Full wwPDB NMR Structure Validation Report (i)

Mar 6, 2022 – 05:02 PM EST

PDB ID	:	2KQN
Title	:	Solution structure of the AL-09 H87Y immunoglobulin light chain variable domain
Authors	:	Volkman, B.F.; Peterson, F.C.; Ramirez-Alvarado, M.; Baden, E.M.
Deposited on	:	2009-11-11

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 (i) symbol.

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

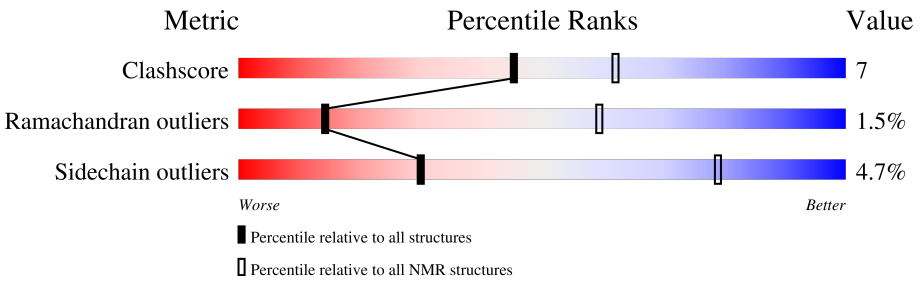
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.27
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.27

1 Overall quality at a glance (i)

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 <=5%

Mol	Chain	Length	Quality of chain
1	A	110	85% 14% •
1	B	110	78% 15% • • •

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 12 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:1-A:108, B:201-B:239, B:243-B:308 (213)	0.40	12

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 4 clusters and 2 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 3297 atoms, of which 1614 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Ig kappa chain V-I region AU.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	108	1648	529	807	136	173	3	0
1	B	108	1649	529	807	136	174	3	0

4 Residue-property plots (i)

4.1 Average score per residue in the NMR ensemble

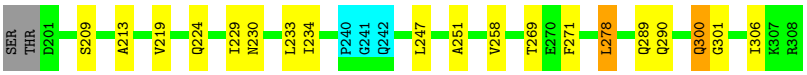
These plots are provided for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic is the same as shown in the summary in section 1 of this report. The second graphic shows the sequence where residues are colour-coded according to the number of geometric quality criteria for 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: Ig kappa chain V-I region AU

Chain A:

• Molecule 1: Ig kappa chain V-I region AU

Chain B:



4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

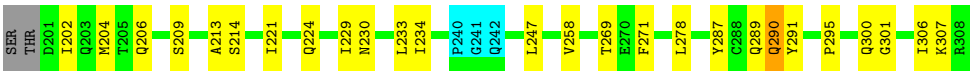
4.2.1 Score per residue for model 1

• Molecule 1: Ig kappa chain V-I region AU

Chain A:

• Molecule 1: Ig kappa chain V-I region AU

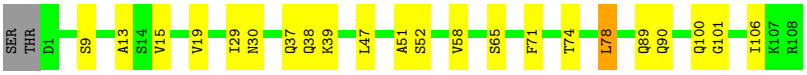
Chain B:



4.2.2 Score per residue for model 2

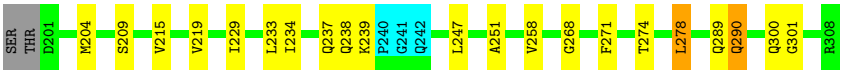
- Molecule 1: Ig kappa chain V-I region AU

Chain A:



- Molecule 1: Ig kappa chain V-I region AU

Chain B:



4.2.3 Score per residue for model 3

- Molecule 1: Ig kappa chain V-I region AU

Chain A:

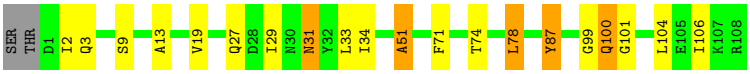
- Molecule 1: Ig kappa chain V-I region AU

