



Full wwPDB NMR Structure Validation Report ⓘ

Mar 8, 2026 – 07:18 AM UTC

PDB ID : 2J5P / pdb_00002j5p
Title : E. coli FtsK gamma domain
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Deposited on : 2006-09-19

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We welcome your comments at validation@mail.wwpdb.org

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<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
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

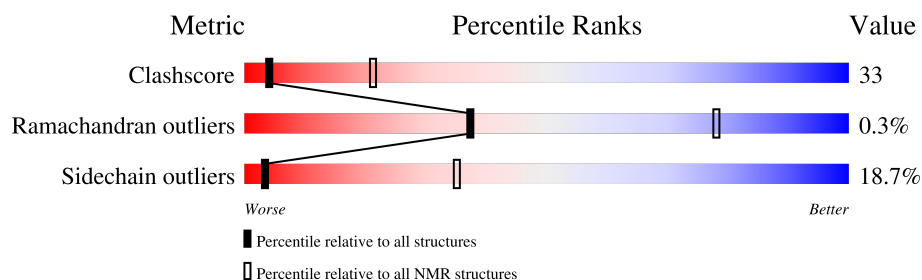
1 Overall quality at a glance

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	76	

2 Ensemble composition and analysis

This entry contains 20 models. Model 11 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:1265-A:1313, A:1319-A:1327 (58)	0.11	11

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 2 clusters. No single-model clusters were found.

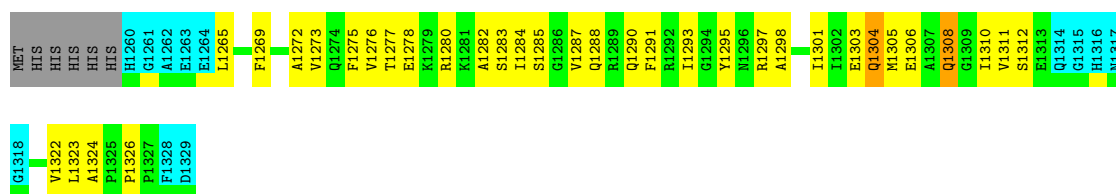
Cluster number	Models
1	1, 2, 4, 6, 7, 8, 9, 10, 11, 12, 14, 17, 20
2	3, 5, 13, 15, 16, 18, 19

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1094 atoms, of which 540 are hydrogens and 0 are deuteriums.

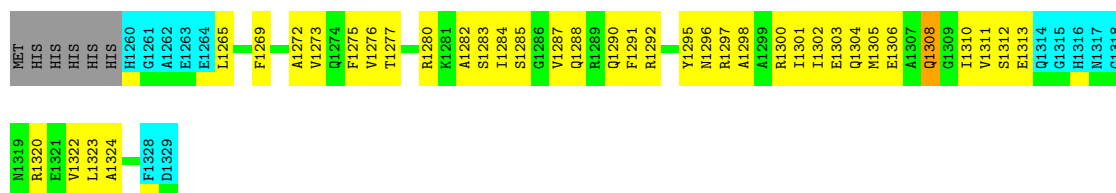
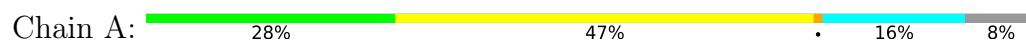
- Molecule 1 is a protein called DNA TRANSLOCASE FTSK.

Mol	Chain	Residues	Atoms						Trace
1	A	70	Total	C	H	N	O	S	0
			1094	343	540	104	106	1	



