Full wwPDB NMR Structure Validation Report (i)

Oct 10, 2021 – 06:13 PM EDT

PDB ID	:	2K6X
Title	:	Autoregulation of a Group 1 Bacterial Sigma Factor Involves the Formation of a Region 1.1- Induced Compacted Structure
Authors	:	Schwartz, E.C.; Shekhtman, A.; Dutta, K.; Pratt, M.R.; Cowburn, D.; Darst, S.; Muir, T.W.
Deposited on	:	2008-07-28

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:

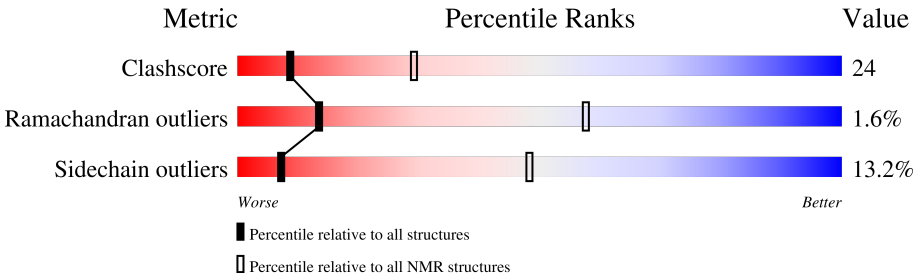
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.23.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.23.2

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	72	43% 35% • 18%

2 Ensemble composition and analysis (i)

This entry contains 20 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: *fewest violations*.

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:28-A:86 (59)	0.42	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 3 clusters and 1 single-model cluster was found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 1165 atoms, of which 578 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called RNA polymerase sigma factor rpoD.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	72	1165	370	578	98	118	1	0

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLY	-	expression tag	UNP P77994
A	26	SER	-	expression tag	UNP P77994
A	27	HIS	-	expression tag	UNP P77994
A	28	MET	-	expression tag	UNP P77994
A	96	GLY	SER	engineered mutation	UNP P77994

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: RNA polymerase sigma factor rpoD

Chain A: 43% 35% • 18%

G25 S26 H27 M28 I31 R34 I35 K36 K37 L38 I39 S40 L41 G42 K43 K44 K45 I48 T49 D52 K55 A56 F57 P58 P59 D60 F61 L68 R71 I72 H73 E74 E75 L76 E77 K78 I81 N82 I83 V84 E87 P88 E89 E90 E91 E92 I93 S94 A95 G96

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: RNA polymerase sigma factor rpoD

Chain A: 42% 35% 6% 18%

G25 S26 H27 I31 R34 I35 K36 K37 L38 I39 S40 L41 G42 K43 K44 K45 I48 D52 K55 A56 F57 P58 P59 N67 L68 R71 I72 H73 E74 E75 L76 E77 K78 I81 N82 I83 V84 E87 P88 E89 E90 E91 E92 I93 S94 A95 G96

4.2.2 Score per residue for model 2

• Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 35% 42% 6% 18%

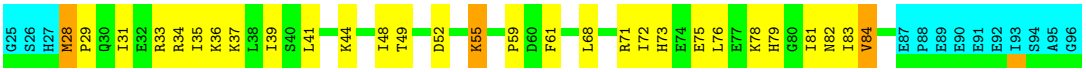
G25 S26 H27 M28 P29 Q30 I31 E32 R33 R34 I35 K36 K37 L38 I39 S40 L41 G42 K43 K44 K45 I48 T49 Y50 E51 D52 I53 D54 K55 A56 F57 P58 P59 D60 F61 D65 L68 I69 E70 R71 I72 H73 E74 E75 H79 I83 V84 E87 P88 E89 E90 E91 E92 I93

S94 A95 G96

4.2.3 Score per residue for model 3

- Molecule 1: RNA polymerase sigma factor rpoD

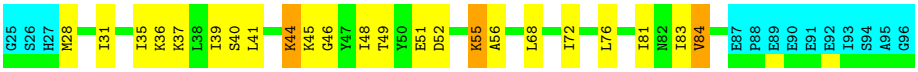
Chain A: 42% 36% • 18%



4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 50% 28% • 18%



4.2.5 Score per residue for model 5

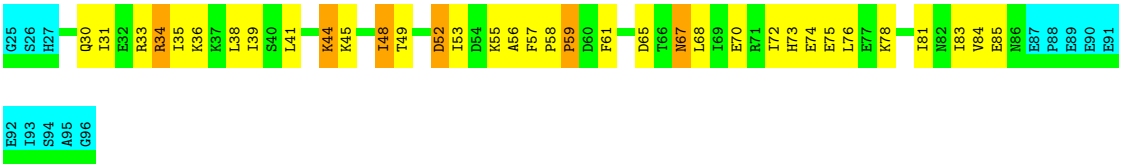
- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 46% 29% 7% 18%