Chain B:

4.2.4 Score per residue for model 4

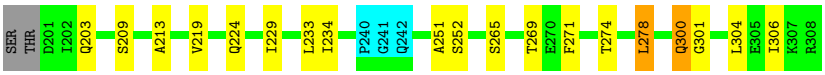
- Molecule 1: Ig kappa chain V-I region AU

Chain A:



- Molecule 1: Ig kappa chain V-I region AU

Chain B:



4.2.5 Score per residue for model 5

- Molecule 1: Ig kappa chain V-I region AU

Chain A:

- Molecule 1: Ig kappa chain V-I region AU

Chain B:

4.2.6 Score per residue for model 6

- Molecule 1: Ig kappa chain V-I region AU

Chain A:

- Molecule 1: Ig kappa chain V-I region AU

Chain B:

4.2.7 Score per residue for model 7

- Molecule 1: Ig kappa chain V-I region AU

Chain A:

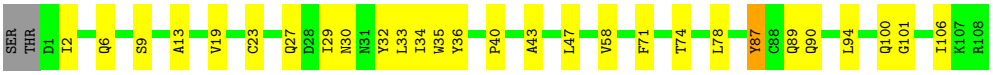
- Molecule 1: Ig kappa chain V-I region AU

Chain B:

4.2.8 Score per residue for model 8

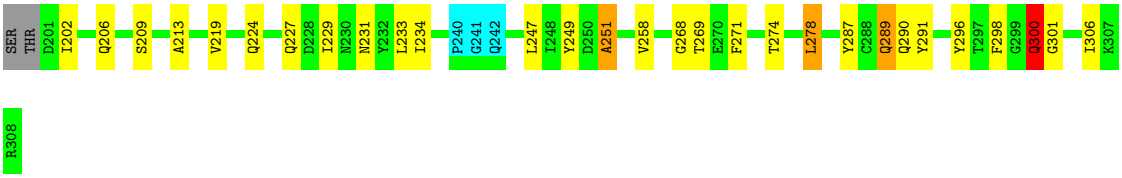
- Molecule 1: Ig kappa chain V-I region AU

Chain A:



- Molecule 1: Ig kappa chain V-I region AU

Chain B:



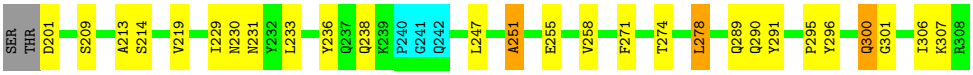
4.2.9 Score per residue for model 9

- Molecule 1: Ig kappa chain V-I region AU

Chain A:

- Molecule 1: Ig kappa chain V-I region AU

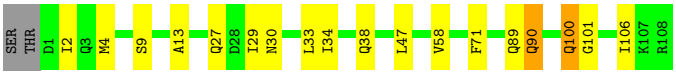
Chain B:



4.2.10 Score per residue for model 10

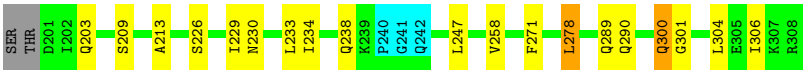
- Molecule 1: Ig kappa chain V-I region AU

Chain A:



- Molecule 1: Ig kappa chain V-I region AU

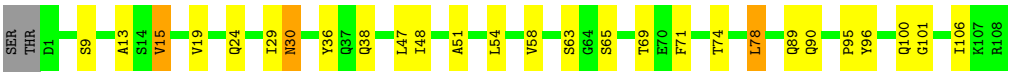
Chain B:



4.2.11 Score per residue for model 11

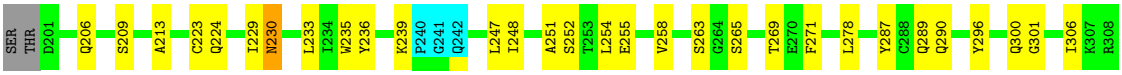
• Molecule 1: Ig kappa chain V-I region AU

