



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 02:43 PM BST

PDB ID : 1GNC
Title : STRUCTURE AND DYNAMICS OF THE HUMAN GRANULOCYTE COLONY-STIMULATING FACTOR DETERMINED BY NMR SPECTROSCOPY. LOOP MOBILITY IN A FOUR-HELIX-BUNDLE PROTEIN
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Deposited on : 1994-03-08

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
<http://wwpdb.org/validation/2016/NMRValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

Cyrange : Kirchner and Güntert (2011)
NmrClust : Kelley et al. (1996)
MolProbity : 4.02b-467
Mogul : unknown
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : rb-20027457
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20027457

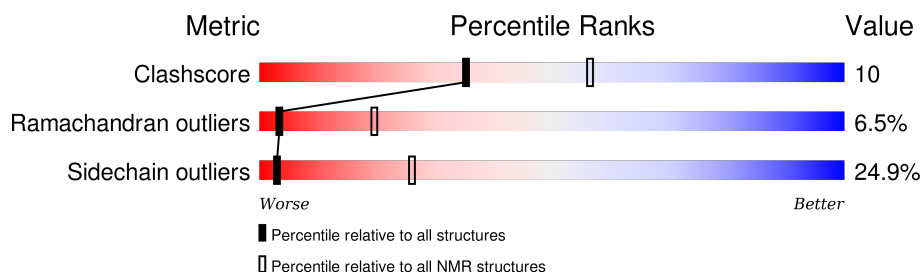
1 Overall quality at a glance

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	114402	11133
Ramachandran outliers	111179	9975
Sidechain outliers	111093	9958

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	178	 44% 30% • 22% •

2 Ensemble composition and analysis

This entry contains 10 models. Model 5 is the overall representative, medoid model (most similar to other models).

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:13-A:62, A:74-A:125, A:138-A:171 (136)	0.98	5

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	2, 5, 7, 9, 10
2	4, 6, 8
3	1, 3

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 2655 atoms, of which 1335 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called GRANULOCYTE COLONY-STIMULATING FACTOR.

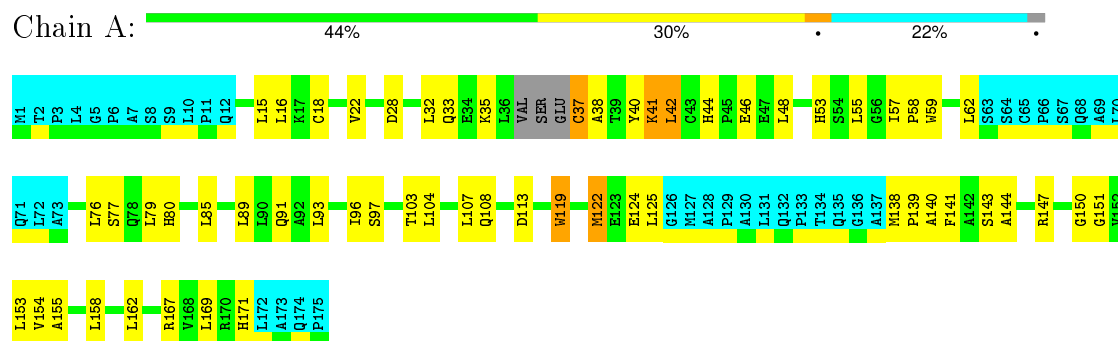
Mol	Chain	Residues	Atoms						Trace
1	A	175	Total	C	H	N	O	S	0
			2655	845	1335	223	243	9	

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: GRANULOCYTE COLONY-STIMULATING FACTOR