4.2.6 Score per residue for model 6

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 33% 40% 8% 18%



4.2.7 Score per residue for model 7

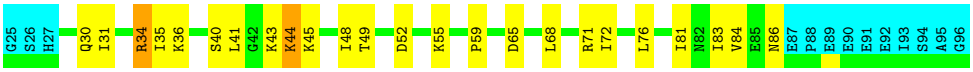
- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 50% 26% 6% 18%

4.2.8 Score per residue for model 8

- Molecule 1: RNA polymerase sigma factor rpoD

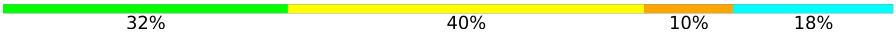
Chain A:

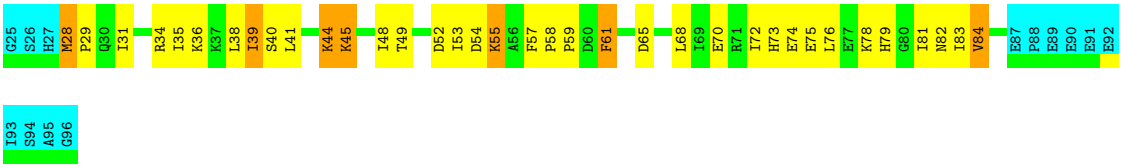


4.2.9 Score per residue for model 9

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A:

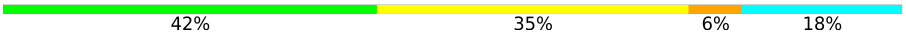


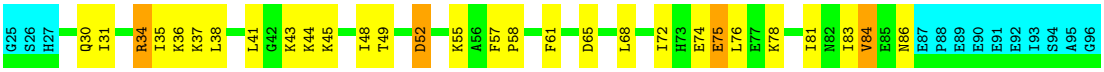


4.2.10 Score per residue for model 10

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A:

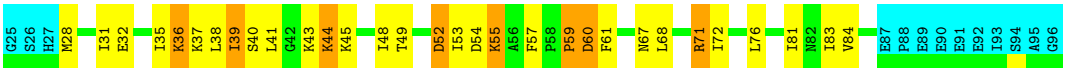




4.2.11 Score per residue for model 11

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A:



4.2.12 Score per residue for model 12

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 40% 36% 6% 18%

G25 S26 H27 M28 P29 Q30 I31 E32 R33 R34 I35 K36 K37 L38 I39 S40 L41 K44 K45 I48 T49 D52 K55 A56 F57 P58 P59 D60 F61 N67 L68 R71 I72 L76 H79 G80 I81 N82 I83 V84 E87 P88 E89 E90 E91 E92 I93 S94 A95 G96

4.2.13 Score per residue for model 13

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 42% 33% 7% 18%

G25 S26 H27 I31 E32 R33 R34 I35 K36 I39 S40 L41 K44 I48 T49 D52 I53 D54 K55 A56 F57 P58 P59 D60 F61 T66 N67 L68 I72 H73 E74 E75 L76 E77 K78 I81 N82 I83 V84 E85 N86 E87 P88 E89 E90 E91 E92 I93 S94 A95 G96

4.2.14 Score per residue for model 14

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 32% 44% 6% 18%

G25 S26 H27 M28 P29 Q30 I31 E32 R33 R34 I35 K36 K37 L38 I39 S40 L41 G42 K43 K44 K45 I48 T49 D52 I53 D54 K55 A56 P59 D60 F61 E62 L68 I69 E70 H73 E74 E75 L76 E77 K78 H79 G80 I81 N82 I83 V84 E85 N86 E87 P88 E89 E90 E91 E92 I93 S94 A95 G96