Chain A:



• Molecule 1: Ig kappa chain V-I region AU

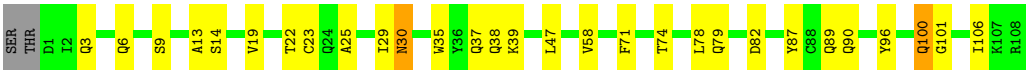
Chain B:



4.2.12 Score per residue for model 12 (medoid)

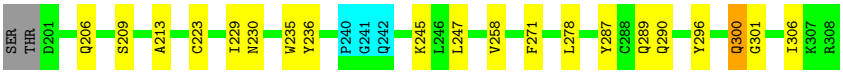
• Molecule 1: Ig kappa chain V-I region AU

Chain A:



• Molecule 1: Ig kappa chain V-I region AU

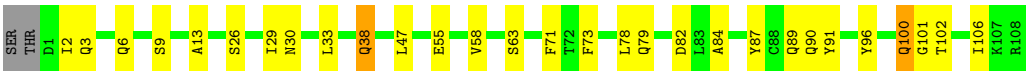
Chain B:



4.2.13 Score per residue for model 13

• Molecule 1: Ig kappa chain V-I region AU

Chain A:



• Molecule 1: Ig kappa chain V-I region AU

Chain B: 78% 15% • • •

SER THR D201 I202 A213 I229 N230 L233 I234 Q238 K239 P240 G241 Q242 L247 A251 V258 S265 F271 L278 A284 Q290 Y291 P295 Q300 I306 K307 R308

4.2.14 Score per residue for model 14

• Molecule 1: Ig kappa chain V-I region AU

Chain A: 76% 22% •

SER THR D1 I2 S9 A13 C23 Q27 D28 I29 N30 N31 W35 Y36 L47 A51 S52 V58 S63 G64 S65 F71 T72 F73 L78 Q89 P95 Y96 Q100 G101 I106 K107 R108

• Molecule 1: Ig kappa chain V-I region AU

Chain B: 71% 23% • • •

SER THR D201 Q206 S209 V219 T222 C223 Q224 I229 N230 W235 Q238 K239 P240 G241 Q242 L247 A251 E255 V258 S263 G264 S265 G268 T269 E270 F271 T272 F273 T274 L278 Q289 T297 F298 G299 Q300 G301 R308

4.2.15 Score per residue for model 15

• Molecule 1: Ig kappa chain V-I region AU

Chain A: 80% 17% • •

SER THR D1 I2 Q3 M4 T5 S9 A13 C23 Q24 I29 N30 N31 Q38 L47 V58 T69 E70 F71 L78 Q90 Q100 G101 L104 E105 I106 K107 R108

• Molecule 1: Ig kappa chain V-I region AU

Chain B: 69% 25% • • •

SER THR D201 I202 Q203 Q206 S209 S212 A213 C223 Q224 I229 N230 N231 Y232 L233 Q238 K239 P240 G241 Q242 L247 S252 V258 G264 T269 E270 F271 L278 A284 Q289 Q290 Y296 Q300 G301 L304 E305 I306 K307 R308

4.2.16 Score per residue for model 16

• Molecule 1: Ig kappa chain V-I region AU

Chain A: 81% 16% • •

SER THR D1 S9 A13 R18 I29 N30 L47 E55 V58 F71 I75 L78 Q89 Q90 Y96 T97 F98 G99 Q100 G101 L104 E105 I106 K107 R108

• Molecule 1: Ig kappa chain V-I region AU

Chain B: 79% 15%

SER THR D201 S209 A213 V219 I229 N230 N231 P240 G241 Q242 L247 A251 V258 F271 T274 L278 Q289 Q290 P295 Y296 Q300 G301 I306 K307 R308