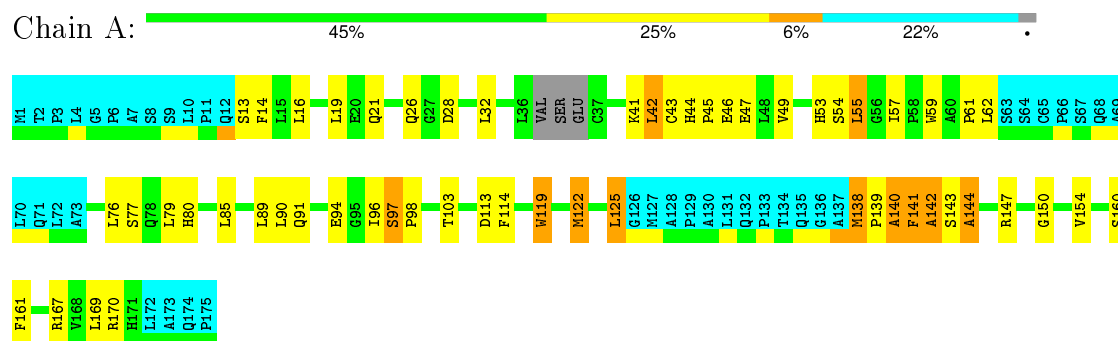


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

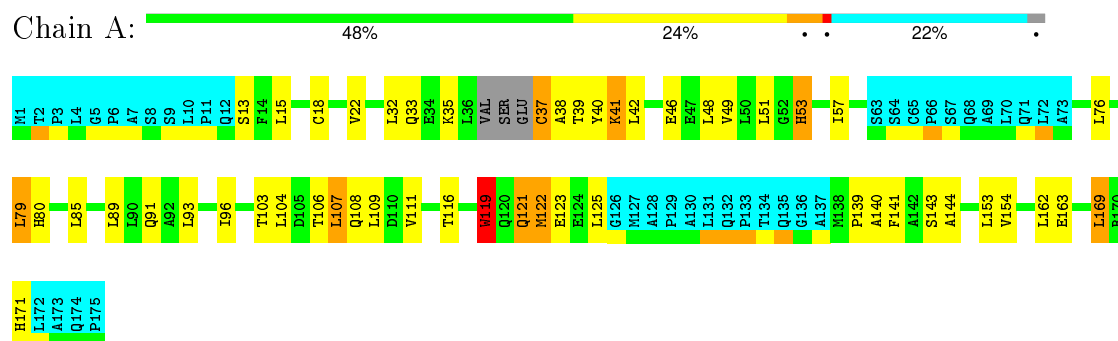
4.2.1 Score per residue for model 1

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



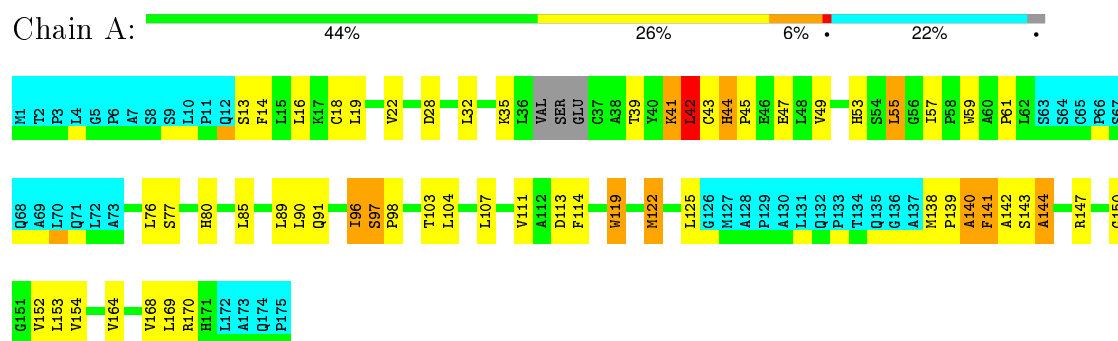
4.2.2 Score per residue for model 2

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