4.2.15 Score per residue for model 15

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 51% 25% 6% 18%

G25 S26 H27 I31 R34 I35 K36 K37 L38 I39 S40 L41 K44 K45 I48 T49 D52 K55 P59 D60 L68 I72 L76 I81 N82 I83 V84 E87 P88 E89 E90 E91 E92 I93 S94 A95 G96

4.2.16 Score per residue for model 16

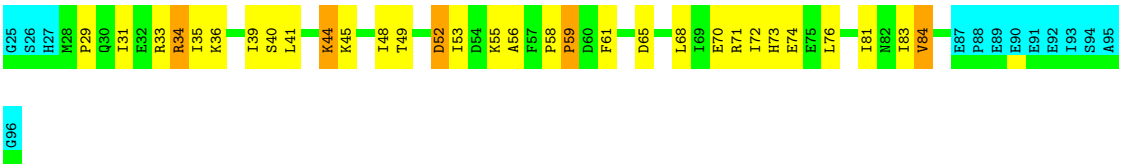
- Molecule 1: RNA polymerase sigma factor rpoD

Chain A: 32% 38% 12% 18%

4.2.17 Score per residue for model 17

- Molecule 1: RNA polymerase sigma factor rpoD

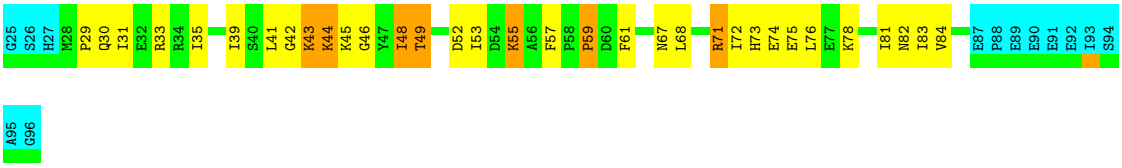
Chain A: 39% 36% 7% 18%



4.2.18 Score per residue for model 18

- Molecule 1: RNA polymerase sigma factor rpoD

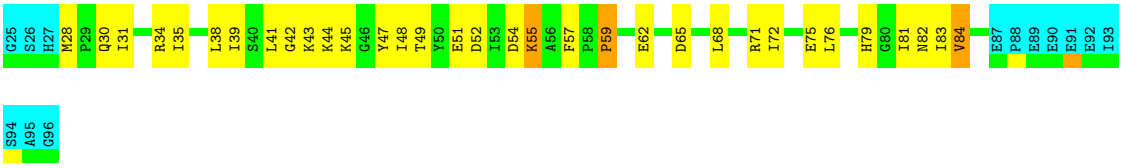
Chain A: 36% 36% 10% 18%



4.2.19 Score per residue for model 19

- Molecule 1: RNA polymerase sigma factor rpoD

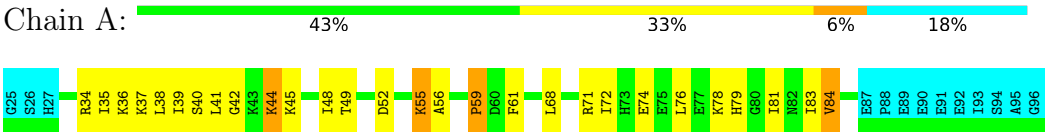
Chain A: 36% 42% • 18%



4.2.20 Score per residue for model 20

- Molecule 1: RNA polymerase sigma factor rpoD

Chain A:


43%
33%
6%
18%
G25 S26 H27 R34 I35 K36 K37 L38 I39 S40 L41 G42 K43 K44 K45 I48 T49 D52 K55 A56 P59 D60 F61 L68 R71 I72 H73 E74 E75 L76 E77 K78 H79 G80 I81 N82 I83 V84 E87 P88 E89 E90 E91 E92 I93 S94 A95 G96

5 Refinement protocol and experimental data overview (i)

The models were refined using the following method: *DGSA-distance geometry simulated annealing*.

