Full wwPDB NMR Structure Validation Report (i)

May 28, 2020 – 10:22 pm BST

PDB ID	:	2K60
Title	:	NMR structure of calcium-loaded STIM1 EF-SAM
Authors	:	Stathopulos, P.B.; Ikura, M.
Deposited on	:	2008-07-02

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 (1)) were used in the production of this report:

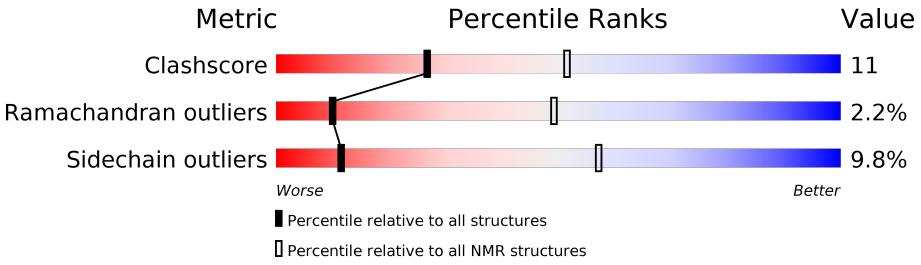
Cyrange	:	Kirchner and Güntert (2011)
NmrClust	:	Kelley et al. (1996)
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	2.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.11

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	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	150	63% 25% • 9%

2 Ensemble composition and analysis

This entry contains 20 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores. Model 20 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:65-A:201 (137)	0.36	20

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 5 single-model clusters were found.

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

3 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2396 atoms, of which 1174 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called PROTEIN (Stromal interaction molecule 1).

Mol	Chain	Residues	Atoms						Trace
1	A	150	Total	C	H	N	O	S	0
			2395	767	1174	206	243	5	

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	GLY	-	EXPRESSION TAG	UNP Q13586
A	-4	SER	-	EXPRESSION TAG	UNP Q13586
A	-3	HIS	-	EXPRESSION TAG	UNP Q13586
A	-2	MET	-	EXPRESSION TAG	UNP Q13586
A	-1	ALA	-	EXPRESSION TAG	UNP Q13586
A	0	SER	-	EXPRESSION TAG	UNP Q13586

- Molecule 2 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	
2	A	1	Total	Ca
			1	1

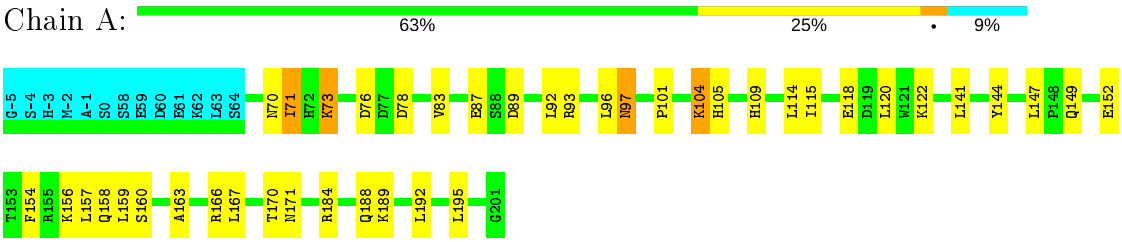
4 Residue-property plots

4.1 Average score per residue in the NMR ensemble

These plots are provided for all protein, RNA and DNA 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: PROTEIN (Stromal interaction molecule 1)

Chain A:



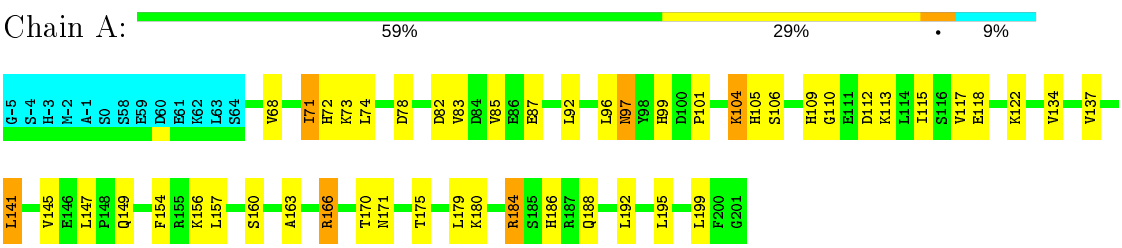
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