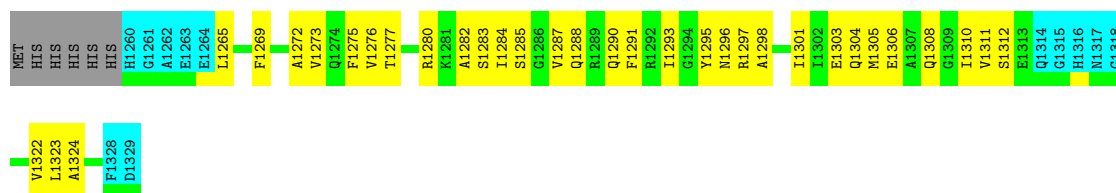
4.2.3 Score per residue for model 3

- Molecule 1: DNA TRANSLOCASE FTSK



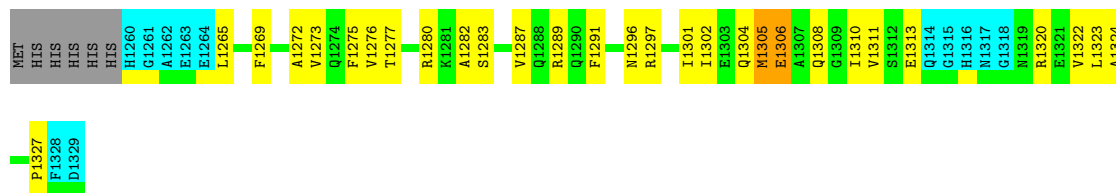
4.2.4 Score per residue for model 4

- Molecule 1: DNA TRANSLOCASE FTSK



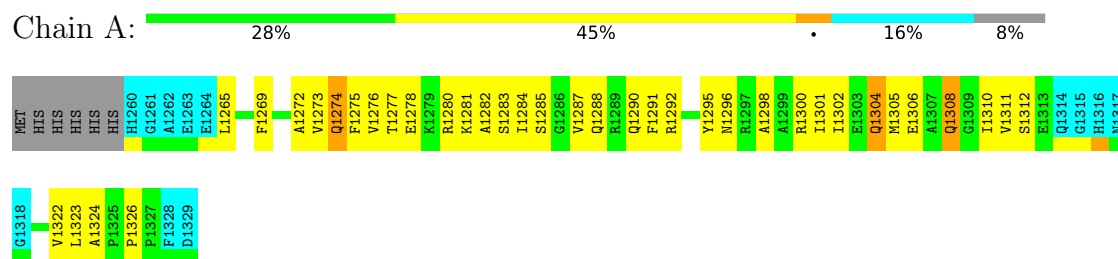
4.2.5 Score per residue for model 5

- Molecule 1: DNA TRANSLOCASE FTSK



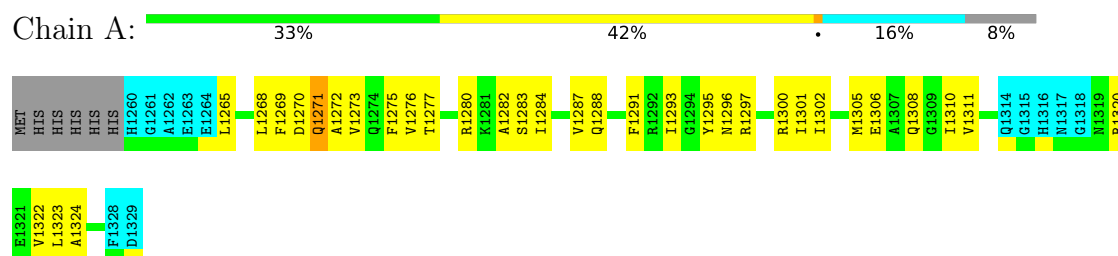
4.2.6 Score per residue for model 6

- Molecule 1: DNA TRANSLOCASE FTSK



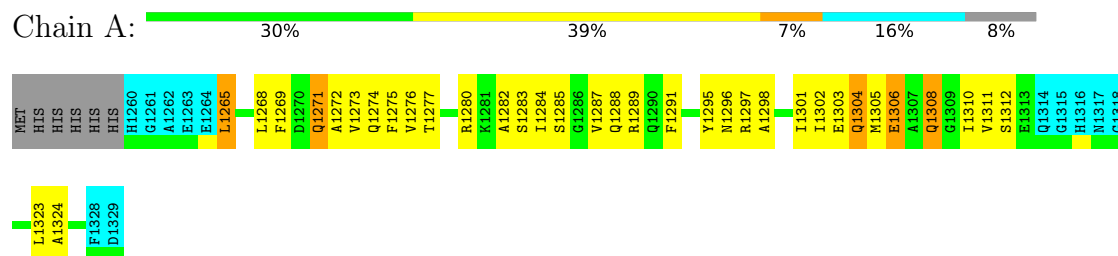
4.2.7 Score per residue for model 7

- Molecule 1: DNA TRANSLOCASE FTSK



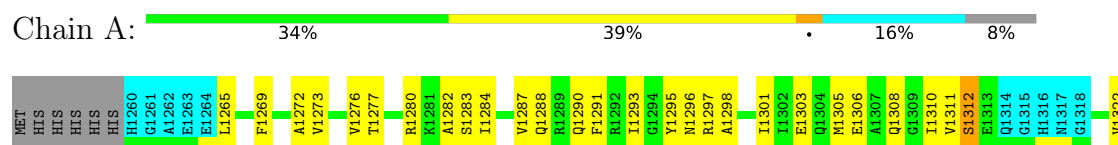
4.2.8 Score per residue for model 8

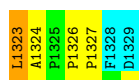
- Molecule 1: DNA TRANSLOCASE FTSK



4.2.9 Score per residue for model 9

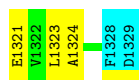
- Molecule 1: DNA TRANSLOCASE FTSK





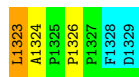
4.2.10 Score per residue for model 10

- Molecule 1: DNA TRANSLOCASE FTSK



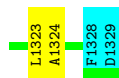
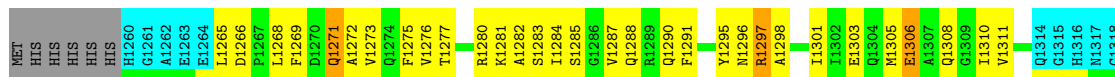
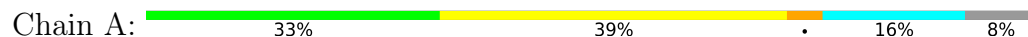
4.2.11 Score per residue for model 11 (medoid)

