



Full wwPDB NMR Structure Validation Report ⓘ

Mar 26, 2026 – 08:59 AM UTC

PDB ID : 2KGL / pdb_00002kgl
Title : NMR solution structure of MESD
Authors : Chen, J.; Wang, J.
Deposited on : 2009-03-12

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 ⓘ 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

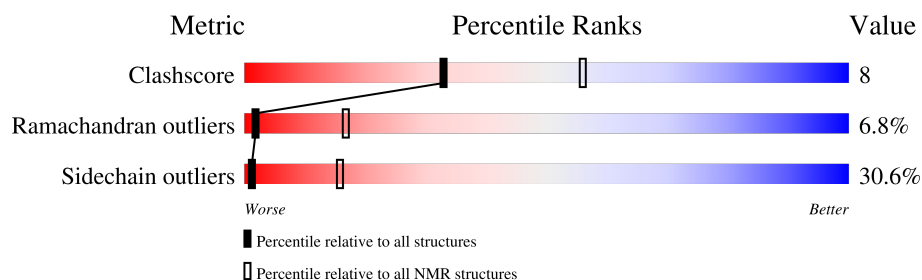
1 Overall quality at a glance

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	195	

2 Ensemble composition and analysis

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: *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:11-A:59, A:64-A:195 (181)	1.26	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 6 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 3073 atoms, of which 1527 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Mesoderm development candidate 2.

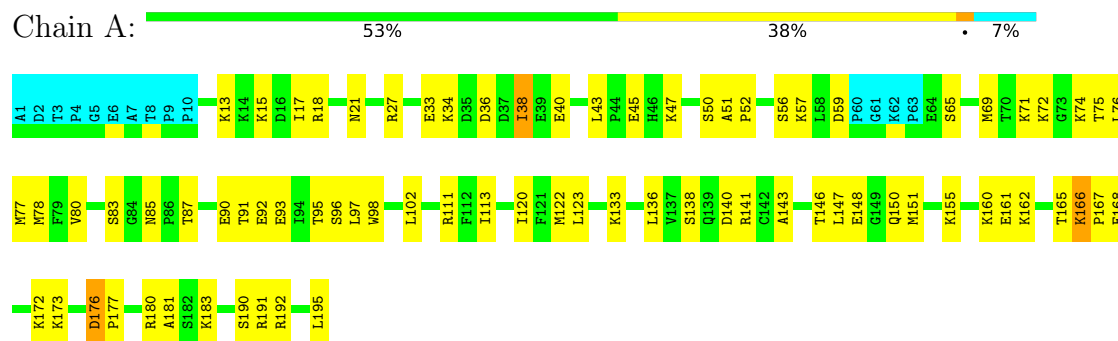
Mol	Chain	Residues	Atoms						Trace
1	A	195	Total	C	H	N	O	S	0
			3073	960	1527	271	308	7	

4 Residue-property plots

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: Mesoderm development candidate 2