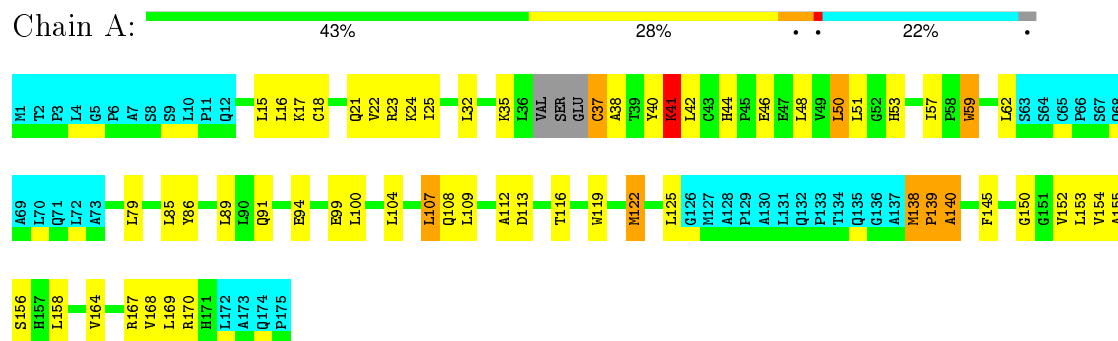
4.2.3 Score per residue for model 3

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



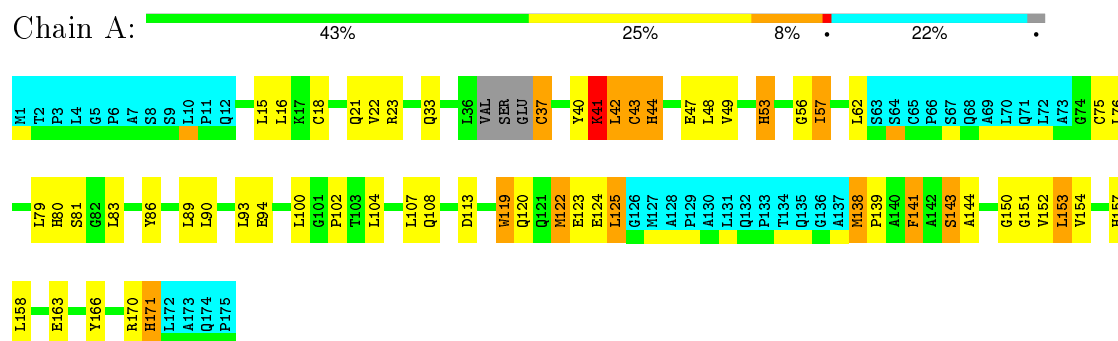
4.2.4 Score per residue for model 4

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



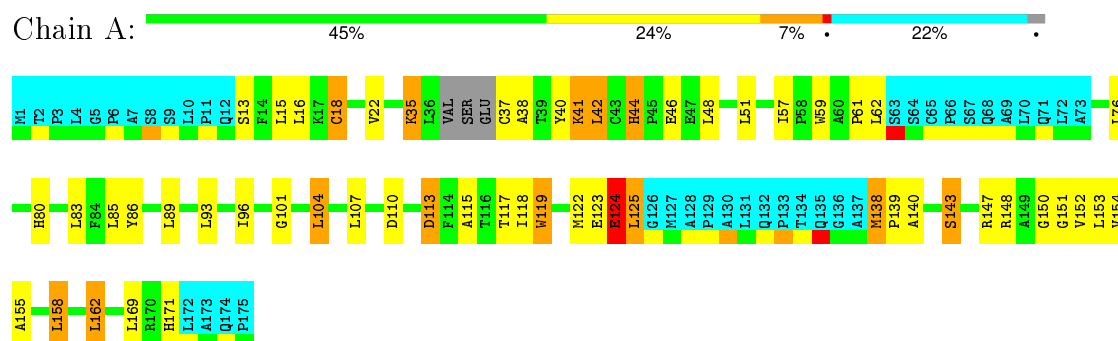
4.2.5 Score per residue for model 5 (medoid)