- Molecule 1: DNA TRANSLOCASE FTSK



4.2.12 Score per residue for model 12

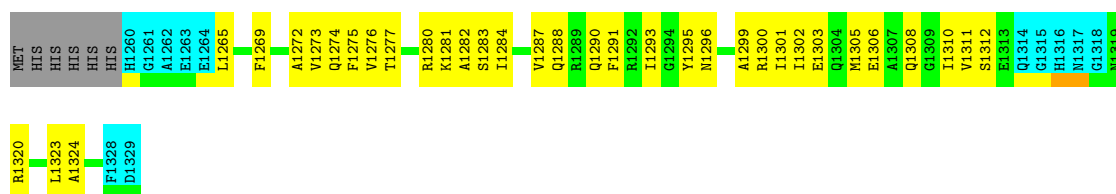
- Molecule 1: DNA TRANSLOCASE FTSK



4.2.13 Score per residue for model 13

- Molecule 1: DNA TRANSLOCASE FTSK

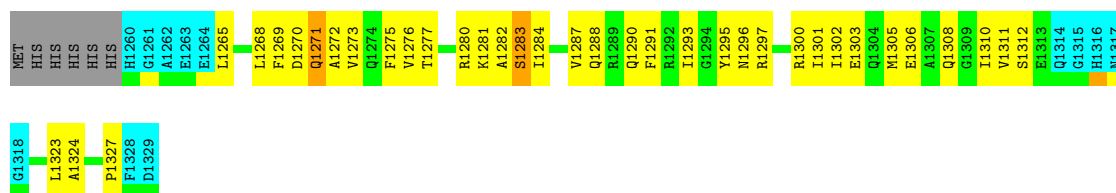




4.2.14 Score per residue for model 14

- Molecule 1: DNA TRANSLOCASE FTSK

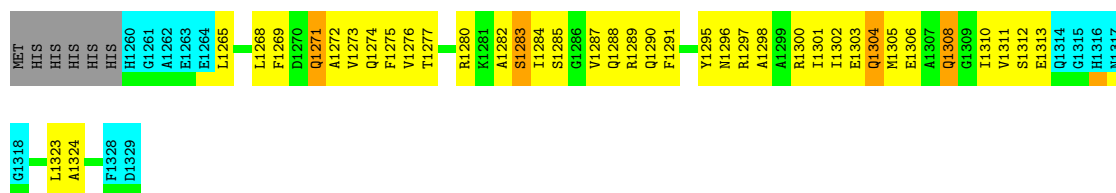
Chain A: 29% 45% 16% 8%



4.2.15 Score per residue for model 15

- Molecule 1: DNA TRANSLOCASE FTSK

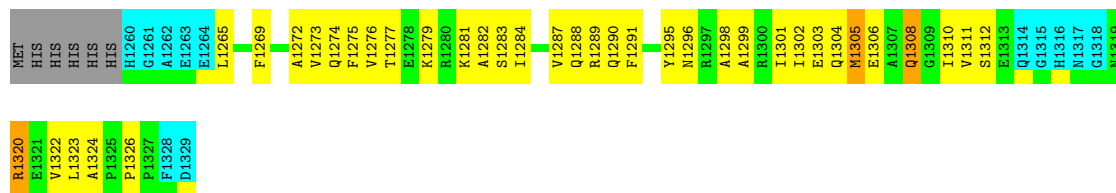
Chain A: 26% 45% 5% 16% 8%



4.2.16 Score per residue for model 16

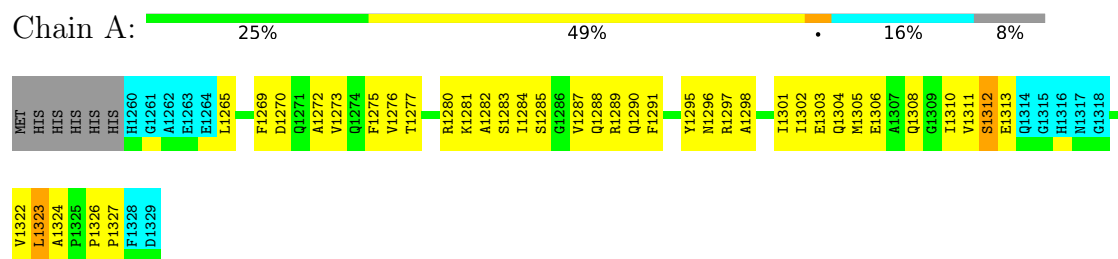
