.42	3.16	11	1
1:A:210:THR:HG22	1:A:213:GLU:OE1	0.42	2.14	16	1
2:B:3:PHE:HA	2:B:6:LEU:CD1	0.42	2.45	20	1
1:A:205:LEU:CB	1:A:214:MET:HE1	0.42	2.45	6	1
1:A:205:LEU:CB	1:A:214:MET:HE3	0.42	2.44	8	1
1:A:169:TYR:O	1:A:173:ARG:HG2	0.42	2.13	15	1
1:A:178:SER:O	1:A:182:LYS:HG3	0.42	2.15	18	1
1:A:211:LEU:HD22	2:B:6:LEU:HA	0.42	1.91	13	1
1:A:205:LEU:HD11	1:A:217:ALA:CB	0.42	2.45	20	2
1:A:211:LEU:HG	1:A:215:MET:SD	0.42	2.55	19	1
1:A:200:THR:HA	1:A:203:LYS:HG2	0.41	1.91	17	1
1:A:155:GLN:HB3	1:A:194:ALA:HA	0.41	1.92	17	2
1:A:195:ASN:HB3	1:A:198:CYS:SG	0.41	2.55	11	1
1:A:177:ALA:CB	1:A:182:LYS:HE3	0.41	2.46	6	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:179:GLN:O	1:A:182:LYS:HG2	0.41	2.15	15	1
1:A:154:ARG:HA	1:A:193:ASN:HB3	0.41	1.93	20	1
1:A:171:THR:O	1:A:175:GLU:HG2	0.41	2.16	19	1
1:A:183:ASN:HB3	2:B:2:THR:CB	0.40	2.46	7	1
1:A:162:ARG:HA	1:A:215:MET:CE	0.40	2.47	13	1
1:A:163:ASP:O	1:A:166:ASP:HB3	0.40	2.16	13	1
1:A:191:VAL:HG12	1:A:199:LYS:HG3	0.40	1.94	17	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	69/105 (66%)	68±1 (99±1%)	1±1 (1±1%)	0±0 (0±1%)	31	76
2	B	7/14 (50%)	7±0 (94±7%)	0±0 (1±4%)	0±0 (4±7%)	3	28
All	All	1520/2380 (64%)	1493 (98%)	16 (1%)	11 (1%)	20	70

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)
2	B	2	THR	6
1	A	150	ILE	5

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	58/86 (67%)	56±1 (97±1%)	2±1 (3±1%)	38	86
2	B	7/11 (64%)	5±0 (69±6%)	2±0 (31±6%)	1	14

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1300/1940 (67%)	1224 (94%)	76 (6%)	20 69

All 18 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)
2	B	2	THR	20
2	B	6	LEU	20
1	A	205	LEU	8
1	A	188	THR	5
1	A	150	ILE	3
2	B	5	ASP	3
1	A	214	MET	2
1	A	169	TYR	2
1	A	162	ARG	2
1	A	183	ASN	2
1	A	152	ASP	2
1	A	176	GLN	1
1	A	189	LEU	1
1	A	175	GLU	1
1	A	180	GLU	1
1	A	159	GLU	1
1	A	170	LYS	1
2	B	7	LEU	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

2 non-standard protein/DNA/RNA residues are 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	MK8	B	8	2	5,8,9	1.15±0.11	0±0 (3±7%)
2	MK8	B	4	2	5,8,9	0.92±0.04	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	MK8	B	8	2	6,10,12	1.42±0.28	1±0 (13±6%)
2	MK8	B	4	2	6,10,12	0.93±0.27	1±0 (10±7%)

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	MK8	B	8	2	-	0±0,6,8,11	-
2	MK8	B	4	2	-	0±0,6,8,11	-

All unique bond outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
2	B	8	MK8	CB-CA	2.09	1.52	1.55	10	3

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
2	B	8	MK8	CG-CB-CA	3.99	109.51	115.41	17	16
2	B	4	MK8	CG-CB-CA	2.54	111.65	115.41	5	9
2	B	4	MK8	CB1-CA-CB	2.35	107.09	110.97	8	4

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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