Full wwPDB NMR Structure Validation Report (i)

Apr 21, 2024 – 12:00 AM EDT

PDB ID	:	2LNC
BMRB ID	:	17523
Title	:	Solution NMR structure of Norwalk virus protease
Authors	:	Takahashi, D.; Hiromasa, Y.; Kim, Y.; Anbanandam, A.; Chang, K.; Prakash, O.
Deposited on	:	2011-12-22

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 types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

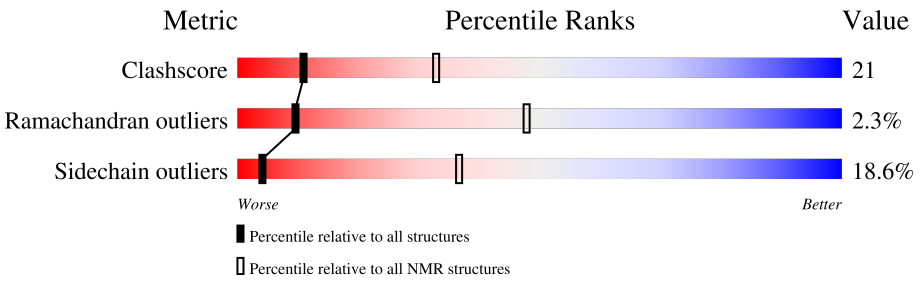
MolProbity	:	4.02b-467
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
wwPDB-RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
wwPDB-ShiftChecker	:	v1.2
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 is 84%.

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	188	

2 Ensemble composition and analysis (i)

This entry contains 20 models. Model 9 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:9-A:112, A:122-A:179 (162)	1.10	9

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 4 single-model clusters were found.

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

3 Entry composition (i)

There is only 1 type of molecule in this entry. The entry contains 2814 atoms, of which 1404 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called 3C-like protease.

Mol	Chain	Residues	Atoms						Trace
			Total	C	H	N	O	S	
1	A	188	2814	890	1404	254	254	12	0

There are 7 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP Q83883
A	2	HIS	-	expression tag	UNP Q83883
A	3	HIS	-	expression tag	UNP Q83883
A	4	HIS	-	expression tag	UNP Q83883
A	5	HIS	-	expression tag	UNP Q83883
A	6	HIS	-	expression tag	UNP Q83883
A	7	HIS	-	expression tag	UNP Q83883

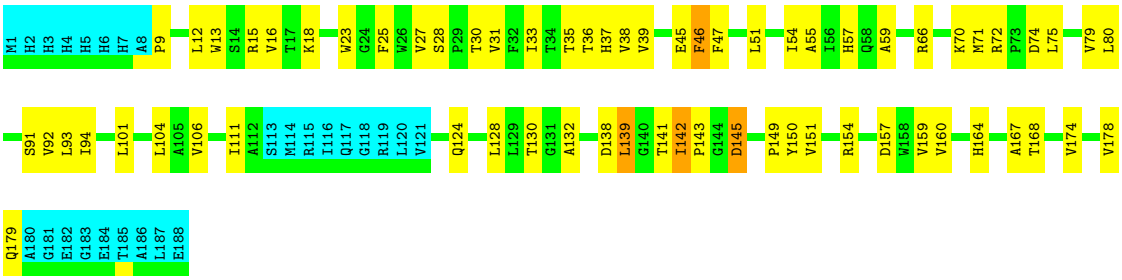
4 Residue-property plots (i)