4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

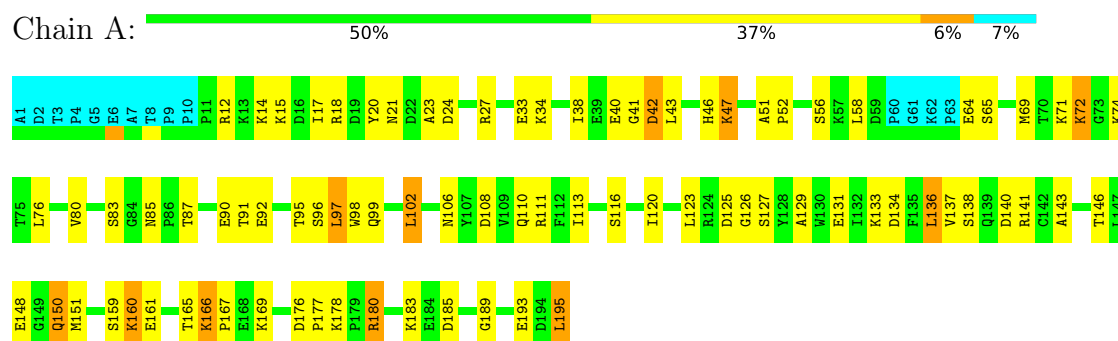
4.2.1 Score per residue for model 1

- Molecule 1: Mesoderm development candidate 2



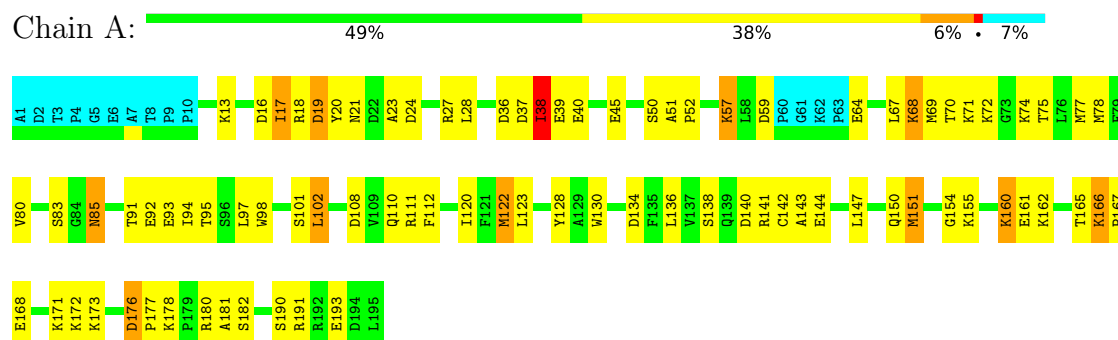
4.2.2 Score per residue for model 2

- Molecule 1: Mesoderm development candidate 2



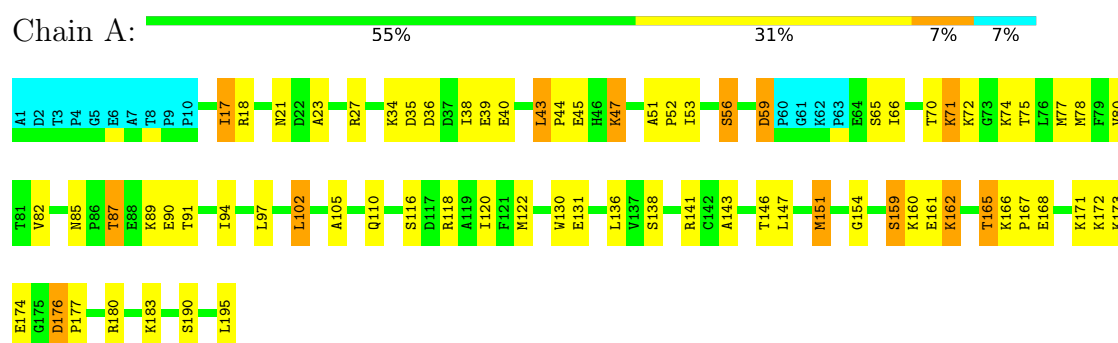
4.2.3 Score per residue for model 3

- Molecule 1: Mesoderm development candidate 2



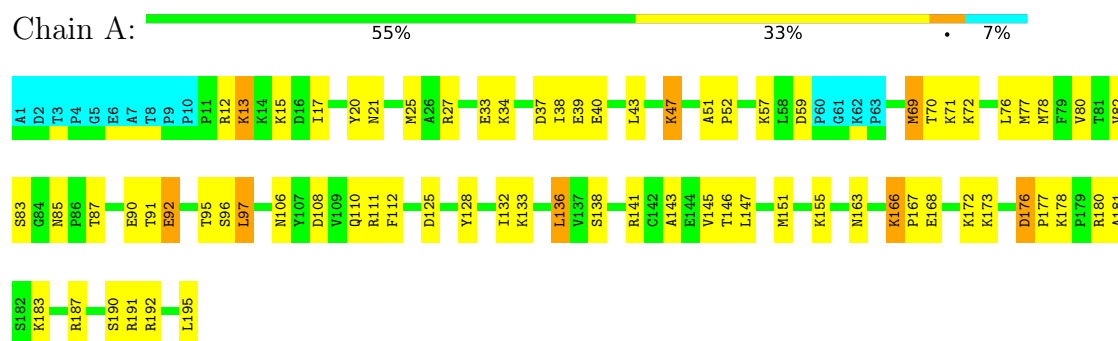
4.2.4 Score per residue for model 4 (medoid)