Of the 512 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
CNS	refinement	

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	491	499	497	23±4
All	All	9820	9980	9940	466

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 24.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:THR:HB	1:A:84:VAL:HG13	1.02	1.25	6	2
1:A:39:ILE:HD11	1:A:83:ILE:HB	0.92	1.41	11	3
1:A:76:LEU:HA	1:A:81:ILE:HG22	0.89	1.44	3	10
1:A:41:LEU:HA	1:A:44:LYS:HE2	0.87	1.44	16	1
1:A:45:LYS:HE3	1:A:56:ALA:HA	0.86	1.46	5	5
1:A:52:ASP:HA	1:A:55:LYS:HD2	0.86	1.46	8	12
1:A:76:LEU:HD23	1:A:81:ILE:HG23	0.83	1.50	8	9
1:A:45:LYS:HE2	1:A:56:ALA:HA	0.80	1.51	12	3
1:A:41:LEU:HA	1:A:44:LYS:HE3	0.80	1.54	3	3
1:A:34:ARG:HD2	1:A:61:PHE:HA	0.77	1.53	3	2
1:A:45:LYS:HE3	1:A:45:LYS:HA	0.74	1.58	9	1
1:A:52:ASP:HA	1:A:55:LYS:CG	0.71	2.15	7	6
1:A:76:LEU:HD21	1:A:83:ILE:HG22	0.71	1.62	8	6
1:A:34:ARG:HD3	1:A:61:PHE:HA	0.70	1.64	16	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:MET:HB3	1:A:29:PRO:HD3	0.69	1.64	9	1
1:A:49:THR:HA	1:A:84:VAL:O	0.68	1.88	15	10
1:A:34:ARG:HA	1:A:34:ARG:HE	0.67	1.50	8	2
1:A:54:ASP:HA	1:A:57:PHE:CD2	0.67	2.24	11	3
1:A:52:ASP:HA	1:A:55:LYS:HG3	0.66	1.67	7	5
1:A:74:GLU:O	1:A:78:LYS:HG2	0.65	1.91	1	5
1:A:49:THR:HG23	1:A:52:ASP:HB2	0.65	1.68	18	1
1:A:29:PRO:O	1:A:33:ARG:HG3	0.65	1.91	18	2
1:A:48:ILE:O	1:A:84:VAL:HG12	0.64	1.93	18	2
1:A:45:LYS:HB3	1:A:55:LYS:HD3	0.63	1.69	5	6
1:A:41:LEU:HA	1:A:44:LYS:CE	0.63	2.22	16	2
1:A:41:LEU:O	1:A:45:LYS:HG2	0.63	1.93	14	17
1:A:45:LYS:HB3	1:A:55:LYS:HE2	0.61	1.71	4	3
1:A:42:GLY:HA2	1:A:52:ASP:OD1	0.61	1.94	18	4
1:A:49:THR:HB	1:A:84:VAL:CG1	0.61	2.13	6	1
1:A:35:ILE:HD11	1:A:71:ARG:HG3	0.61	1.70	20	3
1:A:59:PRO:HG2	1:A:61:PHE:CD2	0.61	2.30	12	1
1:A:31:ILE:O	1:A:35:ILE:HG12	0.61	1.96	9	1
1:A:40:SER:O	1:A:44:LYS:HE3	0.60	1.96	17	9
1:A:32:GLU:HG2	1:A:71:ARG:HD3	0.60	1.72	11	1
1:A:29:PRO:O	1:A:33:ARG:HG2	0.60	1.96	12	3
1:A:45:LYS:HB2	1:A:52:ASP:OD1	0.60	1.96	19	5
1:A:57:PHE:HD1	1:A:59:PRO:HD3	0.60	1.56	11	1
1:A:52:ASP:CG	1:A:55:LYS:HD3	0.59	2.15	19	5
1:A:35:ILE:HG23	1:A:72:ILE:HG12	0.59	1.74	8	2
1:A:31:ILE:O	1:A:35:ILE:HG13	0.59	1.98	17	15
1:A:52:ASP:HA	1:A:55:LYS:CD	0.59	2.27	16	13
1:A:37:LYS:O	1:A:41:LEU:HG	0.59	1.98	15	8
1:A:41:LEU:CA	1:A:44:LYS:HE3	0.58	2.26	3	3