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



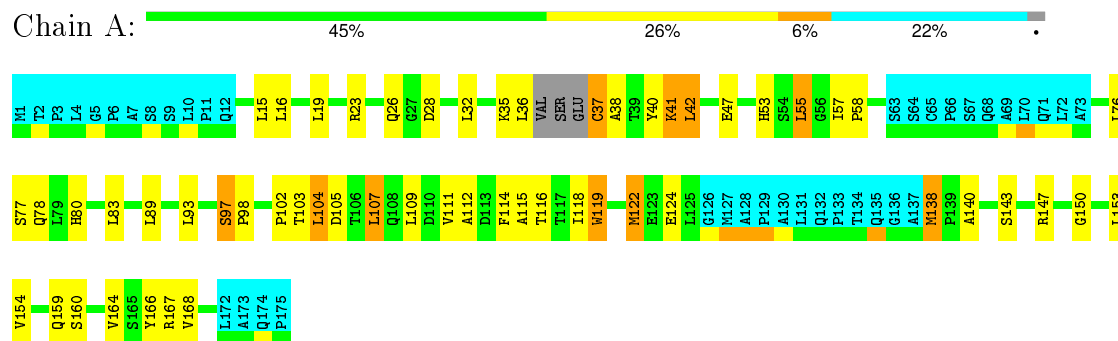
4.2.6 Score per residue for model 6

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



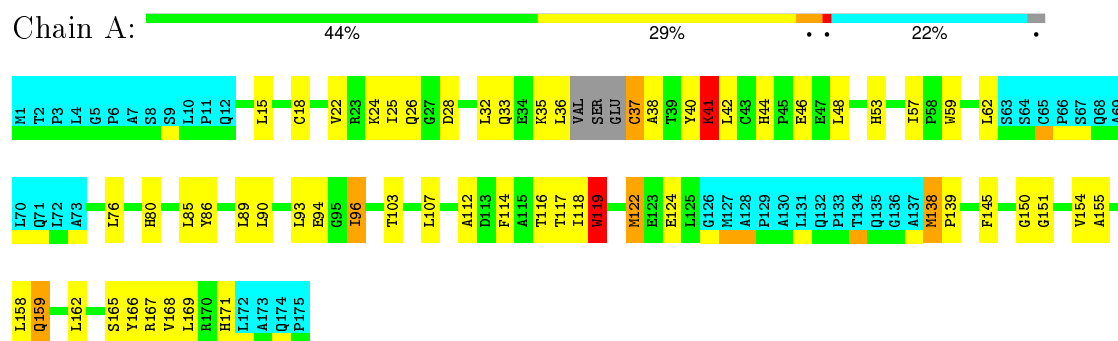
4.2.7 Score per residue for model 7

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



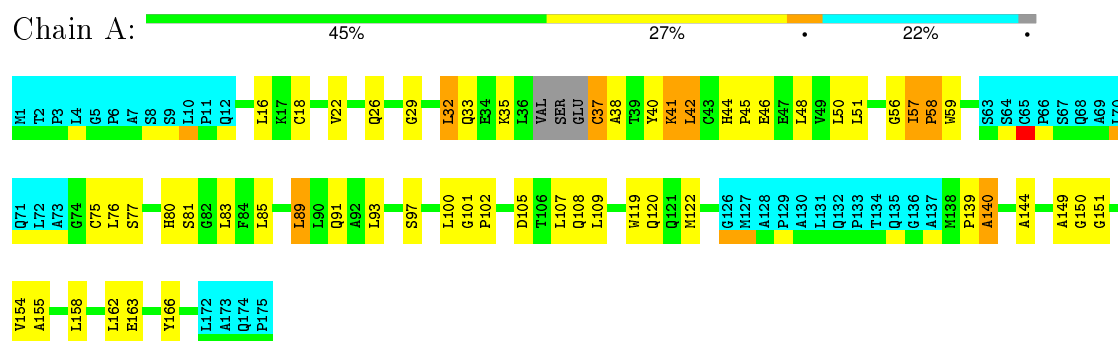
4.2.8 Score per residue for model 8

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



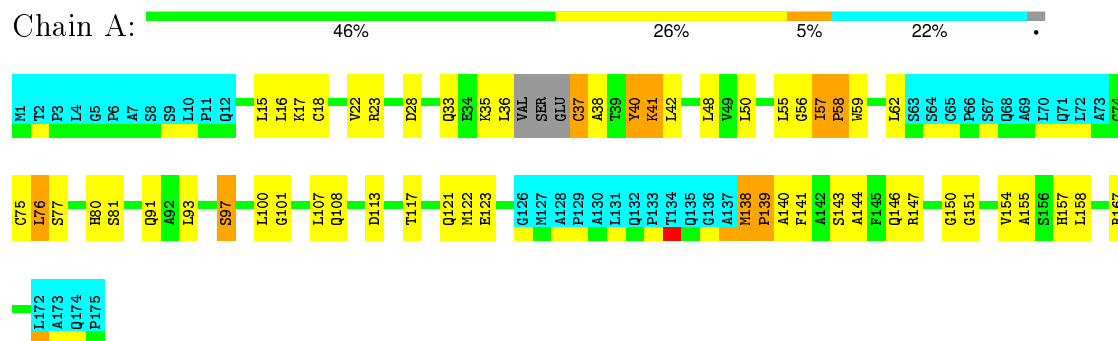
4.2.9 Score per residue for model 9

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



4.2.10 Score per residue for model 10

- Molecule 1: GRANULOCYTE COLONY-STIMULATING FACTOR



5 Refinement protocol and experimental data overview

Of the ? calculated structures, 10 were deposited, based on the following criterion: ?.

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

Software name	Classification	Version
X-PLOR	refinement	

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

6 Model quality [i](#)

6.1 Standard geometry [i](#)

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the (average) root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.02±0.01	0±0/1079 (0.0±0.0%)	0.85±0.01	0±0/1465 (0.0±0.0%)
All	All	1.02	0/10790 (0.0%)	0.85	2/14650 (0.0%)

There are no bond-length outliers.