- Molecule 1: DNA TRANSLOCASE FTSK

Chain A: 28% 45% 16% 8%



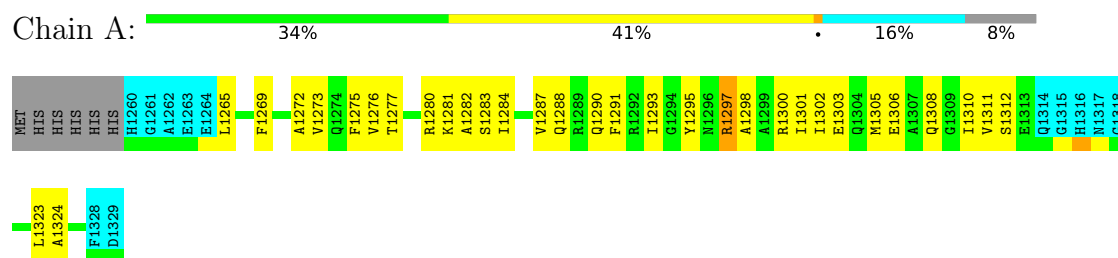
4.2.17 Score per residue for model 17

- Molecule 1: DNA TRANSLOCASE FTSK



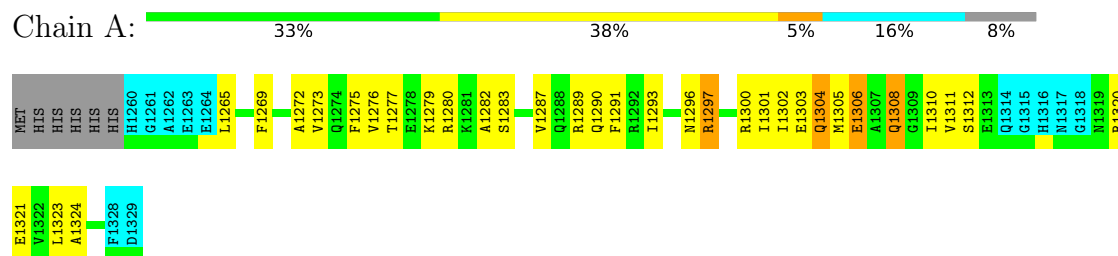
4.2.18 Score per residue for model 18

- Molecule 1: DNA TRANSLOCASE FTSK



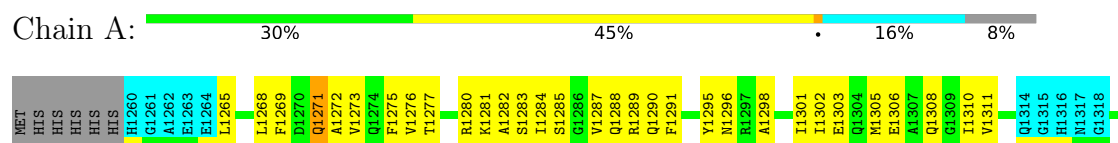
4.2.19 Score per residue for model 19

- Molecule 1: DNA TRANSLOCASE FTSK



4.2.20 Score per residue for model 20

- Molecule 1: DNA TRANSLOCASE FTSK



V1322
L1323
A1324
P1325
P1326
P1327
F1328
D1329

5 Refinement protocol and experimental data overview

The models were refined using the following method: *CNS*.