4.2.17 Score per residue for model 17

- Molecule 1: Ig kappa chain V-I region AU

Chain A: 80% 17%

SER THR D1 M4 S9 A13 I29 N30 L33 I34 W35 P40 L47 V58 F71 L78 Q89 Q90 L94 T97 Q100 G101 I106 K107 R108

- Molecule 1: Ig kappa chain V-I region AU

Chain B: 68% 25%

SER THR D201 I202 Q203 M204 S209 A213 V219 C223 Q224 A225 I229 N230 L233 I234 Q238 K239 P240 G241 Q242 L247 I248 Y249 D250 A251 V258 S265 G266 F271 T274 L278 Q279 D282 Q289 Q290 Q300 G301 L304 E305 I306 K307 R308

4.2.18 Score per residue for model 18

- Molecule 1: Ig kappa chain V-I region AU

Chain A: 79% 19%

SER THR D1 S9 A13 Q24 I29 N30 L33 I34 W35 Y36 Q37 Q38 L46 L47 E55 V58 T69 E70 F71 L78 Q89 Q90 Q100 G101 I106 K107 R108

- Molecule 1: Ig kappa chain V-I region AU

Chain B: 71% 23%

SER THR D201 I202 Q206 S209 A213 I221 Q224 I229 N230 L233 I234 Q238 K239 P240 G241 Q242 L247 E255 V258 G268 T269 E270 F271 L278 Y287 C288 Q289 Q290 Q300 G301 T302 K303 L304 E305 I306 K307 R308

4.2.19 Score per residue for model 19

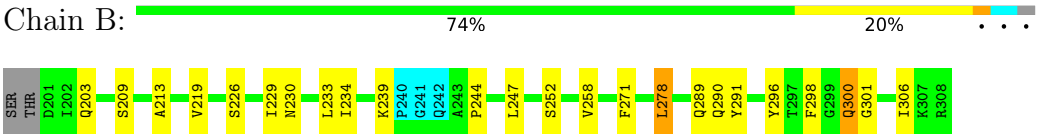
- Molecule 1: Ig kappa chain V-I region AU

Chain A: 77% 21%

SER THR D1 S9 A13 R18 Q24 I29 N30 L33 I34 P44 L47 V58 T69 E70 F71 I75 L78 Q89 Q90 Y91 Y96 T97 F98 G99 Q100 G101 I106 K107 R108

- Molecule 1: Ig kappa chain V-I region AU

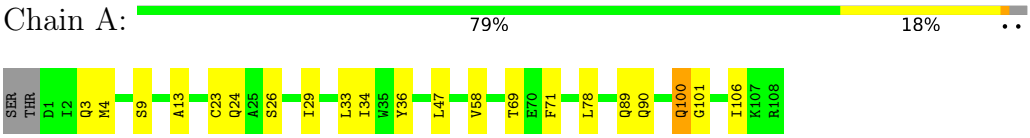
Chain B:



4.2.20 Score per residue for model 20

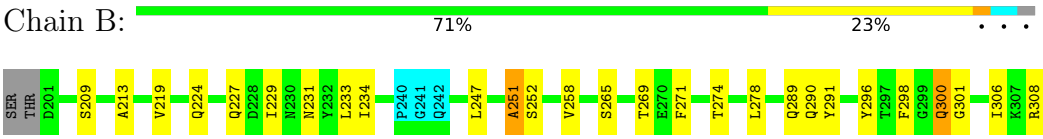
- Molecule 1: Ig kappa chain V-I region AU

Chain A:



- Molecule 1: Ig kappa chain V-I region AU

Chain B:



5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *AUTOMATED METHODS WERE USED FOR BACKBONE CHEMICAL SHIFT ASSIGNMENT AND ITERATIVE NOE REFINEMENT. FINAL STRUCTURES WERE OBTAINED BY MOLECULAR DYNAMICS IN EXPLICIT SOLVENT.*

Of the 100 calculated structures, 20 were deposited, based on the following criterion: *target function.*

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

Software name	Classification	Version
Xplor-NIH	refinement	2.9.3

No chemical shift data was provided.