- Molecule 1: Mesoderm development candidate 2



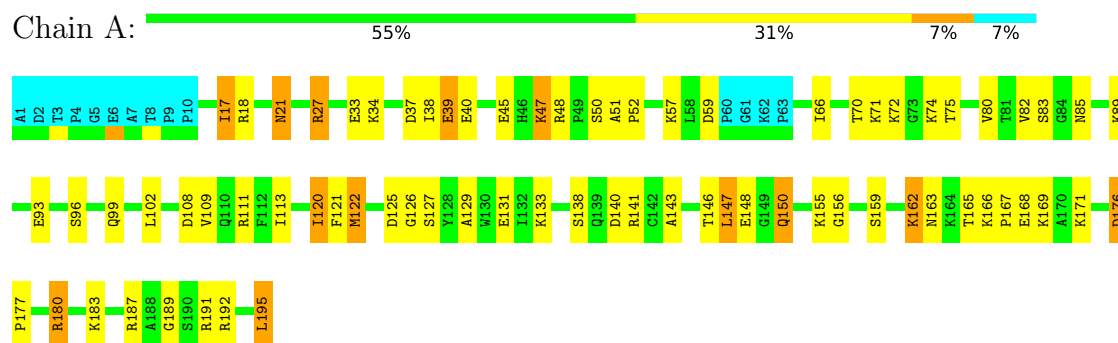
4.2.5 Score per residue for model 5

- Molecule 1: Mesoderm development candidate 2



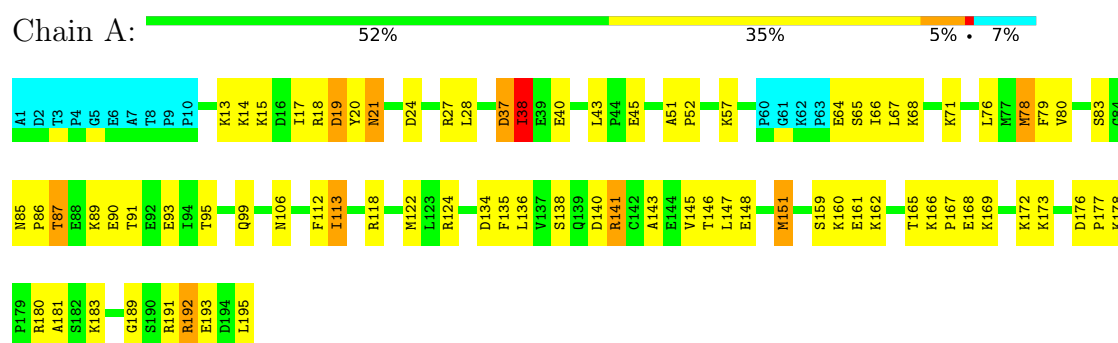
4.2.6 Score per residue for model 6

- Molecule 1: Mesoderm development candidate 2



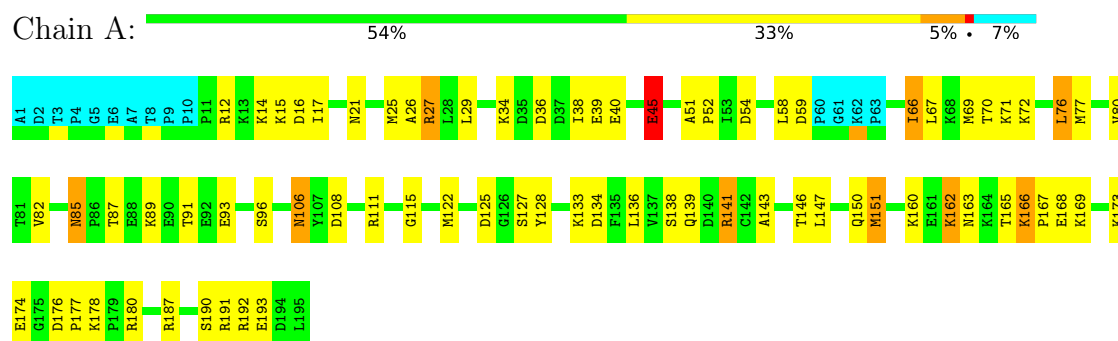
4.2.7 Score per residue for model 7

- Molecule 1: Mesoderm development candidate 2



4.2.8 Score per residue for model 8

- Molecule 1: Mesoderm development candidate 2



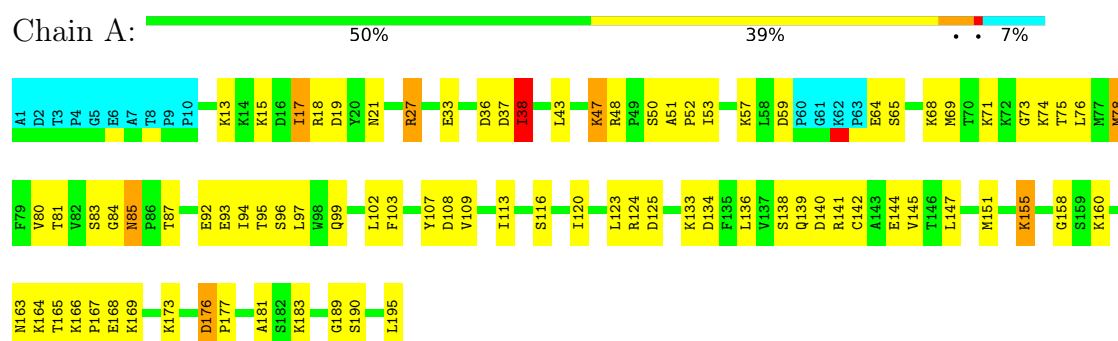
4.2.9 Score per residue for model 9

- Molecule 1: Mesoderm development candidate 2



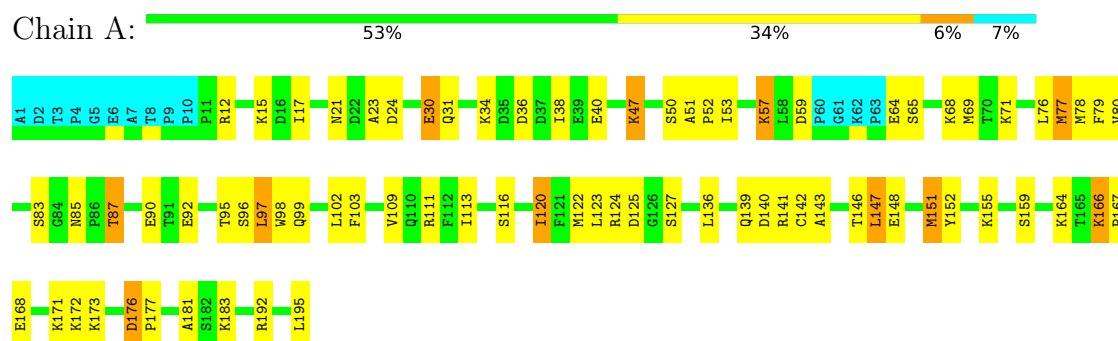
4.2.10 Score per residue for model 10

- Molecule 1: Mesoderm development candidate 2



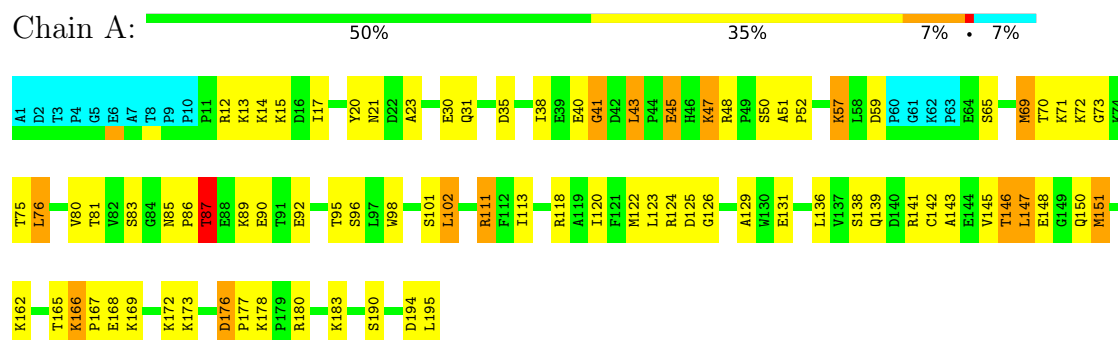
4.2.11 Score per residue for model 11

- Molecule 1: Mesoderm development candidate 2



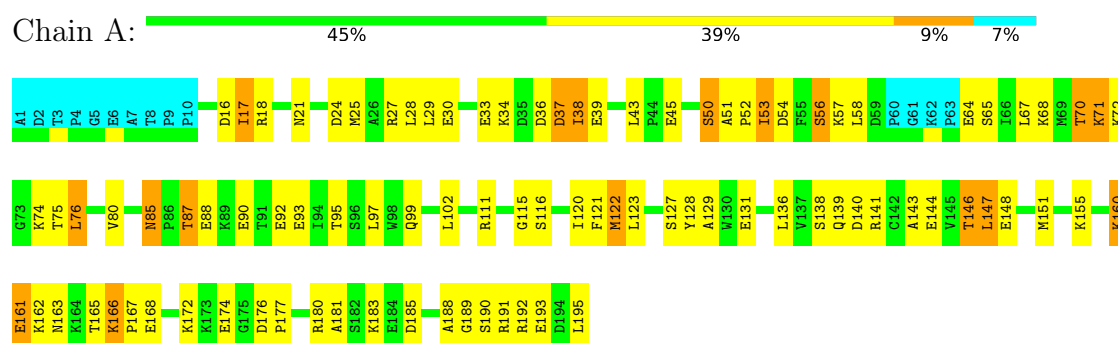
4.2.12 Score per residue for model 12

- Molecule 1: Mesoderm development candidate 2



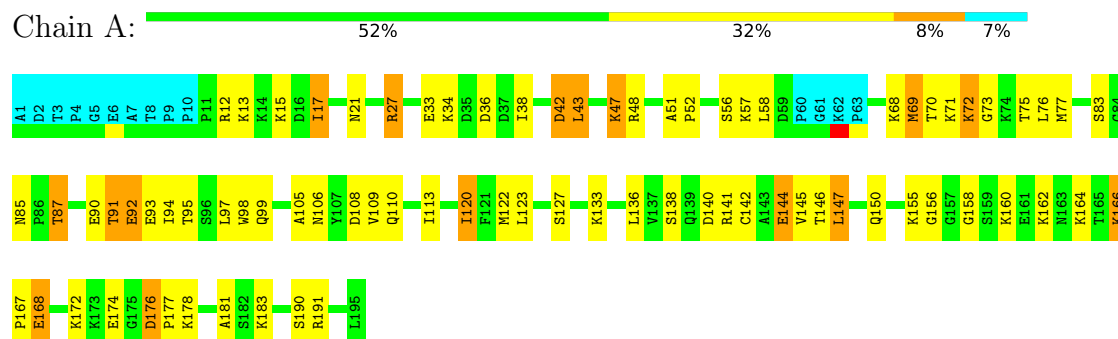
4.2.13 Score per residue for model 13

- Molecule 1: Mesoderm development candidate 2