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: 3C-like protease

Chain A: 52% 32% • 14%



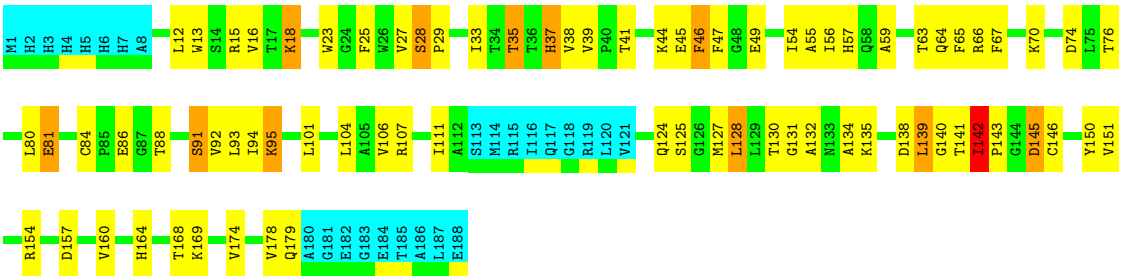
4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

• Molecule 1: 3C-like protease

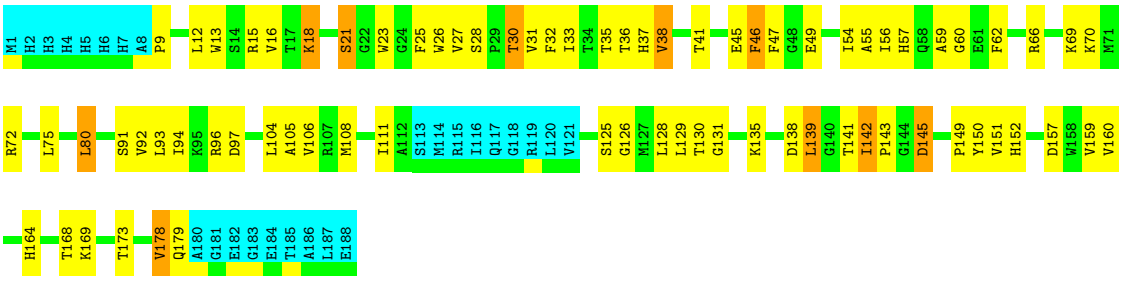
Chain A: 45% 35% 6% • 14%



4.2.2 Score per residue for model 2

- Molecule 1: 3C-like protease

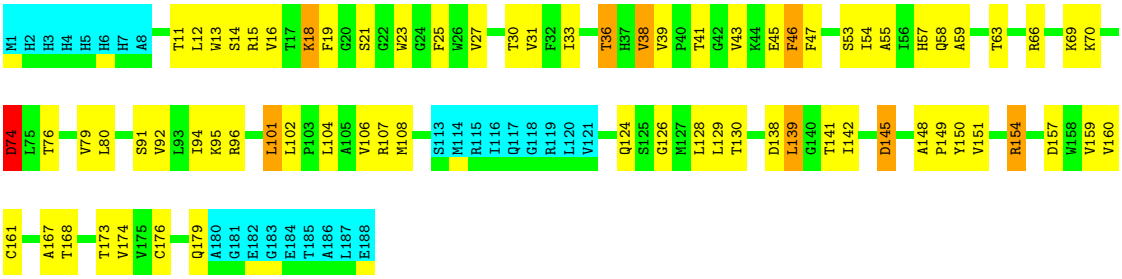
Chain A: 46% 35% 5% 14%



4.2.3 Score per residue for model 3

- Molecule 1: 3C-like protease