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *NO VIOLATIONS*.

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

Software name	Classification	Version
CNS	refinement	
ANSIG	structure solution	

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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	462	469	469	31±3
All	All	9240	9380	9380	613

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 33.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1277:THR:HG22	1:A:1324:ALA:O	0.78	1.78	13	20
1:A:1283:SER:O	1:A:1287:VAL:HG23	0.76	1.80	11	20
1:A:1265:LEU:HD22	1:A:1269:PHE:CD2	0.75	2.15	4	13
1:A:1265:LEU:HD21	1:A:1308:GLN:NE2	0.74	1.97	10	20
1:A:1269:PHE:O	1:A:1273:VAL:HG23	0.73	1.84	15	16
1:A:1284:ILE:HG23	1:A:1298:ALA:HB3	0.70	1.60	9	11
1:A:1265:LEU:HD13	1:A:1269:PHE:CD1	0.69	2.23	2	11
1:A:1284:ILE:HG23	1:A:1298:ALA:CB	0.64	2.22	9	13
1:A:1268:LEU:HD23	1:A:1271:GLN:NE2	0.63	2.08	8	5
1:A:1293:ILE:HG22	1:A:1297:ARG:NH1	0.62	2.10	4	5
1:A:1310:ILE:HG23	1:A:1324:ALA:HB3	0.61	1.70	9	20
1:A:1272:ALA:CB	1:A:1301:ILE:HG21	0.58	2.27	13	20
1:A:1302:ILE:HA	1:A:1305:MET:HE3	0.58	1.74	13	14
1:A:1269:PHE:CZ	1:A:1310:ILE:HD12	0.57	2.34	3	9