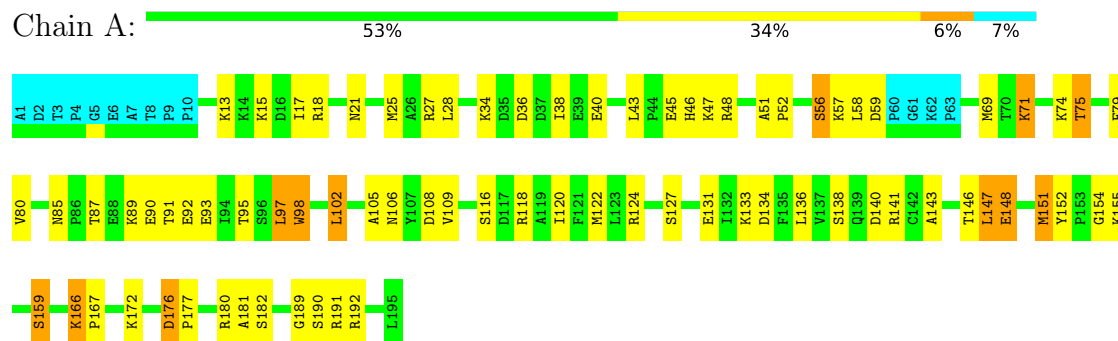
4.2.14 Score per residue for model 14

- Molecule 1: Mesoderm development candidate 2



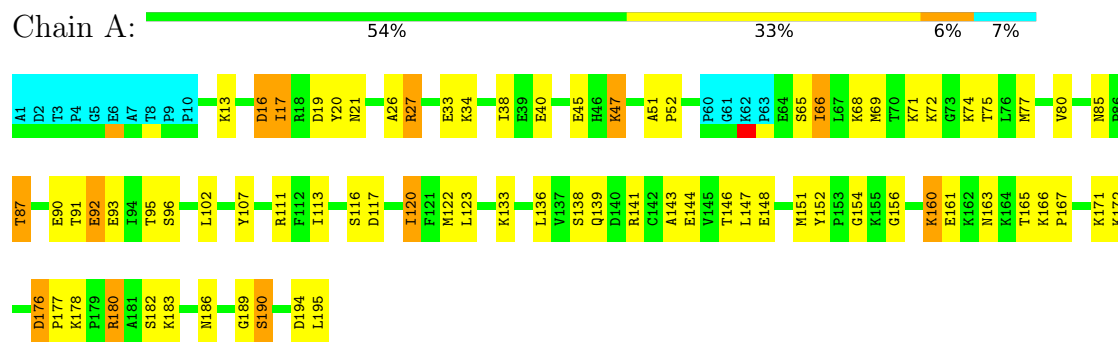
4.2.15 Score per residue for model 15

- Molecule 1: Mesoderm development candidate 2



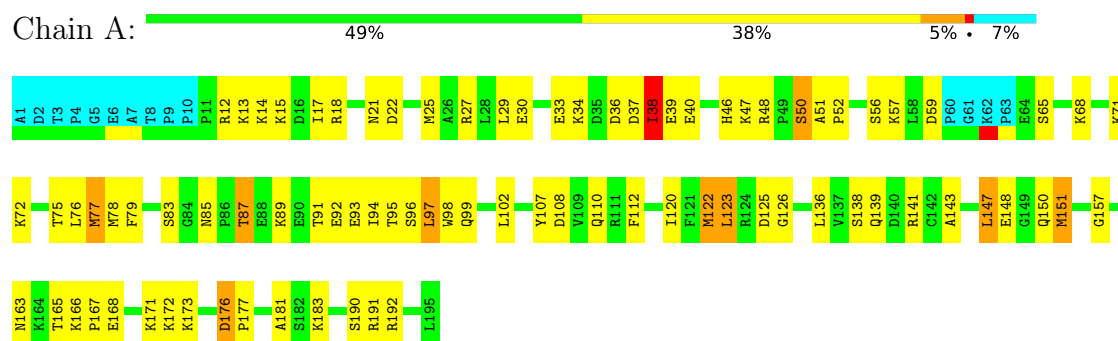
4.2.16 Score per residue for model 16

- Molecule 1: Mesoderm development candidate 2



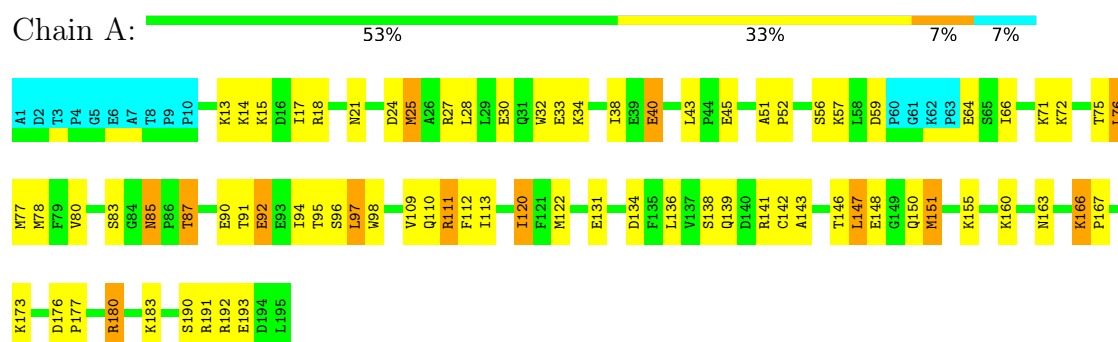
4.2.17 Score per residue for model 17

- Molecule 1: Mesoderm development candidate 2



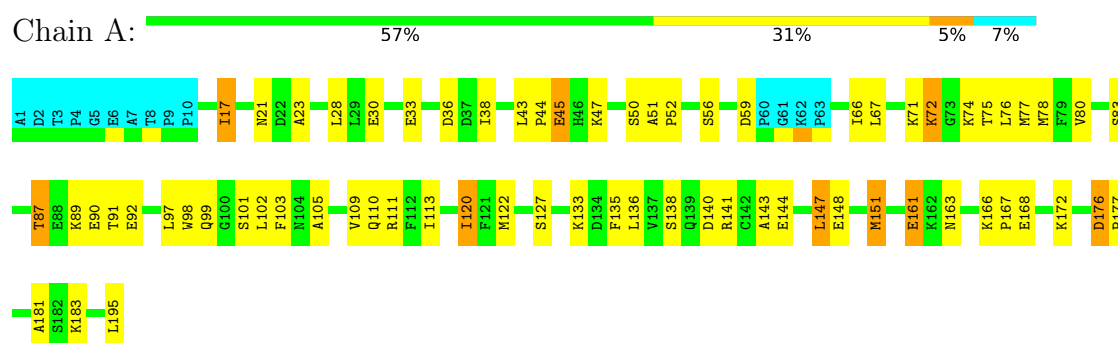
4.2.18 Score per residue for model 18

- Molecule 1: Mesoderm development candidate 2



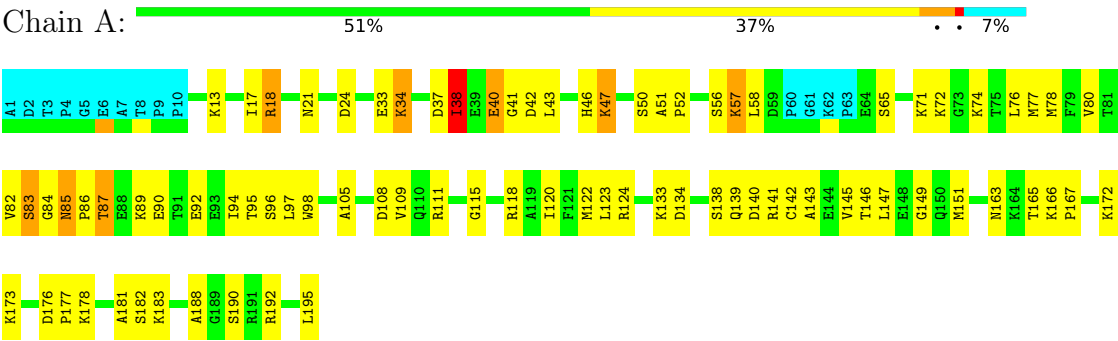
4.2.19 Score per residue for model 19

- Molecule 1: Mesoderm development candidate 2



4.2.20 Score per residue for model 20

- Molecule 1: Mesoderm development candidate 2



5 Refinement protocol and experimental data overview ⓘ

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

Of the 500 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	1.2

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	1453	1439	1439	24±4
All	All	29060	28780	28780	485