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	841	807	809	11±3
1	B	822	789	788	12±3
All	All	33260	31920	31940	440

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:100:GLN:NE2	1:A:100:GLN:H	0.69	1.85	4	1
1:A:9:SER:HA	1:A:101:GLY:O	0.67	1.89	15	19
1:B:213:ALA:O	1:B:306:ILE:HA	0.65	1.92	10	18
1:B:209:SER:HA	1:B:301:GLY:O	0.65	1.92	8	18
1:A:13:ALA:O	1:A:106:ILE:HA	0.65	1.91	10	20
1:B:251:ALA:O	1:B:265:SER:HA	0.64	1.92	7	7
1:B:300:GLN:H	1:B:300:GLN:NE2	0.61	1.93	15	4
1:B:206:GLN:NE2	1:B:287:TYR:HA	0.61	2.10	1	2
1:B:204:MET:SD	1:B:290:GLN:HG3	0.61	2.36	17	2
1:B:289:GLN:NE2	1:B:296:TYR:HB3	0.61	2.11	9	4
1:A:6:GLN:NE2	1:A:87:TYR:HA	0.60	2.12	13	2
1:A:51:ALA:O	1:A:65:SER:HA	0.59	1.97	14	3
1:B:219:VAL:O	1:B:274:THR:HA	0.58	1.98	14	10