1:A:36:LYS:HD3	1:A:81:ILE:HD12	0.58	1.74	13	11
1:A:52:ASP:O	1:A:55:LYS:HG3	0.58	1.98	2	3
1:A:52:ASP:O	1:A:55:LYS:HG2	0.58	1.99	5	7
1:A:38:LEU:HD11	1:A:61:PHE:CZ	0.58	2.33	10	1
1:A:61:PHE:HE2	1:A:68:LEU:HD22	0.58	1.59	9	1
1:A:49:THR:CB	1:A:84:VAL:HG13	0.57	2.17	6	2
1:A:28:MET:HB2	1:A:29:PRO:HD3	0.57	1.77	3	1
1:A:59:PRO:HD2	1:A:61:PHE:CD1	0.57	2.34	7	5
1:A:70:GLU:HA	1:A:73:HIS:CE1	0.56	2.34	9	2
1:A:31:ILE:HD12	1:A:68:LEU:HD13	0.56	1.77	16	1
1:A:67:ASN:O	1:A:71:ARG:HG2	0.56	2.01	12	2
1:A:34:ARG:NH1	1:A:38:LEU:HD11	0.56	2.15	9	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:49:THR:O	1:A:53:ILE:HG12	0.55	2.01	6	10
1:A:39:ILE:HG13	1:A:83:ILE:HG12	0.55	1.78	19	1
1:A:75:GLU:HA	1:A:78:LYS:HG2	0.55	1.79	13	1
1:A:34:ARG:HD3	1:A:60:ASP:O	0.55	2.01	15	1
1:A:39:ILE:HD11	1:A:83:ILE:HG12	0.55	1.79	9	2
1:A:59:PRO:HD2	1:A:61:PHE:HD1	0.55	1.62	11	3
1:A:31:ILE:HG23	1:A:68:LEU:HD13	0.55	1.77	7	2
1:A:68:LEU:O	1:A:72:ILE:HG13	0.54	2.02	13	19
1:A:31:ILE:HG13	1:A:68:LEU:HD13	0.54	1.78	2	1
1:A:49:THR:HG23	1:A:52:ASP:H	0.54	1.63	11	5
1:A:70:GLU:O	1:A:74:GLU:HG2	0.54	2.03	14	2
1:A:34:ARG:CD	1:A:61:PHE:HA	0.53	2.33	13	2
1:A:76:LEU:CA	1:A:81:ILE:HG22	0.53	2.31	20	5
1:A:39:ILE:HG12	1:A:81:ILE:HG12	0.53	1.79	19	2
1:A:36:LYS:HD2	1:A:81:ILE:HD12	0.53	1.79	20	1
1:A:36:LYS:CD	1:A:81:ILE:HD12	0.53	2.34	17	5
1:A:30:GLN:O	1:A:33:ARG:HG2	0.53	2.03	14	2
1:A:49:THR:HG22	1:A:51:GLU:H	0.53	1.64	19	2
1:A:65:ASP:O	1:A:68:LEU:HB3	0.52	2.05	10	9
1:A:57:PHE:HB3	1:A:58:PRO:HA	0.52	1.81	9	1
1:A:34:ARG:HE	1:A:34:ARG:CA	0.52	2.16	8	1
1:A:57:PHE:CD1	1:A:59:PRO:HG3	0.52	2.40	12	2
1:A:35:ILE:HD12	1:A:75:GLU:HG3	0.51	1.81	16	2
1:A:34:ARG:O	1:A:38:LEU:HG	0.51	2.04	9	5
1:A:28:MET:O	1:A:31:ILE:HG22	0.51	2.05	11	5
1:A:41:LEU:HD12	1:A:59:PRO:HB3	0.50	1.81	11	1
1:A:41:LEU:O	1:A:44:LYS:HG2	0.50	2.07	13	2
1:A:39:ILE:HG13	1:A:83:ILE:HB	0.50	1.84	1	8
1:A:35:ILE:HD13	1:A:72:ILE:HA	0.50	1.84	13	2
1:A:76:LEU:HD23	1:A:81:ILE:CG2	0.50	2.34	5	6
1:A:39:ILE:HB	1:A:81:ILE:HD11	0.50	1.83	1	2
1:A:72:ILE:O	1:A:76:LEU:HG	0.49	2.08	8	3
1:A:34:ARG:NH1	1:A:68:LEU:HD21	0.49	2.22	9	1
1:A:48:ILE:HB	1:A:83:ILE:HA	0.48	1.85	14	1
1:A:35:ILE:HG13	1:A:75:GLU:HG3	0.48	1.86	9	1
1:A:34:ARG:HA	1:A:34:ARG:NE	0.48	2.20	8	1
1:A:31:ILE:HG12	1:A:67:ASN:ND2	0.48	2.24	11	1
1:A:39:ILE:HD11	1:A:83:ILE:CB	0.48	2.27	11	1