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 8.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:LEU:HD13	1:A:122:MET:HE3	0.91	1.43	7	1
1:A:76:LEU:HD23	1:A:97:LEU:HD13	0.86	1.46	11	3
1:A:97:LEU:HD13	1:A:147:LEU:HD21	0.81	1.52	17	1
1:A:123:LEU:HD23	1:A:129:ALA:HB2	0.81	1.52	12	1
1:A:76:LEU:HD23	1:A:97:LEU:HD12	0.77	1.56	19	1
1:A:76:LEU:C	1:A:76:LEU:HD22	0.76	2.05	12	2
1:A:147:LEU:HD22	1:A:147:LEU:C	0.72	2.10	19	4
1:A:97:LEU:HD11	1:A:147:LEU:HD23	0.69	1.64	15	1
1:A:27:ARG:HB3	1:A:91:THR:HG21	0.67	1.67	14	5
1:A:87:THR:O	1:A:91:THR:HG23	0.65	1.92	4	7
1:A:76:LEU:HD11	1:A:122:MET:CG	0.64	2.22	8	1
1:A:78:MET:HE1	1:A:90:GLU:HB3	0.64	1.69	11	2
1:A:41:GLY:O	1:A:145:VAL:HG12	0.64	1.93	20	2
1:A:87:THR:HG21	1:A:145:VAL:HG21	0.63	1.68	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:76:LEU:CD2	1:A:97:LEU:HD13	0.63	2.24	9	1
1:A:87:THR:HG22	1:A:90:GLU:HB2	0.62	1.71	14	6
1:A:40:GLU:HB3	1:A:143:ALA:HB3	0.61	1.71	15	4
1:A:87:THR:HG22	1:A:90:GLU:CG	0.61	2.25	12	1
1:A:98:TRP:CZ2	1:A:109:VAL:HG21	0.61	2.30	14	3
1:A:80:VAL:HG21	1:A:85:ASN:CG	0.61	2.20	10	3
1:A:78:MET:CG	1:A:145:VAL:HG13	0.61	2.26	7	1
1:A:147:LEU:N	1:A:147:LEU:HD13	0.61	2.11	12	1
1:A:76:LEU:HD13	1:A:77:MET:N	0.60	2.12	19	4
1:A:29:LEU:HD22	1:A:192:ARG:HA	0.60	1.73	8	2
1:A:97:LEU:HD21	1:A:147:LEU:HD11	0.60	1.72	17	1
1:A:23:ALA:HB1	1:A:111:ARG:NE	0.60	2.12	9	1
1:A:76:LEU:HD11	1:A:122:MET:HG3	0.59	1.74	8	1
1:A:27:ARG:CB	1:A:91:THR:HG21	0.59	2.27	14	4
1:A:120:ILE:HD11	1:A:122:MET:HE3	0.59	1.75	15	2
1:A:85:ASN:OD1	1:A:143:ALA:HB1	0.59	1.98	20	3
1:A:92:GLU:O	1:A:95:THR:HG22	0.58	1.98	13	15
1:A:98:TRP:NE1	1:A:102:LEU:HD23	0.58	2.14	3	2
1:A:132:ILE:HG22	1:A:136:LEU:HD23	0.58	1.73	5	1
1:A:79:PHE:CE1	1:A:123:LEU:HD12	0.58	2.34	17	1
1:A:80:VAL:HG23	1:A:143:ALA:HA	0.57	1.75	1	15
1:A:120:ILE:HG12	1:A:122:MET:HE3	0.57	1.76	11	2
1:A:146:THR:C	1:A:147:LEU:HD13	0.57	2.24	12	1
1:A:69:MET:HE2	1:A:72:LYS:HA	0.57	1.77	2	1
1:A:40:GLU:CB	1:A:143:ALA:HB3	0.57	2.30	17	3
1:A:67:LEU:HD13	1:A:163:ASN:HB2	0.57	1.76	8	1
1:A:120:ILE:HD11	1:A:122:MET:HE2	0.57	1.75	9	1
1:A:93:GLU:HB3	1:A:147:LEU:HD11	0.57	1.77	10	1
1:A:87:THR:HG22	1:A:90:GLU:HG3	0.57	1.77	12	1
1:A:78:MET:CG	1:A:145:VAL:HG23	0.56	2.29	1	3
1:A:120:ILE:HG12	1:A:122:MET:HE2	0.56	1.77	12	2
1:A:75:THR:O	1:A:97:LEU:HD22	0.56	2.01	13	1
1:A:97:LEU:HD11	1:A:147:LEU:HD21	0.56	1.77	14	2
1:A:68:LYS:O	1:A:70:THR:HG23	0.56	2.00	3	1
1:A:98:TRP:CZ2	1:A:102:LEU:HD12	0.56	2.36	17	2
1:A:45:GLU:HG2	1:A:146:THR:HG23	0.56	1.76	8	1
1:A:76:LEU:C	1:A:76:LEU:CD2	0.56	2.79	18	2
1:A:17:ILE:HD11	1:A:109:VAL:O	0.56	2.01	14	2
1:A:56:SER:OG	1:A:105:ALA:HB3	0.56	1.99	15	1
1:A:59:ASP:CB	1:A:105:ALA:HB1	0.56	2.30	4	1
1:A:67:LEU:HD22	1:A:159:SER:CB	0.56	2.30	7	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:29:LEU:HD12	1:A:192:ARG:HG2	0.56	1.76	17	1
1:A:81:THR:HG21	1:A:139:GLN:HB2	0.56	1.77	10	1
1:A:74:LYS:O	1:A:97:LEU:HD22	0.55	2.00	19	2
1:A:120:ILE:CG1	1:A:122:MET:HE3	0.55	2.32	14	2
1:A:69:MET:O	1:A:69:MET:HE3	0.55	2.01	2	1
1:A:67:LEU:HD22	1:A:161:GLU:HG3	0.55	1.79	3	2
1:A:23:ALA:HB1	1:A:111:ARG:CD	0.55	2.32	2	4
1:A:78:MET:HE3	1:A:147:LEU:HB3	0.55	1.78	19	1
1:A:90:GLU:OE2	1:A:147:LEU:HD21	0.55	2.02	19	1
1:A:98:TRP:CH2	1:A:109:VAL:HG21	0.55	2.36	14	2
1:A:94:ILE:HD12	1:A:122:MET:HE2	0.55	1.79	3	1
1:A:97:LEU:CD1	1:A:147:LEU:HD23	0.54	2.32	15	1