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:278:LEU:HD21	1:B:304:LEU:HD21	0.57	1.76	5	6
1:B:231:ASN:O	1:B:251:ALA:HB2	0.57	2.00	9	4
1:A:29:ILE:HD11	1:A:71:PHE:CZ	0.56	2.35	2	19
1:B:229:ILE:HD11	1:B:271:PHE:CZ	0.56	2.36	18	20
1:A:89:GLN:NE2	1:A:96:TYR:HB3	0.55	2.16	13	3
1:B:247:LEU:O	1:B:258:VAL:HG21	0.55	2.02	14	19
1:B:223:CYS:SG	1:B:235:TRP:CH2	0.55	3.00	14	3
1:A:47:LEU:O	1:A:58:VAL:HG21	0.54	2.02	13	19
1:A:78:LEU:HD21	1:A:104:LEU:HD21	0.54	1.80	15	5
1:A:29:ILE:HD11	1:A:71:PHE:CE2	0.53	2.39	19	5
1:A:23:CYS:SG	1:A:35:TRP:CH2	0.52	3.02	12	3
1:B:233:LEU:HD13	1:B:234:ILE:N	0.52	2.19	20	11
1:A:3:GLN:HB2	1:A:26:SER:OG	0.52	2.05	20	1
1:A:100:GLN:H	1:A:100:GLN:NE2	0.52	2.03	7	3
1:A:24:GLN:HA	1:A:69:THR:O	0.51	2.05	1	9
1:B:224:GLN:HA	1:B:269:THR:O	0.51	2.06	7	11
1:B:234:ILE:HD11	1:B:291:TYR:CD1	0.51	2.40	1	3
1:B:289:GLN:HB2	1:B:298:PHE:CD2	0.51	2.40	3	1
1:B:203:GLN:HB2	1:B:226:SER:HB2	0.51	1.83	19	1
1:B:204:MET:HE2	1:B:223:CYS:SG	0.50	2.47	17	1
1:A:63:SER:O	1:A:73:PHE:HA	0.50	2.06	14	2
1:A:79:GLN:HB2	1:A:82:ASP:OD2	0.50	2.07	13	4
1:A:52:SER:HA	1:A:64:GLY:O	0.50	2.07	1	2
1:B:203:GLN:O	1:B:225:ALA:HA	0.50	2.06	17	1
1:A:33:LEU:HD22	1:A:71:PHE:CG	0.50	2.41	9	2
1:A:3:GLN:O	1:A:25:ALA:HA	0.50	2.06	12	1
1:A:2:ILE:HB	1:A:90:GLN:NE2	0.49	2.22	7	1
1:B:223:CYS:HB2	1:B:235:TRP:CH2	0.49	2.43	7	1
1:A:43:ALA:HB2	1:B:300:GLN:HB3	0.49	1.85	8	1
1:B:279:GLN:HB2	1:B:282:ASP:OD2	0.49	2.07	17	1
1:B:229:ILE:HD11	1:B:271:PHE:CE2	0.49	2.42	8	7
1:A:34:ILE:HD11	1:A:91:TYR:CD1	0.49	2.43	9	1
1:B:289:GLN:HE22	1:B:296:TYR:HB3	0.48	1.68	19	4
1:A:19:VAL:O	1:A:74:THR:HA	0.48	2.08	8	8
1:A:31:ASN:O	1:A:51:ALA:HB2	0.48	2.09	4	2
1:A:37:GLN:CD	1:A:39:LYS:HE3	0.48	2.29	12	2
1:B:229:ILE:HD11	1:B:271:PHE:CE1	0.48	2.43	9	2
1:B:212:SER:O	1:B:307:LYS:HE3	0.47	2.08	7	1
1:A:87:TYR:HA	1:A:99:GLY:O	0.47	2.09	4	1
1:A:95:PRO:HB3	1:B:255:GLU:OE2	0.47	2.09	11	1
1:B:219:VAL:CG2	1:B:278:LEU:HD23	0.47	2.40	5	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:300:GLN:NE2	1:B:300:GLN:H	0.47	2.08	12	3
1:B:291:TYR:HA	1:B:296:TYR:CE1	0.47	2.45	9	6
1:A:33:LEU:HD13	1:A:34:ILE:N	0.47	2.24	17	11
1:A:15:VAL:HA	1:A:78:LEU:O	0.47	2.10	11	1
1:A:90:GLN:OE1	1:A:96:TYR:HA	0.47	2.10	5	2
1:A:89:GLN:HB2	1:A:98:PHE:CD1	0.47	2.44	3	1
1:B:206:GLN:OE1	1:B:287:TYR:HA	0.47	2.10	8	3
1:B:206:GLN:HE22	1:B:287:TYR:HA	0.46	1.69	1	2
1:A:94:LEU:HD13	1:B:249:TYR:CD1	0.46	2.44	17	2
1:B:202:ILE:HB	1:B:290:GLN:NE2	0.46	2.26	1	2
1:A:95:PRO:HB3	1:B:255:GLU:OE1	0.46	2.11	14	1
1:A:4:MET:HG3	1:A:97:THR:O	0.46	2.11	17	1
1:B:206:GLN:OE1	1:B:302:THR:HB	0.46	2.10	18	1
1:A:6:GLN:OE1	1:A:87:TYR:HA	0.46	2.11	12	2
1:A:89:GLN:HE22	1:A:96:TYR:HB3	0.46	1.69	13	4
1:A:89:GLN:HB2	1:A:98:PHE:CD2	0.46	2.46	16	1
1:B:202:ILE:HD12	1:B:290:GLN:HE21	0.46	1.71	17	2
1:B:219:VAL:HG21	1:B:278:LEU:HD23	0.46	1.87	2	4
1:A:2:ILE:HD13	1:A:29:ILE:HG22	0.45	1.87	7	3
1:A:44:PRO:HB2	1:B:298:PHE:CE1	0.45	2.46	3	1
1:B:212:SER:O	1:B:307:LYS:HE2	0.45	2.12	15	1
1:B:233:LEU:HD22	1:B:271:PHE:CG	0.45	2.46	9	5