1:A:51:GLU:O	1:A:55:LYS:HG2	0.47	2.08	2	1
1:A:34:ARG:HH11	1:A:68:LEU:HD22	0.47	1.68	1	1
1:A:48:ILE:HD12	1:A:84:VAL:HG12	0.47	1.85	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:GLN:NE2	1:A:62:GLU:HB2	0.47	2.25	14	1
1:A:30:GLN:HB2	1:A:62:GLU:OE1	0.47	2.10	19	1
1:A:70:GLU:HA	1:A:73:HIS:CD2	0.47	2.45	2	1
1:A:67:ASN:O	1:A:71:ARG:HB2	0.47	2.09	18	2
1:A:32:GLU:O	1:A:36:LYS:HG2	0.47	2.10	16	1
1:A:35:ILE:CD1	1:A:71:ARG:HG3	0.47	2.39	19	1
1:A:38:LEU:HB3	1:A:53:ILE:HD12	0.46	1.87	11	1
1:A:65:ASP:OD2	1:A:67:ASN:HB3	0.46	2.10	6	1
1:A:34:ARG:HG2	1:A:61:PHE:CD1	0.46	2.45	2	1
1:A:70:GLU:O	1:A:74:GLU:HG3	0.46	2.11	2	2
1:A:74:GLU:O	1:A:78:LYS:HB3	0.46	2.09	10	2
1:A:31:ILE:HD11	1:A:68:LEU:HB2	0.46	1.86	14	1
1:A:52:ASP:CA	1:A:55:LYS:HG3	0.46	2.40	1	4
1:A:75:GLU:OE2	1:A:78:LYS:HD2	0.46	2.11	6	1
1:A:28:MET:CG	1:A:30:GLN:HG2	0.46	2.40	16	1
1:A:59:PRO:HG2	1:A:61:PHE:HD2	0.46	1.70	2	1
1:A:71:ARG:O	1:A:75:GLU:HG2	0.46	2.10	18	2
1:A:48:ILE:O	1:A:83:ILE:HA	0.46	2.11	6	2
1:A:40:SER:C	1:A:44:LYS:HE2	0.46	2.32	8	1
1:A:73:HIS:O	1:A:76:LEU:HB3	0.45	2.11	3	5
1:A:75:GLU:OE1	1:A:78:LYS:HD2	0.45	2.11	3	1
1:A:61:PHE:CE2	1:A:68:LEU:HD22	0.45	2.44	9	1
1:A:76:LEU:HA	1:A:81:ILE:CG2	0.45	2.31	3	1
1:A:85:GLU:O	1:A:86:ASN:HB3	0.45	2.12	13	2
1:A:41:LEU:CA	1:A:44:LYS:HE2	0.45	2.30	16	1
1:A:39:ILE:CG1	1:A:83:ILE:HB	0.45	2.41	1	4
1:A:84:VAL:HG13	1:A:86:ASN:N	0.45	2.27	5	2
1:A:76:LEU:HA	1:A:81:ILE:O	0.45	2.11	8	1
1:A:45:LYS:NZ	1:A:56:ALA:HA	0.45	2.27	2	1
1:A:44:LYS:N	1:A:44:LYS:HE2	0.45	2.26	6	4
1:A:71:ARG:HA	1:A:71:ARG:HE	0.44	1.72	11	1
1:A:33:ARG:O	1:A:37:LYS:HG2	0.44	2.13	14	1
1:A:71:ARG:O	1:A:74:GLU:HG3	0.44	2.12	1	1
1:A:39:ILE:HD12	1:A:48:ILE:HG22	0.44	1.87	5	1
1:A:39:ILE:HD11	1:A:82:ASN:O	0.44	2.12	16	2
1:A:73:HIS:HA	1:A:76:LEU:HB3	0.44	1.90	17	1
1:A:35:ILE:HG22	1:A:81:ILE:CD1	0.44	2.43	8	4
1:A:36:LYS:HE3	1:A:75:GLU:HG2	0.44	1.88	10	1
1:A:37:LYS:HD3	1:A:60:ASP:OD2	0.44	2.13	16	1
1:A:49:THR:HB	1:A:52:ASP:OD1	0.43	2.14	14	1
1:A:30:GLN:O	1:A:34:ARG:HB2	0.43	2.14	10	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:36:LYS:N	1:A:36:LYS:HD3	0.43	2.27	8	1
1:A:57:PHE:CD2	1:A:59:PRO:HD3	0.43	2.49	19	2
1:A:49:THR:HB	1:A:84:VAL:HG12	0.42	1.91	5	1
1:A:71:ARG:HD2	1:A:74:GLU:OE2	0.42	2.14	17	1
1:A:58:PRO:HA	1:A:59:PRO:HD3	0.42	1.75	17	2