All unique angle outliers are listed below.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	119	TRP	CB-CG-CD2	5.09	133.22	126.60	2	2

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	1055	1065	1065	22±4
All	All	10550	10650	10650	221

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:19:LEU:CD1	1:A:169:LEU:HD23	0.77	2.09	1	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:112:ALA:O	1:A:116:THR:HG23	0.75	1.81	7	3
1:A:93:LEU:HD11	1:A:151:GLY:HA3	0.75	1.58	5	2
1:A:76:LEU:HD13	1:A:76:LEU:O	0.73	1.84	3	2
1:A:89:LEU:HD23	1:A:154:VAL:HG21	0.73	1.59	8	3
1:A:107:LEU:O	1:A:111:VAL:HG23	0.73	1.83	2	3
1:A:150:GLY:O	1:A:154:VAL:HG23	0.72	1.84	7	9
1:A:144:ALA:HB3	1:A:147:ARG:HD3	0.72	1.61	3	2
1:A:160:SER:O	1:A:164:VAL:HG22	0.72	1.85	7	1
1:A:18:CYS:O	1:A:22:VAL:HG23	0.71	1.85	5	7
1:A:33:GLN:NE2	1:A:155:ALA:HB1	0.71	2.01	9	2
1:A:76:LEU:HD11	1:A:118:ILE:CG2	0.70	2.17	7	2
1:A:32:LEU:HD13	1:A:103:THR:HG21	0.69	1.64	3	2
1:A:164:VAL:O	1:A:168:VAL:HG23	0.68	1.89	3	3
1:A:76:LEU:O	1:A:76:LEU:HD13	0.67	1.89	1	2
1:A:85:LEU:O	1:A:85:LEU:HD23	0.67	1.89	3	1
1:A:96:ILE:HD13	1:A:96:ILE:O	0.67	1.90	8	1
1:A:41:LYS:O	1:A:42:LEU:HD23	0.65	1.91	3	1
1:A:32:LEU:HD13	1:A:32:LEU:O	0.64	1.93	2	1
1:A:48:LEU:HD21	1:A:145:PHE:CZ	0.64	2.27	8	1
1:A:93:LEU:HD21	1:A:151:GLY:CA	0.62	2.24	9	2
1:A:48:LEU:HD21	1:A:149:ALA:HB1	0.61	1.71	9	1
1:A:85:LEU:HD23	1:A:85:LEU:O	0.61	1.95	1	1
1:A:76:LEU:O	1:A:76:LEU:HD23	0.60	1.95	2	2
1:A:42:LEU:HD12	1:A:42:LEU:O	0.60	1.95	8	1
1:A:162:LEU:O	1:A:162:LEU:HD13	0.60	1.96	6	1
1:A:32:LEU:HD21	1:A:102:PRO:O	0.60	1.96	9	1
1:A:93:LEU:HD13	1:A:96:ILE:HD12	0.60	1.71	2	1
1:A:35:LYS:O	1:A:38:ALA:HB3	0.59	1.96	2	7
1:A:19:LEU:HD21	1:A:166:TYR:CE1	0.59	2.32	7	1
1:A:40:TYR:O	1:A:42:LEU:N	0.59	2.36	10	8
1:A:55:LEU:HD13	1:A:55:LEU:O	0.58	1.98	3	2
1:A:89:LEU:CD2	1:A:154:VAL:HG21	0.57	2.30	8	1
1:A:37:CYS:O	1:A:41:LYS:N	0.56	2.37	7	8
1:A:93:LEU:HD21	1:A:151:GLY:HA3	0.56	1.77	6	2
1:A:104:LEU:O	1:A:104:LEU:HD23	0.56	2.01	2	1
1:A:76:LEU:HD13	1:A:76:LEU:C	0.55	2.22	10	5
1:A:80:HIS:CD2	1:A:118:ILE:HG22	0.55	2.37	7	1
1:A:115:ALA:O	1:A:119:TRP:CD1	0.55	2.60	6	2
1:A:89:LEU:HD13	1:A:154:VAL:HG11	0.55	1.79	4	1
1:A:113:ASP:O	1:A:117:THR:HG22	0.54	2.02	6	1