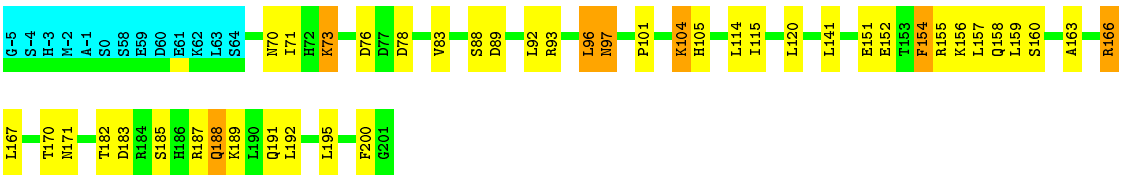
Chain A:



4.2.2 Score per residue for model 2

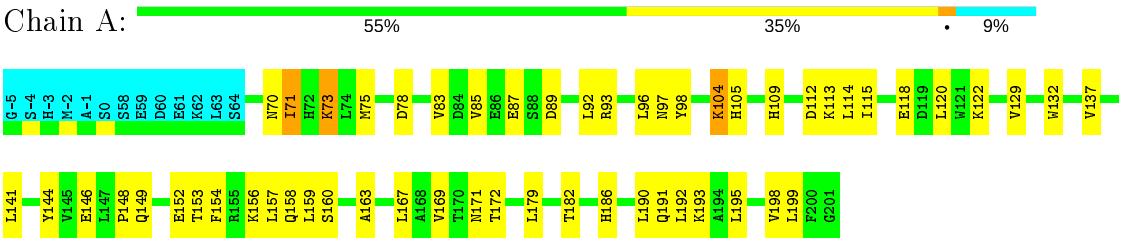
• Molecule 1: PROTEIN (Stromal interaction molecule 1)

Chain A:



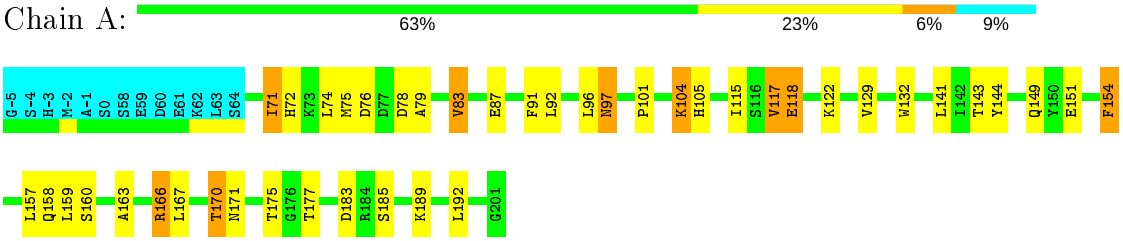
4.2.3 Score per residue for model 3

• Molecule 1: PROTEIN (Stromal interaction molecule 1)



4.2.4 Score per residue for model 4

• Molecule 1: PROTEIN (Stromal interaction molecule 1)



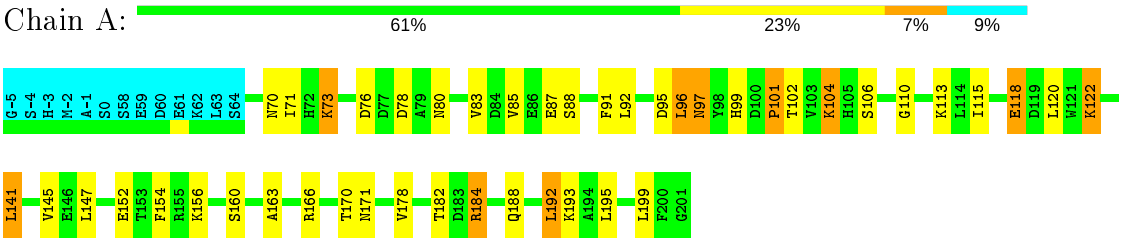
4.2.5 Score per residue for model 5

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

4.2.6 Score per residue for model 6

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

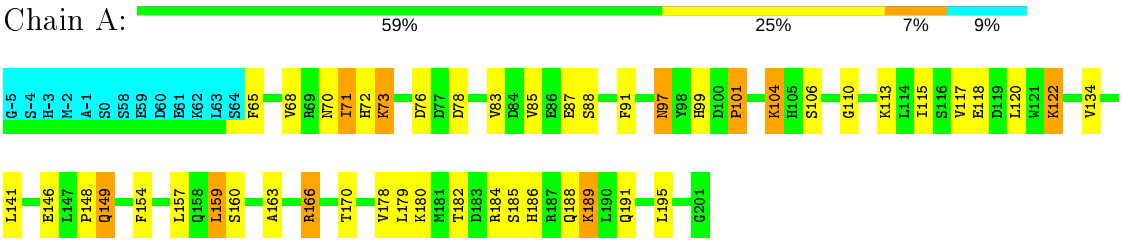
Chain A:



4.2.7 Score per residue for model 7

- Molecule 1: PROTEIN (Stromal interaction molecule 1)

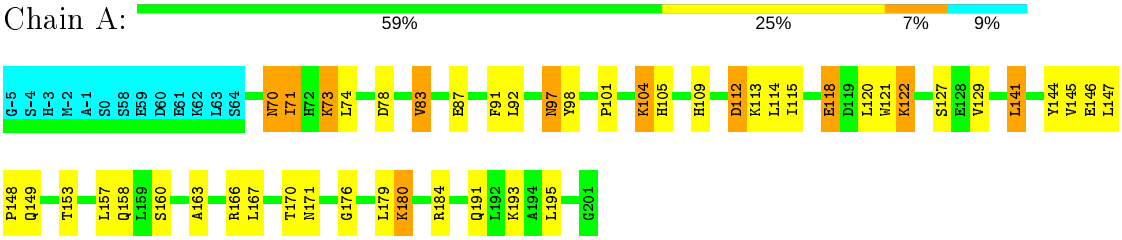
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: PROTEIN (Stromal interaction molecule 1)

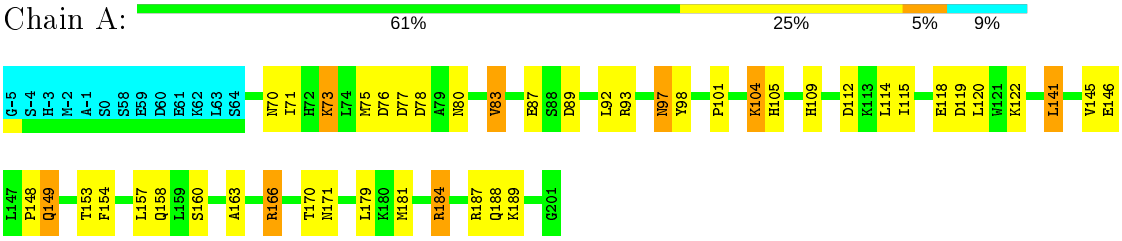
Chain A:



4.2.9 Score per residue for model 9

- Molecule 1: PROTEIN (Stromal interaction molecule 1)

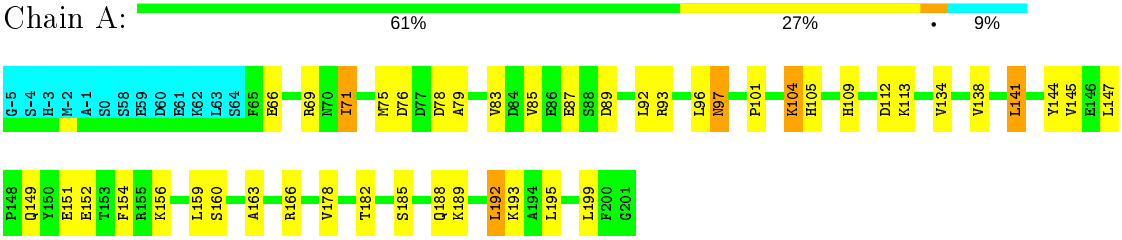
Chain A:



4.2.10 Score per residue for model 10

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

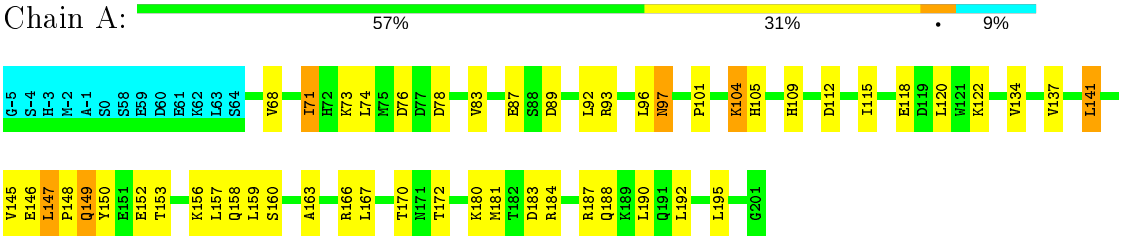
Chain A:



4.2.11 Score per residue for model 11

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

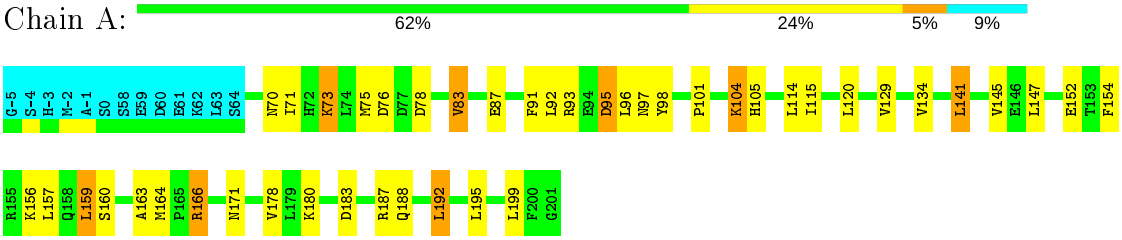
Chain A:



4.2.12 Score per residue for model 12

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

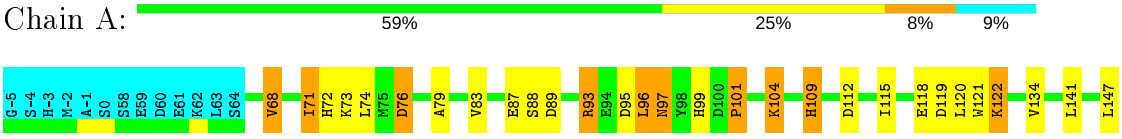
Chain A:

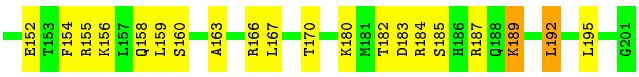


4.2.13 Score per residue for model 13

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

Chain A:

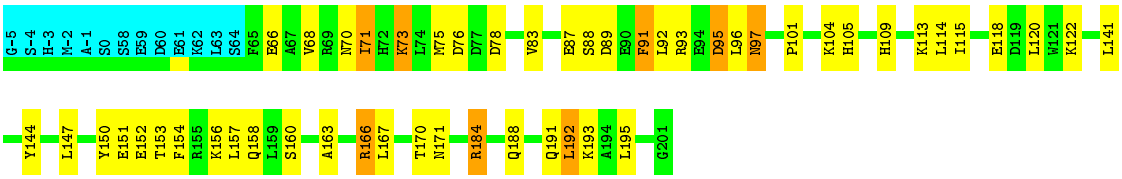




4.2.14 Score per residue for model 14

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

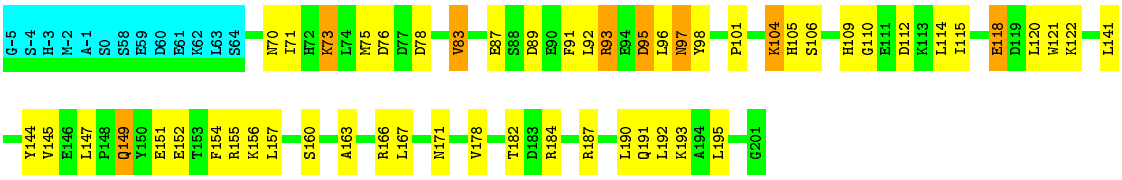
Chain A:



4.2.15 Score per residue for model 15

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

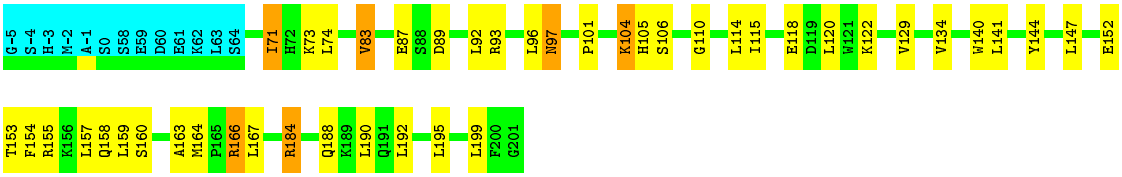
Chain A:



4.2.16 Score per residue for model 16

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

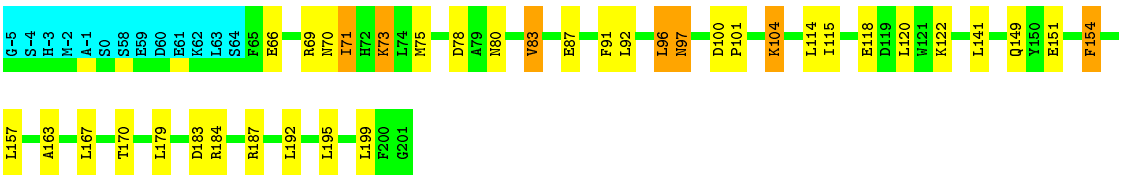
Chain A:



4.2.17 Score per residue for model 17

• Molecule 1: PROTEIN (Stromal interaction molecule 1)

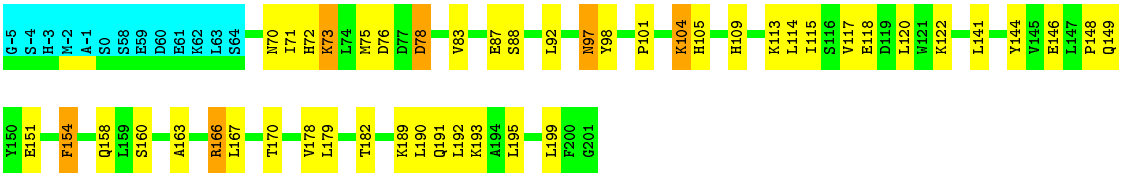
Chain A:



4.2.18 Score per residue for model 18

- Molecule 1: PROTEIN (Stromal interaction molecule 1)

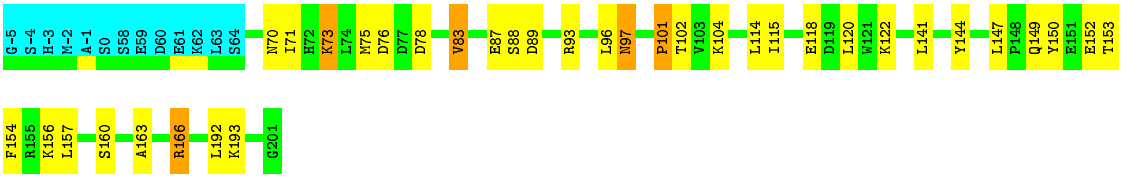
Chain A:



4.2.19 Score per residue for model 19

- Molecule 1: PROTEIN (Stromal interaction molecule 1)

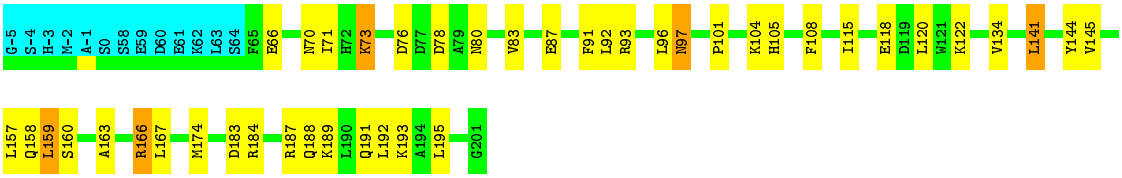
Chain A:



4.2.20 Score per residue for model 20 (medoid)

- Molecule 1: PROTEIN (Stromal interaction molecule 1)

Chain A:



5 Refinement protocol and experimental data overview

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

Of the 250 calculated structures, 20 were deposited, based on the following criterion: *20 structures for lowest energy.*

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

Software name	Classification	Version
CNS	refinement	v1.1
CYANA	structure solution	v2.1

No chemical shift data was provided. No validations of the models with respect to experimental NMR restraints is performed at this time.

COVALENT-GEOMETRY INFOmissingINFO

5.1 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	1127	1088	1088	24±4
2	A	1	0	0	1±1
All	All	22560	21760	21760	489

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 11.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:89:ASP:O	1:A:93:ARG:HG3	0.70	1.87	5	11
1:A:76:ASP:OD1	2:A:686:CA:CA	0.67	1.72	10	2
1:A:96:LEU:HA	1:A:192:LEU:HD13	0.67	1.67	11	11
1:A:78:ASP:OD1	2:A:686:CA:CA	0.62	1.77	15	9
1:A:184:ARG:O	1:A:188:GLN:HG2	0.62	1.95	7	7
1:A:76:ASP:HB2	1:A:83:VAL:HG12	0.61	1.73	10	7
1:A:83:VAL:O	1:A:114:LEU:HA	0.60	1.96	12	10
1:A:70:ASN:O	1:A:73:LYS:HG3	0.59	1.97	15	13