1:A:76:LEU:HD21	1:A:122:MET:HB2	0.54	1.79	13	1
1:A:27:ARG:CZ	1:A:120:ILE:HG21	0.54	2.32	16	1
1:A:25:MET:HG3	1:A:28:LEU:HD12	0.54	1.80	18	1
1:A:94:ILE:HD12	1:A:122:MET:CE	0.54	2.33	3	2
1:A:75:THR:HG22	1:A:154:GLY:CA	0.54	2.33	15	1
1:A:76:LEU:HD22	1:A:97:LEU:CB	0.54	2.32	2	1
1:A:16:ASP:C	1:A:17:ILE:HD12	0.54	2.28	16	3
1:A:43:LEU:HD11	1:A:144:GLU:CG	0.54	2.31	14	1
1:A:48:ARG:CZ	1:A:146:THR:HG21	0.53	2.33	12	1
1:A:70:THR:HG23	1:A:162:LYS:HB3	0.53	1.78	13	1
1:A:78:MET:HG3	1:A:145:VAL:HG13	0.53	1.79	7	1
1:A:58:LEU:HD23	1:A:105:ALA:O	0.53	2.03	14	1
1:A:26:ALA:HB2	1:A:190:SER:CB	0.53	2.34	16	1
1:A:29:LEU:HD13	1:A:192:ARG:HB3	0.53	1.81	8	1
1:A:121:PHE:CE1	1:A:129:ALA:HB1	0.53	2.37	13	2
1:A:147:LEU:HD22	1:A:148:GLU:N	0.53	2.19	11	2
1:A:67:LEU:HD13	1:A:163:ASN:CB	0.53	2.34	8	1
1:A:39:GLU:HG2	1:A:82:VAL:HG21	0.52	1.80	6	3
1:A:102:LEU:O	1:A:102:LEU:HD23	0.52	2.04	16	1
1:A:147:LEU:C	1:A:147:LEU:CD2	0.52	2.82	19	4
1:A:97:LEU:CD2	1:A:147:LEU:HD11	0.52	2.34	17	1
1:A:166:LYS:CB	1:A:167:PRO:CD	0.52	2.87	15	17
1:A:70:THR:HG23	1:A:162:LYS:CB	0.52	2.34	13	2
1:A:29:LEU:HD13	1:A:192:ARG:CB	0.52	2.35	8	1
1:A:113:ILE:HG22	1:A:118:ARG:CZ	0.52	2.35	7	1
1:A:26:ALA:HB2	1:A:190:SER:HB3	0.52	1.82	16	1
1:A:147:LEU:HD22	1:A:147:LEU:O	0.51	2.05	6	4
1:A:102:LEU:O	1:A:102:LEU:HD13	0.51	2.05	12	3
1:A:45:GLU:HG3	1:A:146:THR:HG22	0.51	1.82	13	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:70:THR:HG23	1:A:162:LYS:HB2	0.51	1.83	4	2
1:A:27:ARG:NE	1:A:120:ILE:HD13	0.51	2.21	6	1
1:A:166:LYS:N	1:A:167:PRO:HD2	0.51	2.21	19	15
1:A:76:LEU:HD22	1:A:76:LEU:O	0.51	2.06	18	2
1:A:102:LEU:HD11	1:A:176:ASP:OD2	0.51	2.06	11	1
1:A:109:VAL:HG22	1:A:122:MET:CB	0.51	2.36	19	2
1:A:120:ILE:CG1	1:A:122:MET:HE2	0.51	2.36	12	1
1:A:28:LEU:HG	1:A:91:THR:HG21	0.51	1.83	19	3
1:A:147:LEU:HD13	1:A:147:LEU:C	0.50	2.32	11	8
1:A:67:LEU:HD13	1:A:161:GLU:HG2	0.50	1.82	9	1
1:A:109:VAL:HG22	1:A:122:MET:HB2	0.50	1.82	19	1
1:A:97:LEU:HD21	1:A:147:LEU:HD21	0.49	1.83	18	2
1:A:17:ILE:HG23	1:A:23:ALA:HB2	0.49	1.84	4	1
1:A:111:ARG:HA	1:A:120:ILE:HD12	0.49	1.84	19	2
1:A:39:GLU:CG	1:A:82:VAL:HG21	0.49	2.37	8	1
1:A:87:THR:HG21	1:A:145:VAL:HG11	0.49	1.84	14	2
1:A:77:MET:HE3	1:A:146:THR:HB	0.49	1.85	9	1
1:A:75:THR:HG21	1:A:124:ARG:NH2	0.49	2.23	10	1
1:A:109:VAL:HG13	1:A:122:MET:HB3	0.49	1.83	19	2
1:A:51:ALA:HB1	1:A:52:PRO:HD2	0.49	1.85	15	20
1:A:78:MET:SD	1:A:145:VAL:HG23	0.49	2.48	10	2
1:A:108:ASP:OD2	1:A:129:ALA:HB3	0.49	2.07	2	1
1:A:43:LEU:HB3	1:A:145:VAL:HG13	0.49	1.85	12	1
1:A:29:LEU:HD13	1:A:192:ARG:HB2	0.48	1.84	13	1
1:A:80:VAL:CG2	1:A:82:VAL:HG12	0.48	2.38	20	1
1:A:27:ARG:HD3	1:A:120:ILE:HD12	0.48	1.84	3	1
1:A:50:SER:OG	1:A:77:MET:HE1	0.48	2.09	17	2
1:A:147:LEU:HD13	1:A:148:GLU:N	0.48	2.24	17	1
1:A:18:ARG:NH1	1:A:188:ALA:HB1	0.48	2.24	20	1
1:A:17:ILE:HG23	1:A:23:ALA:CB	0.48	2.38	4	2
1:A:23:ALA:HB1	1:A:111:ARG:HG2	0.48	1.85	11	1
1:A:97:LEU:HD21	1:A:147:LEU:CD2	0.48	2.39	15	1
1:A:39:GLU:HG2	1:A:82:VAL:HG11	0.47	1.85	1	3
1:A:98:TRP:CE2	1:A:102:LEU:HD23	0.47	2.44	2	1
1:A:76:LEU:HD13	1:A:76:LEU:C	0.47	2.34	11	2
1:A:27:ARG:CD	1:A:120:ILE:HD12	0.47	2.38	3	1
1:A:147:LEU:C	1:A:147:LEU:HD13	0.47	2.34	1	2
1:A:86:PRO:O	1:A:87:THR:HG23	0.47	2.09	12	3
1:A:58:LEU:HD23	1:A:106:ASN:OD1	0.47	2.09	8	1
1:A:27:ARG:HB2	1:A:91:THR:HG21	0.47	1.86	9	1
1:A:78:MET:SD	1:A:94:ILE:HD11	0.47	2.49	4	2