1:A:39:ILE:HG13	1:A:83:ILE:CG1	0.42	2.44	19	1
1:A:31:ILE:CG1	1:A:68:LEU:HD13	0.42	2.44	2	1
1:A:75:GLU:HA	1:A:78:LYS:CG	0.42	2.45	14	1
1:A:34:ARG:HD3	1:A:68:LEU:HD13	0.42	1.90	5	1
1:A:57:PHE:HA	1:A:58:PRO:C	0.42	2.35	10	2
1:A:38:LEU:HA	1:A:41:LEU:HD12	0.42	1.90	19	1
1:A:47:TYR:HD2	1:A:49:THR:HG1	0.42	1.54	19	1
1:A:43:LYS:HD2	1:A:48:ILE:HG23	0.42	1.91	18	1
1:A:57:PHE:CD1	1:A:59:PRO:HD3	0.42	2.50	6	2
1:A:49:THR:OG1	1:A:86:ASN:HB2	0.42	2.15	13	1
1:A:36:LYS:HE3	1:A:75:GLU:CG	0.42	2.45	10	1
1:A:49:THR:HG22	1:A:84:VAL:HG12	0.41	1.92	9	1
1:A:74:GLU:O	1:A:78:LYS:HG3	0.41	2.15	16	1
1:A:39:ILE:HG12	1:A:83:ILE:HD11	0.41	1.91	2	1
1:A:39:ILE:CD1	1:A:48:ILE:HG22	0.41	2.45	2	2
1:A:35:ILE:HD12	1:A:72:ILE:HG12	0.41	1.92	9	1
1:A:45:LYS:HE2	1:A:55:LYS:HG3	0.41	1.91	10	1
1:A:37:LYS:HG2	1:A:60:ASP:HB2	0.41	1.93	11	1
1:A:38:LEU:HD11	1:A:61:PHE:HZ	0.41	1.75	12	1
1:A:44:LYS:HE3	1:A:44:LYS:N	0.41	2.30	15	1
1:A:75:GLU:HA	1:A:79:HIS:HB2	0.41	1.91	19	1
1:A:36:LYS:NZ	1:A:75:GLU:OE1	0.41	2.52	2	1
1:A:31:ILE:HD12	1:A:68:LEU:HB2	0.41	1.93	18	1
1:A:38:LEU:HD12	1:A:53:ILE:HG23	0.41	1.93	2	1
1:A:75:GLU:CD	1:A:78:LYS:HD2	0.41	2.36	16	1
1:A:49:THR:CG2	1:A:86:ASN:HB2	0.40	2.47	8	1
1:A:52:ASP:OD1	1:A:55:LYS:HD3	0.40	2.16	20	1
1:A:49:THR:CB	1:A:84:VAL:HG12	0.40	2.47	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	59/72 (82%)	54±1 (92±2%)	4±1 (6±2%)	1±1 (2±1%)	13 57
All	All	1180/1440 (82%)	1086 (92%)	75 (6%)	19 (2%)	13 57

All 3 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	59	PRO	15
1	A	28	MET	2
1	A	46	GLY	2

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	54/64 (84%)	47±2 (87±4%)	7±2 (13±4%)	7 48
All	All	1080/1280 (84%)	937 (87%)	143 (13%)	7 48

All 28 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	48	ILE	20
1	A	84	VAL	18
1	A	44	LYS	17
1	A	43	LYS	10
1	A	55	LYS	10
1	A	34	ARG	10
1	A	52	ASP	9
1	A	79	HIS	7
1	A	39	ILE	6
1	A	82	ASN	6
1	A	54	ASP	3
1	A	36	LYS	3
1	A	71	ARG	3
1	A	85	GLU	2

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Mol	Chain	Res	Type	Models (Total)
1	A	60	ASP	2
1	A	45	LYS	2
1	A	61	PHE	2
1	A	75	GLU	2
1	A	32	GLU	2
1	A	74	GLU	1
1	A	28	MET	1
1	A	65	ASP	1
1	A	67	ASN	1
1	A	66	THR	1
1	A	78	LYS	1
1	A	30	GLN	1
1	A	49	THR	1
1	A	73	HIS	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