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:115:ILE:HG22	1:A:120:LEU:HD11	0.58	1.76	5	16
1:A:93:ARG:HG2	1:A:101:PRO:HD3	0.58	1.75	13	7
1:A:160:SER:H	1:A:163:ALA:HB3	0.58	1.59	7	19
1:A:76:ASP:HB2	1:A:83:VAL:HG22	0.57	1.77	7	8
1:A:163:ALA:HA	1:A:166:ARG:HG3	0.57	1.76	9	11
1:A:109:HIS:CD2	1:A:112:ASP:HB3	0.57	2.35	3	4
1:A:167:LEU:HD13	1:A:190:LEU:HD12	0.56	1.76	11	5
1:A:118:GLU:O	1:A:122:LYS:HD3	0.56	2.00	9	17
1:A:151:GLU:HA	1:A:154:PHE:CE2	0.56	2.35	14	7
1:A:152:GLU:O	1:A:156:LYS:HG2	0.56	2.01	15	10
1:A:144:TYR:O	1:A:193:LYS:HE2	0.56	2.01	3	3
1:A:97:ASN:OD1	1:A:101:PRO:HA	0.55	2.01	7	18
1:A:112:ASP:OD1	1:A:114:LEU:HG	0.54	2.02	3	2
1:A:75:MET:SD	1:A:92:LEU:HD13	0.54	2.43	10	8
1:A:188:GLN:O	1:A:192:LEU:HB2	0.53	2.03	12	3
1:A:183:ASP:O	1:A:187:ARG:HG2	0.53	2.03	17	6
1:A:163:ALA:HA	1:A:166:ARG:CG	0.53	2.34	16	11
1:A:129:VAL:HA	1:A:132:TRP:CE3	0.53	2.39	3	2
1:A:149:GLN:HG3	1:A:149:GLN:O	0.53	2.03	3	4
1:A:71:ILE:O	1:A:74:LEU:HB2	0.52	2.04	4	7
1:A:104:LYS:HA	1:A:104:LYS:HE2	0.52	1.82	15	6
1:A:149:GLN:O	1:A:149:GLN:HG3	0.52	2.04	15	3
1:A:70:ASN:ND2	1:A:169:VAL:HG21	0.51	2.19	3	1
1:A:191:GLN:O	1:A:195:LEU:HB3	0.51	2.05	7	8
1:A:129:VAL:HG13	1:A:164:MET:SD	0.51	2.45	16	2
1:A:109:HIS:CD2	1:A:113:LYS:HB2	0.51	2.41	14	2
1:A:104:LYS:O	1:A:104:LYS:HE2	0.51	2.06	10	7
1:A:104:LYS:CE	1:A:200:PHE:HB2	0.51	2.35	2	1
1:A:144:TYR:HB3	1:A:193:LYS:HG2	0.50	1.83	18	5
1:A:91:PHE:O	1:A:95:ASP:HB2	0.50	2.07	15	4
1:A:145:VAL:HG12	1:A:147:LEU:HD23	0.50	1.81	11	2
1:A:152:GLU:O	1:A:155:ARG:HG2	0.50	2.06	13	3
1:A:171:ASN:ND2	1:A:180:LYS:HG3	0.50	2.22	8	1
1:A:104:LYS:HE2	1:A:104:LYS:HA	0.50	1.83	18	6
1:A:185:SER:O	1:A:189:LYS:HD3	0.50	2.07	7	2
1:A:145:VAL:HG13	1:A:189:LYS:HB3	0.50	1.83	20	1
1:A:85:VAL:HG12	1:A:113:LYS:HB2	0.50	1.84	10	4
1:A:75:MET:O	1:A:88:SER:HA	0.50	2.07	19	1
1:A:83:VAL:CG1	1:A:88:SER:HB3	0.49	2.37	18	6
1:A:147:LEU:HD12	1:A:149:GLN:OE1	0.49	2.08	11	1
1:A:71:ILE:HG22	1:A:195:LEU:HD13	0.49	1.83	17	5