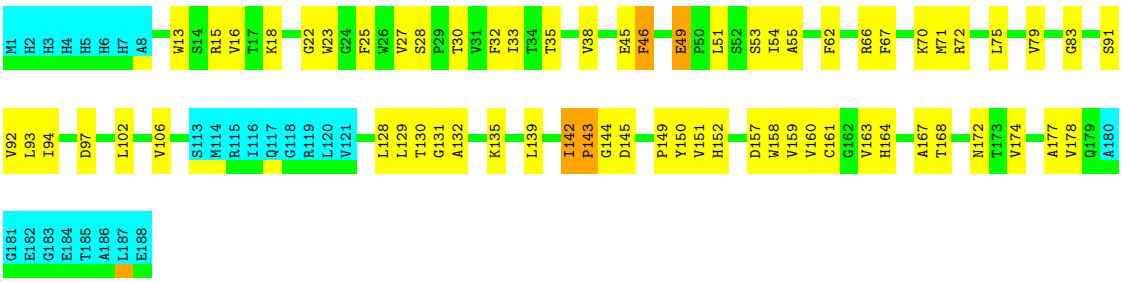
Chain A: 47% 34% • • 14%



4.2.4 Score per residue for model 4

- Molecule 1: 3C-like protease

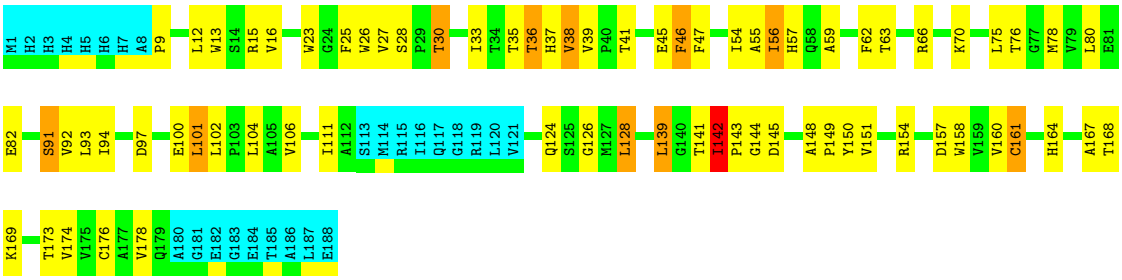
Chain A: 52% 32% • 14%



4.2.5 Score per residue for model 5

- Molecule 1: 3C-like protease

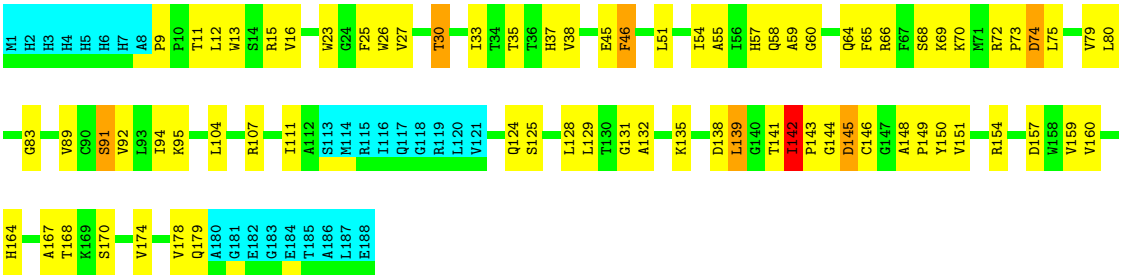
Chain A: 48% 32% 5% • 14%



4.2.6 Score per residue for model 6

- Molecule 1: 3C-like protease

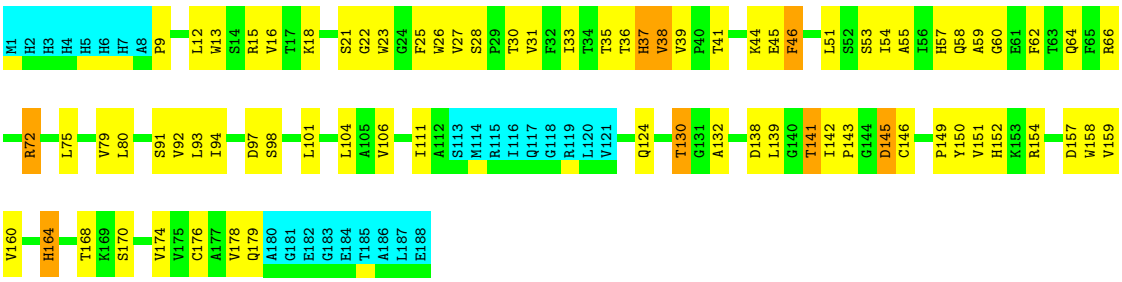
Chain A: 46% 36% • • 14%