1:A:76:LEU:HD11	1:A:118:ILE:HG23	0.54	1.78	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:LEU:HD22	1:A:76:LEU:O	0.54	2.03	10	1
1:A:80:HIS:CE1	1:A:119:TRP:CE2	0.54	2.96	7	1
1:A:85:LEU:HD13	1:A:85:LEU:C	0.54	2.24	6	1
1:A:159:GLN:HA	1:A:162:LEU:HD12	0.53	1.79	8	1
1:A:22:VAL:HG11	1:A:166:TYR:CD1	0.53	2.39	5	1
1:A:76:LEU:C	1:A:76:LEU:HD13	0.53	2.23	7	1
1:A:32:LEU:HD13	1:A:32:LEU:C	0.53	2.23	2	1
1:A:57:ILE:HB	1:A:58:PRO:CD	0.53	2.34	9	2
1:A:25:ILE:HD12	1:A:26:GLN:N	0.52	2.19	8	1
1:A:125:LEU:O	1:A:125:LEU:HD23	0.52	2.04	5	1
1:A:25:ILE:HD11	1:A:107:LEU:HA	0.52	1.80	4	1
1:A:29:GLY:CA	1:A:107:LEU:HD11	0.52	2.35	9	1
1:A:41:LYS:C	1:A:42:LEU:HD23	0.52	2.25	3	1
1:A:93:LEU:HD11	1:A:151:GLY:CA	0.52	2.33	5	2
1:A:158:LEU:O	1:A:158:LEU:HD13	0.52	2.05	6	1
1:A:55:LEU:HD23	1:A:141:PHE:CD1	0.51	2.40	10	1
1:A:141:PHE:O	1:A:142:ALA:HB3	0.51	2.06	3	2
1:A:50:LEU:HD13	1:A:53:HIS:CE1	0.51	2.41	4	1
1:A:96:ILE:HG21	1:A:147:ARG:HD3	0.51	1.83	6	1
1:A:158:LEU:HD13	1:A:158:LEU:C	0.50	2.27	9	1
1:A:139:PRO:O	1:A:140:ALA:HB2	0.50	2.06	4	3
1:A:143:SER:O	1:A:144:ALA:HB3	0.50	2.06	5	1
1:A:101:GLY:N	1:A:104:LEU:HD21	0.50	2.22	6	1
1:A:35:LYS:O	1:A:39:THR:HG23	0.50	2.07	3	1
1:A:49:VAL:HG12	1:A:53:HIS:CD2	0.50	2.41	3	2
1:A:141:PHE:O	1:A:142:ALA:CB	0.50	2.60	1	2
1:A:32:LEU:HD22	1:A:104:LEU:CD2	0.49	2.37	7	1
1:A:80:HIS:CD2	1:A:119:TRP:CE3	0.49	3.00	6	1
1:A:141:PHE:CD1	1:A:141:PHE:N	0.49	2.79	10	1
1:A:89:LEU:CD1	1:A:154:VAL:HG21	0.49	2.37	9	1
1:A:57:ILE:CB	1:A:58:PRO:CD	0.49	2.91	10	2
1:A:49:VAL:HG22	1:A:53:HIS:CD2	0.49	2.42	5	1
1:A:59:TRP:HB3	1:A:85:LEU:HD21	0.48	1.85	4	1
1:A:29:GLY:HA3	1:A:107:LEU:HD11	0.48	1.84	9	1
1:A:89:LEU:HD13	1:A:154:VAL:HG21	0.48	1.85	9	1
1:A:42:LEU:C	1:A:42:LEU:HD12	0.48	2.29	8	1
1:A:139:PRO:O	1:A:140:ALA:HB3	0.48	2.09	9	1
1:A:80:HIS:NE2	1:A:119:TRP:CD2	0.48	2.82	7	1
1:A:42:LEU:HD12	1:A:44:HIS:HB2	0.48	1.84	3	1
1:A:80:HIS:NE2	1:A:119:TRP:CE3	0.48	2.82	8	4
1:A:15:LEU:N	1:A:15:LEU:HD22	0.47	2.24	5	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:LEU:HD12	1:A:121:GLN:HG2	0.47	1.86	2	1
1:A:55:LEU:HD23	1:A:55:LEU:O	0.47	2.09	7	1
1:A:19:LEU:HD13	1:A:169:LEU:HD23	0.47	1.83	3	1
1:A:86:TYR:CD1	1:A:158:LEU:CD2	0.47	2.98	6	1
1:A:76:LEU:C	1:A:76:LEU:HD23	0.46	2.31	2	2
1:A:169:LEU:C	1:A:169:LEU:HD23	0.46	2.30	8	1