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:134:VAL:HA	1:A:159:LEU:O	0.49	2.07	12	6
1:A:104:LYS:CE	1:A:104:LYS:HA	0.49	2.37	15	5
1:A:95:ASP:O	1:A:192:LEU:HD22	0.49	2.08	14	4
1:A:171:ASN:ND2	1:A:183:ASP:HB2	0.49	2.23	12	1
1:A:85:VAL:CG1	1:A:113:LYS:HA	0.49	2.37	5	1
1:A:141:LEU:O	1:A:145:VAL:HB	0.49	2.08	5	8
1:A:104:LYS:HA	1:A:104:LYS:CE	0.49	2.37	4	4
1:A:195:LEU:O	1:A:199:LEU:HG	0.48	2.08	17	7
1:A:78:ASP:OD2	1:A:80:ASN:HB3	0.48	2.09	9	4
1:A:92:LEU:HD12	1:A:96:LEU:HD11	0.48	1.84	2	2
1:A:85:VAL:CG1	1:A:113:LYS:HB2	0.48	2.39	7	2
1:A:92:LEU:HD23	1:A:105:HIS:CD2	0.48	2.44	10	15
1:A:153:THR:HB	1:A:179:LEU:HD11	0.48	1.86	9	1
1:A:112:ASP:O	1:A:113:LYS:HG3	0.47	2.09	8	1
1:A:106:SER:O	1:A:110:GLY:HA2	0.47	2.10	1	5
1:A:109:HIS:HB3	1:A:112:ASP:O	0.47	2.08	3	5
1:A:141:LEU:O	1:A:145:VAL:HG12	0.47	2.10	9	1
1:A:185:SER:O	1:A:189:LYS:HG2	0.47	2.09	2	3
1:A:74:LEU:O	1:A:91:PHE:HB3	0.47	2.10	4	1
1:A:150:TYR:HA	1:A:153:THR:HG22	0.47	1.86	14	3
1:A:104:LYS:HE3	1:A:200:PHE:HB2	0.47	1.87	2	1
1:A:115:ILE:CG2	1:A:120:LEU:HD11	0.47	2.39	15	9
1:A:163:ALA:O	1:A:167:LEU:HG	0.46	2.10	11	8
1:A:93:ARG:CG	1:A:101:PRO:HD3	0.46	2.40	13	1
1:A:118:GLU:O	1:A:121:TRP:HB3	0.46	2.11	13	3
1:A:66:GLU:O	1:A:70:ASN:HB2	0.46	2.10	14	2
1:A:156:LYS:HA	1:A:156:LYS:HE2	0.46	1.88	1	1
1:A:153:THR:O	1:A:157:LEU:HG	0.46	2.11	3	2
1:A:188:GLN:HA	1:A:188:GLN:HE21	0.46	1.71	2	2
1:A:118:GLU:HG3	1:A:119:ASP:N	0.45	2.26	9	1
1:A:104:LYS:HE2	1:A:104:LYS:O	0.45	2.11	9	1
1:A:72:HIS:CG	1:A:117:VAL:HG12	0.45	2.47	4	1
1:A:151:GLU:HA	1:A:154:PHE:CD2	0.45	2.47	18	4
1:A:68:VAL:HA	1:A:71:ILE:CD1	0.45	2.42	14	1
1:A:66:GLU:O	1:A:69:ARG:HG2	0.45	2.11	10	2
1:A:68:VAL:HA	1:A:71:ILE:HD12	0.44	1.88	11	3
1:A:167:LEU:HB2	1:A:174:MET:SD	0.44	2.52	20	1
1:A:65:PHE:HA	1:A:68:VAL:HG22	0.44	1.89	7	1
1:A:71:ILE:CG2	1:A:195:LEU:HD13	0.44	2.43	17	5
1:A:144:TYR:O	1:A:193:LYS:HE3	0.44	2.12	14	2
1:A:108:PHE:CE2	1:A:115:ILE:HA	0.43	2.48	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:180:LYS:HG3	1:A:181:MET:O	0.43	2.13	11	1
1:A:93:ARG:HG2	1:A:101:PRO:CD	0.43	2.43	11	1
1:A:76:ASP:OD2	1:A:79:ALA:HA	0.43	2.13	10	1
1:A:163:ALA:HA	1:A:166:ARG:HB3	0.43	1.89	15	1
1:A:146:GLU:O	1:A:148:PRO:HD3	0.43	2.13	9	6
1:A:72:HIS:O	1:A:75:MET:HE3	0.43	2.14	18	1
1:A:151:GLU:O	1:A:155:ARG:HG2	0.43	2.13	15	1
1:A:193:LYS:N	1:A:193:LYS:HD2	0.43	2.28	6	1
1:A:171:ASN:O	1:A:175:THR:HG22	0.43	2.13	1	2
1:A:73:LYS:C	1:A:73:LYS:HD2	0.43	2.34	6	1
1:A:140:TRP:O	1:A:144:TYR:HB2	0.43	2.13	16	1
1:A:171:ASN:HB2	1:A:186:HIS:HD1	0.42	1.74	3	1
1:A:96:LEU:HA	1:A:192:LEU:CD1	0.42	2.44	4	1
1:A:109:HIS:ND1	1:A:113:LYS:HB2	0.42	2.29	8	1
1:A:134:VAL:O	1:A:137:VAL:HG12	0.42	2.15	11	2
1:A:188:GLN:OE1	1:A:188:GLN:HA	0.42	2.14	10	1
1:A:179:LEU:HG	1:A:186:HIS:NE2	0.42	2.30	1	1
1:A:104:LYS:NZ	1:A:199:LEU:HB3	0.42	2.30	10	1
1:A:72:HIS:CG	1:A:117:VAL:HG22	0.42	2.50	1	1
1:A:104:LYS:C	1:A:104:LYS:HE2	0.42	2.35	10	1
1:A:92:LEU:HD12	1:A:96:LEU:HD21	0.41	1.91	4	1
1:A:138:VAL:HA	1:A:141:LEU:HD23	0.41	1.92	10	1
1:A:83:VAL:HG12	1:A:115:ILE:HB	0.41	1.93	1	1
1:A:195:LEU:HA	1:A:198:VAL:HG12	0.41	1.93	3	1
1:A:143:THR:HG23	1:A:144:TYR:CD2	0.41	2.51	4	1
1:A:83:VAL:HG22	1:A:115:ILE:HG12	0.41	1.91	4	1
1:A:72:HIS:HB2	1:A:117:VAL:HG12	0.41	1.90	7	2
1:A:184:ARG:CZ	1:A:188:GLN:HG3	0.41	2.46	14	1
1:A:171:ASN:HB3	1:A:187:ARG:HB3	0.41	1.92	15	2
1:A:180:LYS:HB3	1:A:186:HIS:CD2	0.41	2.51	7	1
1:A:82:ASP:HA	1:A:115:ILE:O	0.40	2.17	1	1
1:A:179:LEU:HD23	1:A:186:HIS:NE2	0.40	2.31	3	1
1:A:163:ALA:HA	1:A:166:ARG:HG2	0.40	1.92	12	1
1:A:153:THR:HB	1:A:179:LEU:HD13	0.40	1.93	8	1
1:A:93:ARG:HG2	1:A:101:PRO:HG3	0.40	1.93	20	1
1:A:137:VAL:HG11	1:A:159:LEU:C	0.40	2.37	3	1
1:A:127:SER:OG	1:A:129:VAL:HG23	0.40	2.16	8	1
1:A:149:GLN:HG2	1:A:179:LEU:HD12	0.40	1.92	8	1
1:A:68:VAL:HG22	1:A:72:HIS:NE2	0.40	2.31	13	1
1:A:92:LEU:CD1	1:A:96:LEU:HD21	0.40	2.46	15	1