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:50:SER:HB3	1:A:75:THR:HG21	0.47	1.86	13	1
1:A:27:ARG:NE	1:A:120:ILE:HG21	0.47	2.23	16	2
1:A:27:ARG:CZ	1:A:120:ILE:HD13	0.47	2.39	6	1
1:A:67:LEU:HD22	1:A:159:SER:HB3	0.47	1.87	7	1
1:A:23:ALA:HB1	1:A:111:ARG:HD2	0.47	1.86	2	1
1:A:76:LEU:HD22	1:A:97:LEU:C	0.47	2.35	17	1
1:A:176:ASP:N	1:A:177:PRO:HD2	0.47	2.25	16	20
1:A:65:SER:HA	1:A:165:THR:HG21	0.47	1.87	9	1
1:A:34:LYS:CE	1:A:38:ILE:HD12	0.47	2.40	20	1
1:A:78:MET:CB	1:A:122:MET:HE3	0.47	2.40	20	1
1:A:79:PHE:HB3	1:A:136:LEU:HD13	0.47	1.87	11	4
1:A:97:LEU:HD11	1:A:147:LEU:CD2	0.47	2.40	14	2
1:A:37:ASP:O	1:A:38:ILE:C	0.46	2.58	3	6
1:A:176:ASP:CB	1:A:177:PRO:CD	0.46	2.94	13	20
1:A:109:VAL:HG23	1:A:122:MET:HB3	0.46	1.84	9	1
1:A:66:ILE:HG12	1:A:102:LEU:HD23	0.46	1.86	4	1
1:A:78:MET:SD	1:A:122:MET:HE3	0.46	2.51	9	1
1:A:111:ARG:NH1	1:A:113:ILE:HD12	0.46	2.26	18	1
1:A:24:ASP:O	1:A:91:THR:HG23	0.46	2.11	3	1
1:A:17:ILE:HG12	1:A:109:VAL:HG23	0.46	1.86	10	1
1:A:30:GLU:OE2	1:A:113:ILE:HG23	0.46	2.11	11	1
1:A:66:ILE:HD11	1:A:99:GLN:O	0.46	2.11	7	1
1:A:76:LEU:HD13	1:A:94:ILE:HD12	0.46	1.87	10	1
1:A:69:MET:HE1	1:A:103:PHE:CD1	0.45	2.46	10	1
1:A:165:THR:HG22	1:A:167:PRO:HD2	0.45	1.88	4	1
1:A:69:MET:O	1:A:70:THR:C	0.45	2.60	14	4
1:A:94:ILE:HG21	1:A:122:MET:HE1	0.45	1.88	18	1
1:A:147:LEU:HD13	1:A:147:LEU:O	0.45	2.11	11	1
1:A:78:MET:HE3	1:A:147:LEU:HB2	0.45	1.89	5	1
1:A:17:ILE:HD13	1:A:109:VAL:CG1	0.45	2.42	6	1
1:A:76:LEU:HD23	1:A:147:LEU:HD23	0.45	1.89	5	1
1:A:136:LEU:C	1:A:136:LEU:HD13	0.45	2.36	4	1
1:A:136:LEU:HD23	1:A:137:VAL:N	0.44	2.26	2	1
1:A:19:ASP:O	1:A:20:TYR:C	0.44	2.60	7	3
1:A:75:THR:HG22	1:A:154:GLY:N	0.44	2.27	4	3
1:A:159:SER:O	1:A:160:LYS:C	0.44	2.60	9	2
1:A:43:LEU:HD22	1:A:43:LEU:N	0.44	2.27	19	1
1:A:80:VAL:HG21	1:A:85:ASN:OD1	0.44	2.12	18	1
1:A:34:LYS:HE3	1:A:38:ILE:HD12	0.44	1.89	20	1
1:A:27:ARG:CD	1:A:120:ILE:HG21	0.44	2.42	10	2
1:A:82:VAL:O	1:A:83:SER:C	0.44	2.59	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:69:MET:HE3	1:A:99:GLN:O	0.44	2.12	11	1
1:A:78:MET:HB2	1:A:122:MET:HE3	0.44	1.90	4	1
1:A:21:ASN:OD1	1:A:95:THR:HG23	0.44	2.13	7	1
1:A:78:MET:HE2	1:A:147:LEU:HB2	0.44	1.89	17	1
1:A:98:TRP:CZ2	1:A:102:LEU:HD13	0.44	2.48	11	1
1:A:44:PRO:O	1:A:45:GLU:C	0.43	2.61	4	2
1:A:191:ARG:O	1:A:192:ARG:C	0.43	2.61	13	7
1:A:78:MET:HB3	1:A:122:MET:HE3	0.43	1.89	20	1
1:A:43:LEU:HD12	1:A:144:GLU:HA	0.43	1.89	13	1
1:A:45:GLU:CG	1:A:146:THR:HG23	0.43	2.43	8	1
1:A:41:GLY:C	1:A:145:VAL:HG12	0.43	2.38	20	1
1:A:126:GLY:O	1:A:129:ALA:HB3	0.43	2.13	6	1
1:A:75:THR:HG21	1:A:124:ARG:CD	0.43	2.43	9	1
1:A:98:TRP:CH2	1:A:109:VAL:HG11	0.43	2.49	14	2
1:A:78:MET:HG2	1:A:145:VAL:HG23	0.43	1.90	1	1
1:A:78:MET:HE3	1:A:94:ILE:HD11	0.43	1.91	9	1
1:A:147:LEU:CD1	1:A:147:LEU:N	0.43	2.82	13	3
1:A:78:MET:HE2	1:A:145:VAL:HB	0.43	1.91	9	1
1:A:29:LEU:HD22	1:A:192:ARG:CA	0.43	2.43	13	1
1:A:76:LEU:HD13	1:A:122:MET:CE	0.42	2.29	7	1
1:A:120:ILE:CD1	1:A:122:MET:HE2	0.42	2.44	9	1
1:A:121:PHE:HE1	1:A:129:ALA:HB1	0.42	1.73	13	1
1:A:76:LEU:HD12	1:A:94:ILE:HG23	0.42	1.91	14	1
1:A:82:VAL:HG13	1:A:84:GLY:O	0.42	2.14	20	1
1:A:79:PHE:CZ	1:A:123:LEU:HD13	0.42	2.49	9	1
1:A:147:LEU:N	1:A:147:LEU:CD1	0.42	2.81	12	2
1:A:76:LEU:HD12	1:A:77:MET:N	0.42	2.30	8	1
1:A:66:ILE:HD13	1:A:103:PHE:CE2	0.42	2.50	19	1
1:A:150:GLN:CG	1:A:151:MET:HE2	0.42	2.44	2	1
1:A:39:GLU:CG	1:A:82:VAL:HG11	0.42	2.44	4	1
1:A:28:LEU:HD12	1:A:28:LEU:C	0.42	2.40	7	2
1:A:98:TRP:CZ3	1:A:102:LEU:HD23	0.42	2.49	15	1
1:A:40:GLU:HB2	1:A:143:ALA:HB3	0.42	1.90	17	1
1:A:66:ILE:HD13	1:A:102:LEU:C	0.42	2.39	4	1
1:A:98:TRP:CZ2	1:A:109:VAL:HG11	0.42	2.49	15	1
1:A:78:MET:CE	1:A:94:ILE:HD11	0.42	2.44	10	2
1:A:102:LEU:HD11	1:A:176:ASP:CG	0.41	2.40	11	1
1:A:121:PHE:CA	1:A:122:MET:HE2	0.41	2.46	6	1
1:A:26:ALA:HB3	1:A:27:ARG:NH2	0.41	2.30	8	1
1:A:78:MET:HE1	1:A:90:GLU:CB	0.41	2.42	11	1
1:A:17:ILE:HG13	1:A:109:VAL:HG23	0.41	1.91	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:166:LYS:CB	1:A:167:PRO:HD3	0.41	2.45	15	2
1:A:193:GLU:OE2	1:A:195:LEU:HD23	0.41	2.14	2	1
1:A:76:LEU:HD12	1:A:76:LEU:C	0.41	2.41	7	1
1:A:166:LYS:N	1:A:167:PRO:CD	0.41	2.84	11	1
1:A:185:ASP:O	1:A:188:ALA:HB3	0.41	2.15	13	1
1:A:87:THR:HG22	1:A:90:GLU:CB	0.41	2.46	16	1
1:A:80:VAL:HG23	1:A:143:ALA:CB	0.41	2.46	4	2
1:A:76:LEU:HD11	1:A:122:MET:HG2	0.41	1.90	8	1
1:A:27:ARG:HH22	1:A:119:ALA:N	0.41	2.14	9	1
1:A:69:MET:HE3	1:A:155:LYS:HD3	0.41	1.92	10	1
1:A:166:LYS:C	1:A:168:GLU:H	0.41	2.24	14	1
1:A:39:GLU:HG3	1:A:82:VAL:HG21	0.40	1.94	5	1
1:A:195:LEU:O	1:A:195:LEU:HD23	0.40	2.15	6	1
1:A:67:LEU:HD22	1:A:161:GLU:CB	0.40	2.46	19	1
1:A:58:LEU:HD22	1:A:105:ALA:O	0.40	2.15	20	1
1:A:43:LEU:HD23	1:A:44:PRO:HD2	0.40	1.92	4	1
1:A:66:ILE:CG1	1:A:69:MET:HE2	0.40	2.47	8	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	180/195 (92%)	131±4 (73±2%)	37±4 (20±2%)	12±2 (7±1%)	2	17
All	All	3600/3900 (92%)	2620 (73%)	735 (20%)	245 (7%)	2	17