1:A:165:SER:O	1:A:168:VAL:HG12	0.46	2.11	8	1
1:A:85:LEU:C	1:A:85:LEU:HD23	0.46	2.31	8	1
1:A:124:GLU:O	1:A:125:LEU:CB	0.46	2.64	6	1
1:A:96:ILE:HG22	1:A:98:PRO:HD2	0.45	1.88	3	1
1:A:86:TYR:CD1	1:A:158:LEU:HD12	0.45	2.46	5	2
1:A:152:VAL:O	1:A:155:ALA:HB3	0.45	2.11	6	2
1:A:79:LEU:HD13	1:A:79:LEU:O	0.45	2.11	2	1
1:A:86:TYR:CD2	1:A:158:LEU:HD13	0.45	2.46	8	1
1:A:22:VAL:HG11	1:A:166:TYR:CE2	0.45	2.47	8	1
1:A:80:HIS:NE2	1:A:119:TRP:CZ3	0.45	2.84	1	2
1:A:115:ALA:O	1:A:119:TRP:CB	0.45	2.65	6	1
1:A:56:GLY:O	1:A:58:PRO:HD2	0.45	2.11	9	2
1:A:80:HIS:CD2	1:A:119:TRP:CD2	0.44	3.05	6	1
1:A:119:TRP:CE3	1:A:119:TRP:HA	0.44	2.47	8	3
1:A:57:ILE:HG22	1:A:58:PRO:HD3	0.44	1.89	9	1
1:A:144:ALA:HB3	1:A:147:ARG:CD	0.43	2.39	3	1
1:A:59:TRP:CH2	1:A:154:VAL:HG22	0.43	2.48	8	1
1:A:152:VAL:HG23	1:A:153:LEU:N	0.43	2.28	4	4
1:A:57:ILE:CG2	1:A:58:PRO:HD3	0.43	2.43	9	1
1:A:56:GLY:O	1:A:57:ILE:HB	0.43	2.14	5	1
1:A:153:LEU:HD12	1:A:157:HIS:NE2	0.43	2.28	5	1
1:A:119:TRP:CE3	1:A:122:MET:HB3	0.43	2.48	4	1
1:A:93:LEU:O	1:A:96:ILE:HG22	0.43	2.13	8	1
1:A:55:LEU:HD23	1:A:141:PHE:CE1	0.43	2.49	10	1
1:A:119:TRP:CZ3	1:A:122:MET:HG3	0.43	2.49	5	2
1:A:89:LEU:O	1:A:93:LEU:HD12	0.42	2.15	7	1
1:A:115:ALA:O	1:A:119:TRP:CG	0.42	2.73	6	1
1:A:139:PRO:O	1:A:140:ALA:CB	0.42	2.68	4	1
1:A:138:MET:N	1:A:139:PRO:HD3	0.42	2.30	8	1
1:A:83:LEU:HD22	1:A:115:ALA:HB2	0.42	1.92	6	1
1:A:117:THR:HG23	1:A:118:ILE:HG13	0.42	1.90	6	1
1:A:138:MET:N	1:A:139:PRO:CD	0.41	2.83	10	2
1:A:80:HIS:CD2	1:A:118:ILE:CG2	0.41	3.02	7	1
1:A:141:PHE:O	1:A:147:ARG:CG	0.41	2.68	1	2
1:A:28:ASP:OD1	1:A:103:THR:HG21	0.41	2.16	8	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:15:LEU:N	1:A:15:LEU:CD2	0.41	2.83	5	1
1:A:151:GLY:O	1:A:155:ALA:HB2	0.41	2.16	8	1
1:A:119:TRP:HA	1:A:119:TRP:CE3	0.41	2.50	1	1
1:A:76:LEU:O	1:A:80:HIS:CB	0.41	2.68	2	1
1:A:50:LEU:HD13	1:A:53:HIS:HE1	0.41	1.74	4	1
1:A:49:VAL:O	1:A:53:HIS:CG	0.41	2.74	2	1
1:A:147:ARG:N	1:A:147:ARG:HD2	0.41	2.30	1	1
1:A:80:HIS:NE2	1:A:119:TRP:CG	0.41	2.88	9	1
1:A:143:SER:O	1:A:144:ALA:CB	0.40	2.69	5	1
1:A:89:LEU:HD23	1:A:154:VAL:CG1	0.40	2.46	2	1
1:A:44:HIS:N	1:A:44:HIS:ND1	0.40	2.69	6	1
1:A:119:TRP:O	1:A:122:MET:CG	0.40	2.69	8	1
1:A:19:LEU:CD2	1:A:170:ARG:NH1	0.40	2.85	1	1
1:A:62:LEU:O	1:A:161:PHE:CD2	0.40	2.75	1	1