1:A:55:GLU:OE1	1:B:295:PRO:HB3	0.45	2.12	13	3
1:A:19:VAL:HG21	1:A:78:LEU:HD23	0.45	1.89	9	3
1:B:261:ARG:NH1	1:B:279:GLN:HG3	0.45	2.27	7	1
1:B:201:ASP:N	1:B:295:PRO:HD2	0.45	2.27	9	1
1:B:234:ILE:O	1:B:288:CYS:HA	0.44	2.11	18	1
1:A:3:GLN:HB2	1:A:26:SER:HB2	0.44	1.89	7	2
1:B:202:ILE:HD13	1:B:229:ILE:CG2	0.44	2.42	13	1
1:A:14:SER:HA	1:A:106:ILE:HG23	0.44	1.90	12	1
1:B:238:GLN:O	1:B:284:ALA:HB1	0.44	2.13	13	1
1:B:206:GLN:OE1	1:B:221:ILE:HG21	0.44	2.13	18	2
1:B:237:GLN:CD	1:B:239:LYS:HE3	0.44	2.33	2	1
1:B:206:GLN:HG3	1:B:223:CYS:SG	0.44	2.52	15	1
1:B:229:ILE:HG12	1:B:268:GLY:O	0.44	2.12	7	3
1:B:203:GLN:HB3	1:B:226:SER:HB2	0.44	1.90	10	1
1:A:48:ILE:HG12	1:A:54:LEU:HD23	0.44	1.89	11	1
1:A:91:TYR:HA	1:A:96:TYR:CE1	0.44	2.48	13	3
1:A:36:TYR:CE2	1:B:298:PHE:HE1	0.44	2.31	8	1
1:A:36:TYR:CE1	1:B:298:PHE:HE1	0.44	2.31	14	1
1:A:44:PRO:HG2	1:B:298:PHE:CE2	0.43	2.48	19	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:B:252:SER:OG	1:B:265:SER:HA	0.43	2.13	20	1
1:A:5:THR:O	1:A:23:CYS:HA	0.43	2.12	15	1
1:A:12:SER:O	1:A:107:LYS:HE2	0.43	2.14	3	1
1:B:236:TYR:HE2	1:B:289:GLN:CB	0.43	2.26	11	1
1:A:29:ILE:HD11	1:A:71:PHE:CE1	0.43	2.49	7	1
1:A:33:LEU:HD22	1:A:71:PHE:CD1	0.43	2.48	7	1
1:A:6:GLN:OE1	1:A:102:THR:HB	0.43	2.13	13	1
1:A:18:ARG:HA	1:A:75:ILE:O	0.43	2.14	16	2
1:B:236:TYR:HE1	1:B:289:GLN:HB3	0.43	1.73	9	1
1:B:248:ILE:HG12	1:B:254:LEU:HD23	0.43	1.91	11	1
1:A:4:MET:SD	1:A:90:GLN:HG3	0.42	2.54	10	1
1:B:202:ILE:HG12	1:B:227:GLN:HB2	0.42	1.90	8	1
1:B:206:GLN:HA	1:B:222:THR:O	0.42	2.14	14	1
1:B:214:SER:HB2	1:B:307:LYS:HB2	0.42	1.92	1	1
1:B:202:ILE:HD13	1:B:229:ILE:HG22	0.42	1.92	1	1
1:B:214:SER:OG	1:B:307:LYS:HB2	0.42	2.15	9	1
1:A:33:LEU:HD22	1:A:71:PHE:CD2	0.42	2.50	13	1
1:A:2:ILE:HG12	1:A:27:GLN:HB2	0.42	1.91	8	1
1:A:38:GLN:O	1:A:84:ALA:HB1	0.41	2.14	13	1
1:B:239:LYS:HE2	1:B:239:LYS:HA	0.41	1.91	19	1
1:A:33:LEU:HD12	1:A:35:TRP:NE1	0.41	2.30	17	1
1:A:36:TYR:CE1	1:B:298:PHE:HE2	0.41	2.33	20	1
1:B:212:SER:HA	1:B:305:GLU:O	0.41	2.14	5	1
1:A:6:GLN:HA	1:A:22:THR:O	0.41	2.15	12	1
1:B:289:GLN:HA	1:B:297:THR:O	0.41	2.15	14	1
1:B:289:GLN:HB3	1:B:298:PHE:CD1	0.41	2.49	5	1
1:B:236:TYR:HE2	1:B:289:GLN:HB3	0.41	1.75	11	1
1:B:236:TYR:HA	1:B:245:LYS:O	0.41	2.15	12	1
1:A:98:PHE:CE2	1:B:244:PRO:HG2	0.41	2.51	19	1
1:A:2:ILE:HG12	1:A:27:GLN:HB3	0.41	1.93	4	4
1:A:36:TYR:HE2	1:A:89:GLN:HB3	0.41	1.75	11	2
1:B:263:SER:O	1:B:273:PHE:HA	0.41	2.16	14	1
1:B:266:GLY:HA3	1:B:271:PHE:HA	0.41	1.92	17	1
1:A:34:ILE:CG2	1:A:46:LEU:HG	0.40	2.46	18	1
1:A:4:MET:CE	1:A:23:CYS:SG	0.40	3.09	20	1
1:B:252:SER:HA	1:B:264:GLY:O	0.40	2.16	15	1
1:A:29:ILE:HD12	1:A:32:TYR:O	0.40	2.16	8	1
1:A:29:ILE:HG12	1:A:68:GLY:O	0.40	2.16	1	1
1:A:37:GLN:HB3	1:A:86:TYR:CE1	0.40	2.51	7	1
1:A:6:GLN:HE22	1:A:87:TYR:HA	0.40	1.73	13	1
1:B:284:ALA:O	1:B:304:LEU:HB3	0.40	2.17	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	106/110 (96%)	98±2 (92±2%)	7±2 (6±2%)	1±1 (1±1%)	15 61
1	B	103/110 (94%)	95±2 (92±2%)	6±2 (6±2%)	2±1 (2±1%)	13 57
All	All	4180/4400 (95%)	3859 (92%)	259 (6%)	62 (1%)	14 59