All 38 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	17	ILE	20
1	A	21	ASN	20
1	A	38	ILE	20
1	A	71	LYS	20
1	A	141	ARG	20

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Mol	Chain	Res	Type	Models (Total)
1	A	47	LYS	15
1	A	151	MET	15
1	A	181	ALA	13
1	A	160	LYS	9
1	A	45	GLU	8
1	A	75	THR	8
1	A	56	SER	7
1	A	180	ARG	7
1	A	189	GLY	7
1	A	57	LYS	6
1	A	150	GLN	4
1	A	115	GLY	4
1	A	194	ASP	3
1	A	41	GLY	3
1	A	42	ASP	3
1	A	126	GLY	3
1	A	53	ILE	3
1	A	156	GLY	3
1	A	73	GLY	3
1	A	107	TYR	3
1	A	72	LYS	3
1	A	159	SER	2
1	A	162	LYS	2
1	A	158	GLY	2
1	A	55	PHE	1
1	A	13	LYS	1
1	A	84	GLY	1
1	A	87	THR	1
1	A	58	LEU	1
1	A	157	GLY	1
1	A	191	ARG	1
1	A	83	SER	1
1	A	149	GLY	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	158/168 (94%)	110±5 (69±3%)	48±5 (31±3%)	1	16
All	All	3160/3360 (94%)	2193 (69%)	967 (31%)	1	16

All 129 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	85	ASN	19
1	A	138	SER	18
1	A	183	LYS	17
1	A	146	THR	15
1	A	172	LYS	15
1	A	34	LYS	14
1	A	72	LYS	14
1	A	165	THR	14
1	A	87	THR	14
1	A	168	GLU	14
1	A	83	SER	13
1	A	151	MET	13
1	A	173	LYS	13
1	A	195	LEU	13
1	A	176	ASP	13
1	A	190	SER	13
1	A	15	LYS	12
1	A	18	ARG	12
1	A	33	GLU	12
1	A	43	LEU	12
1	A	47	LYS	12
1	A	96	SER	12
1	A	140	ASP	12
1	A	40	GLU	12
1	A	136	LEU	12
1	A	59	ASP	12
1	A	27	ARG	11
1	A	36	ASP	11
1	A	166	LYS	11
1	A	65	SER	11
1	A	133	LYS	11
1	A	13	LYS	11
1	A	57	LYS	11
1	A	50	SER	10
1	A	77	MET	10
1	A	89	LYS	10

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Mol	Chain	Res	Type	Models (Total)
1	A	93	GLU	10
1	A	120	ILE	10
1	A	127	SER	10
1	A	180	ARG	10
1	A	148	GLU	10
1	A	178	LYS	10
1	A	155	LYS	10
1	A	147	LEU	10
1	A	74	LYS	9
1	A	110	GLN	9
1	A	113	ILE	9
1	A	97	LEU	9
1	A	102	LEU	9
1	A	123	LEU	9
1	A	108	ASP	9
1	A	163	ASN	9
1	A	12	ARG	8
1	A	25	MET	8
1	A	99	GLN	8
1	A	111	ARG	8
1	A	171	LYS	8
1	A	64	GLU	8
1	A	116	SER	8
1	A	125	ASP	8
1	A	131	GLU	8
1	A	134	ASP	8
1	A	68	LYS	8
1	A	139	GLN	8
1	A	90	GLU	7
1	A	162	LYS	7
1	A	193	GLU	7
1	A	14	LYS	7
1	A	24	ASP	7
1	A	150	GLN	7
1	A	161	GLU	7
1	A	169	LYS	7
1	A	69	MET	7
1	A	142	CYS	7
1	A	48	ARG	6
1	A	118	ARG	6
1	A	122	MET	6
1	A	128	TYR	6

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Mol	Chain	Res	Type	Models (Total)
1	A	106	ASN	6
1	A	92	GLU	6
1	A	30	GLU	6
1	A	45	GLU	5
1	A	46	HIS	5
1	A	78	MET	5
1	A	159	SER	5
1	A	174	GLU	5
1	A	38	ILE	5
1	A	39	GLU	5
1	A	112	PHE	5
1	A	144	GLU	5
1	A	56	SER	5
1	A	124	ARG	5
1	A	76	LEU	5
1	A	58	LEU	4
1	A	101	SER	4
1	A	42	ASP	4
1	A	160	LYS	4
1	A	182	SER	4
1	A	37	ASP	4
1	A	16	ASP	3
1	A	31	GLN	3
1	A	35	ASP	3
1	A	135	PHE	3
1	A	20	TYR	3
1	A	19	ASP	3
1	A	191	ARG	3
1	A	71	LYS	3
1	A	187	ARG	3
1	A	66	ILE	3
1	A	192	ARG	3
1	A	164	LYS	3
1	A	152	TYR	3
1	A	21	ASN	2
1	A	91	THR	2
1	A	130	TRP	2
1	A	141	ARG	2
1	A	54	ASP	2
1	A	32	TRP	2
1	A	117	ASP	2
1	A	53	ILE	2

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Mol	Chain	Res	Type	Models (Total)
1	A	185	ASP	1
1	A	28	LEU	1
1	A	103	PHE	1
1	A	81	THR	1
1	A	70	THR	1
1	A	88	GLU	1
1	A	98	TRP	1
1	A	186	ASN	1
1	A	22	ASP	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 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