6.3 Torsion angles ⓘ

6.3.1 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	136/178 (76%)	117±3 (86±2%)	10±3 (7±2%)	9±3 (7±2%)	3	19
All	All	1360/1780 (76%)	1169 (86%)	102 (8%)	89 (7%)	3	19

All 26 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	57	ILE	10
1	A	140	ALA	8
1	A	41	LYS	8
1	A	143	SER	5
1	A	144	ALA	5
1	A	138	MET	5
1	A	97	SER	5
1	A	44	HIS	4

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Mol	Chain	Res	Type	Models (Total)
1	A	139	PRO	4
1	A	125	LEU	4
1	A	47	GLU	4
1	A	45	PRO	3
1	A	61	PRO	3
1	A	58	PRO	3
1	A	98	PRO	2
1	A	46	GLU	2
1	A	96	ILE	2
1	A	103	THR	2
1	A	101	GLY	2
1	A	42	LEU	2
1	A	142	ALA	1
1	A	102	PRO	1
1	A	124	GLU	1
1	A	141	PHE	1
1	A	171	HIS	1
1	A	43	CYS	1

6.3.2 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	113/145 (78%)	85±4 (75±4%)	28±4 (25±4%)	3	26
All	All	1130/1450 (78%)	849 (75%)	281 (25%)	3	26

All 87 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	122	MET	8
1	A	16	LEU	8
1	A	37	CYS	7
1	A	107	LEU	7
1	A	119	TRP	7
1	A	138	MET	7
1	A	113	ASP	6

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Mol	Chain	Res	Type	Models (Total)
1	A	42	LEU	6
1	A	59	TRP	6
1	A	15	LEU	6
1	A	91	GLN	6
1	A	104	LEU	5
1	A	48	LEU	5
1	A	167	ARG	5
1	A	108	GLN	5
1	A	41	LYS	5
1	A	77	SER	5
1	A	44	HIS	4
1	A	28	ASP	4
1	A	23	ARG	4
1	A	51	LEU	4
1	A	94	GLU	4
1	A	141	PHE	4
1	A	109	LEU	4
1	A	13	SER	4
1	A	124	GLU	4
1	A	114	PHE	4
1	A	79	LEU	4
1	A	123	GLU	4
1	A	97	SER	4
1	A	100	LEU	4
1	A	62	LEU	4
1	A	53	HIS	4
1	A	46	GLU	4
1	A	171	HIS	4
1	A	90	LEU	4
1	A	55	LEU	3
1	A	36	LEU	3
1	A	83	LEU	3
1	A	21	GLN	3
1	A	125	LEU	3
1	A	32	LEU	3
1	A	26	GLN	3
1	A	50	LEU	3
1	A	43	CYS	3
1	A	33	GLN	3
1	A	170	ARG	3
1	A	81	SER	3
1	A	162	LEU	3

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Mol	Chain	Res	Type	Models (Total)
1	A	89	LEU	3
1	A	143	SER	3
1	A	163	GLU	3
1	A	75	CYS	3
1	A	169	LEU	3
1	A	153	LEU	3
1	A	120	GLN	2
1	A	159	GLN	2
1	A	18	CYS	2
1	A	85	LEU	2
1	A	105	ASP	2
1	A	14	PHE	2
1	A	117	THR	2
1	A	24	LYS	2
1	A	158	LEU	2
1	A	17	LYS	2
1	A	147	ARG	2
1	A	121	GLN	2
1	A	35	LYS	1
1	A	80	HIS	1
1	A	99	GLU	1
1	A	157	HIS	1
1	A	96	ILE	1
1	A	116	THR	1
1	A	145	PHE	1
1	A	106	THR	1
1	A	148	ARG	1
1	A	160	SER	1
1	A	54	SER	1
1	A	40	TYR	1
1	A	166	TYR	1
1	A	76	LEU	1
1	A	39	THR	1
1	A	102	PRO	1
1	A	78	GLN	1
1	A	110	ASP	1
1	A	156	SER	1
1	A	146	GLN	1

6.3.3 RNA ⓘ

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 carbohydrates 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