4.2.7 Score per residue for model 7

- Molecule 1: 3C-like protease

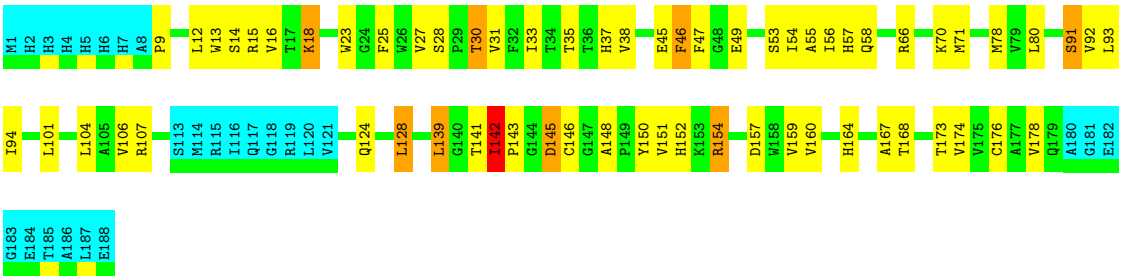
Chain A: 46% 36% • 14%



4.2.8 Score per residue for model 8

- Molecule 1: 3C-like protease

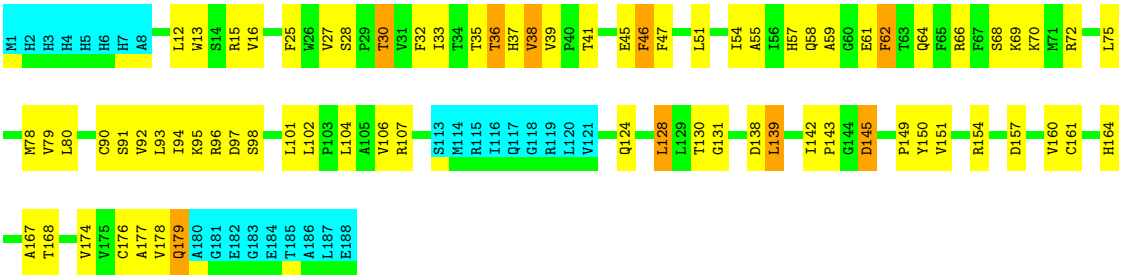
Chain A: 53% 29% • • 14%



4.2.9 Score per residue for model 9 (medoid)

- Molecule 1: 3C-like protease

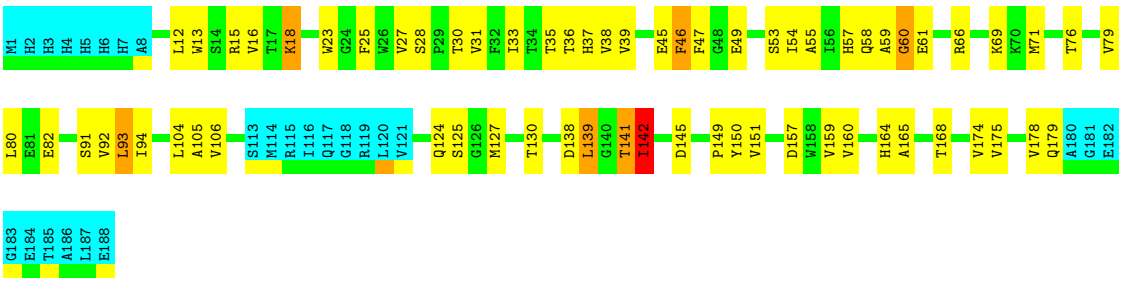
Chain A: 46% 35% 5% 14%



4.2.10 Score per residue for model 10

- Molecule 1: 3C-like protease