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1306:GLU:N	1:A:1311:VAL:HG22	0.56	2.15	12	20
1:A:1305:MET:C	1:A:1311:VAL:HG22	0.56	2.25	5	20
1:A:1269:PHE:CE2	1:A:1304:GLN:HB3	0.56	2.34	16	7
1:A:1265:LEU:HD22	1:A:1269:PHE:CG	0.56	2.36	5	3
1:A:1297:ARG:HH12	1:A:1301:ILE:HD11	0.55	1.61	12	1
1:A:1272:ALA:HA	1:A:1291:PHE:CZ	0.55	2.36	9	20
1:A:1269:PHE:CE1	1:A:1273:VAL:CG2	0.54	2.90	8	20
1:A:1288:GLN:NE2	1:A:1295:TYR:HB2	0.54	2.17	6	13
1:A:1284:ILE:CG2	1:A:1298:ALA:HB3	0.54	2.33	4	13
1:A:1305:MET:HB3	1:A:1311:VAL:HG13	0.54	1.80	10	16
1:A:1284:ILE:HD13	1:A:1299:ALA:HB2	0.53	1.80	16	2
1:A:1273:VAL:O	1:A:1277:THR:HG23	0.52	2.04	11	20
1:A:1273:VAL:HG13	1:A:1310:ILE:HD13	0.51	1.81	1	10
1:A:1273:VAL:CG1	1:A:1310:ILE:HD13	0.51	2.36	1	15
1:A:1269:PHE:CE1	1:A:1273:VAL:HG21	0.51	2.41	8	8
1:A:1283:SER:C	1:A:1302:ILE:HD11	0.50	2.31	13	1
1:A:1295:TYR:C	1:A:1295:TYR:CD1	0.50	2.90	9	1
1:A:1271:GLN:HB3	1:A:1291:PHE:CE2	0.50	2.41	12	2
1:A:1302:ILE:HA	1:A:1305:MET:HE2	0.49	1.85	5	2
1:A:1287:VAL:O	1:A:1291:PHE:HB2	0.48	2.08	1	13
1:A:1273:VAL:HG13	1:A:1310:ILE:HG21	0.48	1.85	14	8
1:A:1291:PHE:CD1	1:A:1291:PHE:N	0.48	2.82	3	13
1:A:1276:VAL:HG12	1:A:1282:ALA:HA	0.47	1.84	5	20
1:A:1282:ALA:HB2	1:A:1322:VAL:HG22	0.47	1.86	9	11
1:A:1284:ILE:HG21	1:A:1295:TYR:CE1	0.47	2.45	3	14
1:A:1284:ILE:CG2	1:A:1295:TYR:CE1	0.46	2.98	13	3
1:A:1311:VAL:HG21	1:A:1320:ARG:HD2	0.46	1.88	5	3
1:A:1297:ARG:NH1	1:A:1301:ILE:HD11	0.46	2.26	12	1
1:A:1273:VAL:CG2	1:A:1310:ILE:HD13	0.45	2.41	8	3
1:A:1288:GLN:NE2	1:A:1295:TYR:CB	0.45	2.80	9	4
1:A:1268:LEU:HD12	1:A:1297:ARG:NH1	0.45	2.26	12	1
1:A:1275:PHE:CD2	1:A:1291:PHE:CE1	0.45	3.04	16	14
1:A:1305:MET:HB3	1:A:1311:VAL:HG22	0.44	1.90	16	1
1:A:1284:ILE:HG12	1:A:1302:ILE:HD12	0.44	1.89	18	1
1:A:1265:LEU:CD2	1:A:1308:GLN:NE2	0.44	2.80	2	7
1:A:1291:PHE:N	1:A:1291:PHE:CD1	0.43	2.87	14	7
1:A:1306:GLU:N	1:A:1311:VAL:CG2	0.43	2.81	7	13
1:A:1285:SER:HA	1:A:1288:GLN:OE1	0.43	2.14	11	11
1:A:1269:PHE:HA	1:A:1301:ILE:HG23	0.43	1.91	12	4
1:A:1282:ALA:N	1:A:1322:VAL:CG2	0.43	2.82	9	10
1:A:1269:PHE:CE2	1:A:1304:GLN:CB	0.43	3.02	5	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:1288:GLN:CG	1:A:1293:ILE:O	0.43	2.67	14	3
1:A:1265:LEU:HD13	1:A:1269:PHE:CG	0.42	2.48	2	1
1:A:1277:THR:HB	1:A:1326:PRO:N	0.42	2.29	2	8
1:A:1312:SER:CB	1:A:1323:LEU:HD11	0.42	2.44	11	3
1:A:1276:VAL:O	1:A:1280:ARG:N	0.42	2.52	19	19
1:A:1302:ILE:HG21	1:A:1320:ARG:HG3	0.42	1.90	10	1
1:A:1275:PHE:CD1	1:A:1275:PHE:C	0.41	2.98	12	14
1:A:1268:LEU:HD23	1:A:1271:GLN:HE21	0.41	1.74	20	2
1:A:1288:GLN:NE2	1:A:1295:TYR:HA	0.41	2.30	9	1
1:A:1266:ASP:OD2	1:A:1297:ARG:NH2	0.41	2.54	12	1
1:A:1288:GLN:NE2	1:A:1295:TYR:CA	0.41	2.84	9	1
1:A:1274:GLN:O	1:A:1278:GLU:HB2	0.40	2.16	6	1
1:A:1272:ALA:HB3	1:A:1301:ILE:HG21	0.40	1.92	12	1
1:A:1281:LYS:C	1:A:1322:VAL:CG2	0.40	2.95	16	1
1:A:1293:ILE:CG2	1:A:1297:ARG:NH1	0.40	2.83	9	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	58/76 (76%)	57±1 (99±1%)	1±1 (1±1%)	0±0 (0±1%)	37	78
All	All	1160/1520 (76%)	1143 (99%)	13 (1%)	4 (0%)	37	78

All 1 unique Ramachandran outliers are listed below.

Mol	Chain	Res	Type	Models (Total)
1	A	1327	PRO	4

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	49/63 (78%)	40±2 (81±5%)	9±2 (19±5%)	3	35
All	All	980/1260 (78%)	797 (81%)	183 (19%)	3	35

All 25 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	1323	LEU	20
1	A	1290	GLN	16
1	A	1303	GLU	16
1	A	1312	SER	16
1	A	1296	ASN	16
1	A	1297	ARG	13
1	A	1300	ARG	10
1	A	1281	LYS	9
1	A	1289	ARG	9
1	A	1304	GLN	7
1	A	1308	GLN	7
1	A	1271	GLN	7
1	A	1320	ARG	5
1	A	1313	GLU	5
1	A	1274	GLN	5
1	A	1306	GLU	4
1	A	1270	ASP	3
1	A	1279	LYS	3
1	A	1278	GLU	2
1	A	1292	ARG	2
1	A	1305	MET	2
1	A	1321	GLU	2
1	A	1283	SER	2
1	A	1265	LEU	1
1	A	1288	GLN	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

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