5.2 Torsion angles

5.2.1 Protein backbone

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	136/150 (91%)	118±2 (87±1%)	15±2 (11±2%)	3±2 (2±1%)	10	49
All	All	2720/3000 (91%)	2363 (87%)	297 (11%)	60 (2%)	10	49

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	170	THR	12
1	A	158	GLN	11
1	A	98	TYR	6
1	A	178	VAL	6
1	A	91	PHE	5
1	A	101	PRO	4
1	A	99	HIS	4
1	A	180	LYS	2
1	A	102	THR	2
1	A	79	ALA	2
1	A	179	LEU	2
1	A	177	THR	1
1	A	112	ASP	1
1	A	76	ASP	1
1	A	176	GLY	1

5.2.2 Protein sidechains

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	126/137 (92%)	114±2 (90±2%)	12±2 (10±2%)	11	57
All	All	2520/2740 (92%)	2273 (90%)	247 (10%)	11	57

All 35 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	97	ASN	20
1	A	104	LYS	20
1	A	141	LEU	20
1	A	71	ILE	20
1	A	73	LYS	18
1	A	166	ARG	15
1	A	157	LEU	14
1	A	154	PHE	13
1	A	83	VAL	10
1	A	147	LEU	10
1	A	182	THR	9
1	A	149	GLN	8
1	A	184	ARG	8
1	A	96	LEU	7
1	A	159	LEU	7
1	A	192	LEU	7
1	A	78	ASP	5
1	A	122	LYS	4
1	A	118	GLU	4
1	A	171	ASN	4
1	A	189	LYS	4
1	A	95	ASP	3
1	A	180	LYS	2
1	A	172	THR	2
1	A	70	ASN	2
1	A	188	GLN	2
1	A	156	LYS	1
1	A	117	VAL	1
1	A	181	MET	1
1	A	119	ASP	1
1	A	183	ASP	1
1	A	109	HIS	1
1	A	68	VAL	1
1	A	179	LEU	1
1	A	100	ASP	1

5.2.3 RNA

There are no RNA molecules in this entry.

5.3 Non-standard residues in protein, DNA, RNA chains

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

5.4 Carbohydrates

There are no carbohydrates in this entry.

5.5 Ligand geometry

Of 1 ligands modelled in this entry, 1 is monoatomic - leaving 0 for Mogul analysis.

5.6 Other polymers

There are no such molecules in this entry.

5.7 Polymer linkage issues

There are no chain breaks in this entry.

6 Chemical shift validation

No chemical shift data were provided