All 15 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	30	ASN	13
1	B	230	ASN	12
1	B	251	ALA	5
1	A	31	ASN	5
1	B	252	SER	4
1	B	268	GLY	4
1	B	231	ASN	4
1	B	300	GLN	3
1	A	100	GLN	3
1	A	52	SER	2
1	A	51	ALA	2
1	A	40	PRO	2
1	A	68	GLY	1
1	A	63	SER	1
1	B	263	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	95/97 (98%)	91±1 (95±1%)	4±1 (5±1%)	31 79

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	93/97 (96%)	89±1 (95±1%)	4±1 (5±1%)	30	79
All	All	3760/3880 (97%)	3584 (95%)	176 (5%)	30	79

All 29 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	100	GLN	20
1	B	278	LEU	20
1	A	78	LEU	19
1	B	300	GLN	19
1	A	90	GLN	17
1	B	290	GLN	17
1	B	238	GLN	9
1	B	289	GLN	8
1	A	38	GLN	8
1	A	89	GLN	7
1	A	3	GLN	4
1	B	203	GLN	4
1	A	4	MET	2
1	A	15	VAL	2
1	A	87	TYR	2
1	A	55	GLU	2
1	B	255	GLU	2
1	A	30	ASN	2
1	B	308	ARG	2
1	B	204	MET	1
1	B	215	VAL	1
1	A	28	ASP	1
1	A	81	GLU	1
1	B	281	GLU	1
1	B	282	ASP	1
1	B	307	LYS	1
1	B	230	ASN	1
1	A	108	ARG	1
1	B	227	GLN	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)

No chemical shift data were provided