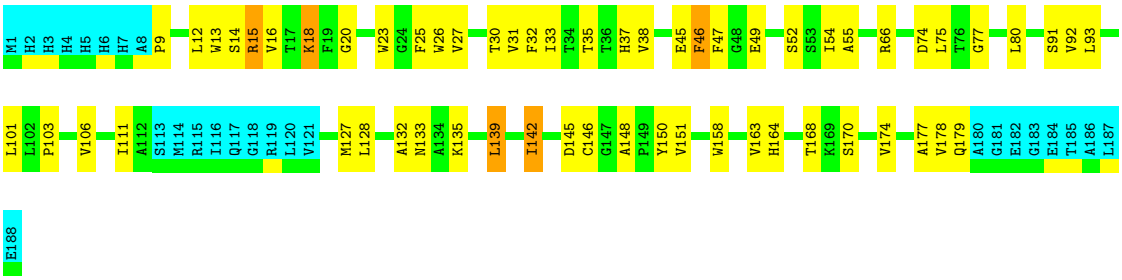
Chain A: 52% 31% • • 14%



4.2.11 Score per residue for model 11

- Molecule 1: 3C-like protease

Chain A: 55% 29% • 14%



4.2.12 Score per residue for model 12

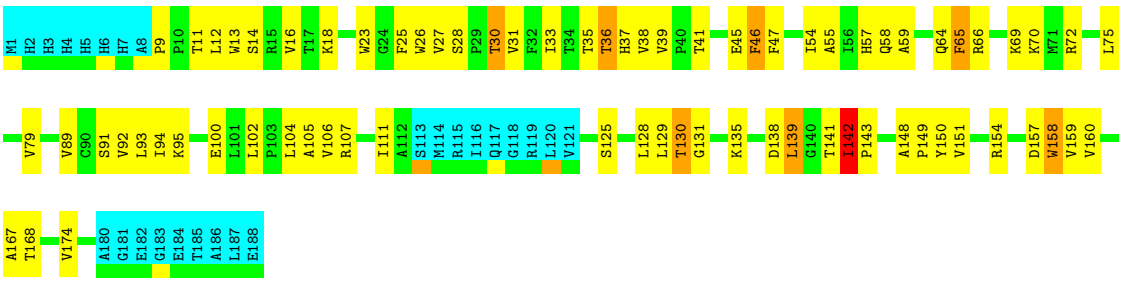
- Molecule 1: 3C-like protease

Chain A: 49% 33% • 14%

4.2.13 Score per residue for model 13

- Molecule 1: 3C-like protease

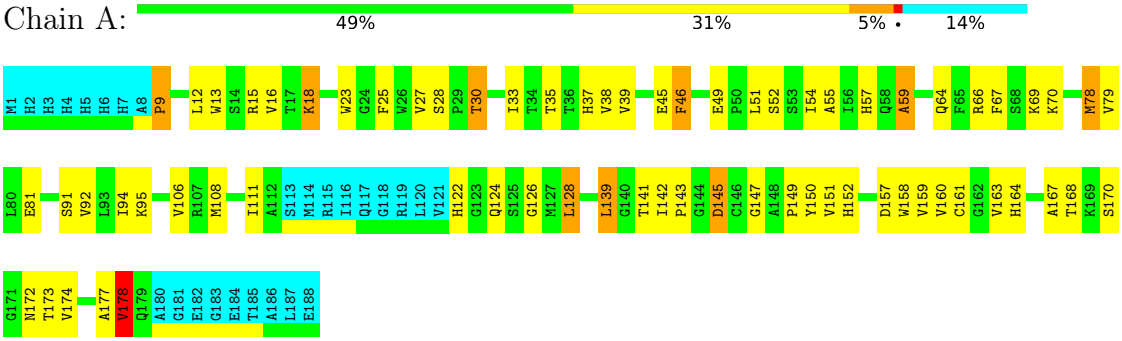
Chain A: 47% 35% • • 14%



4.2.14 Score per residue for model 14

- Molecule 1: 3C-like protease

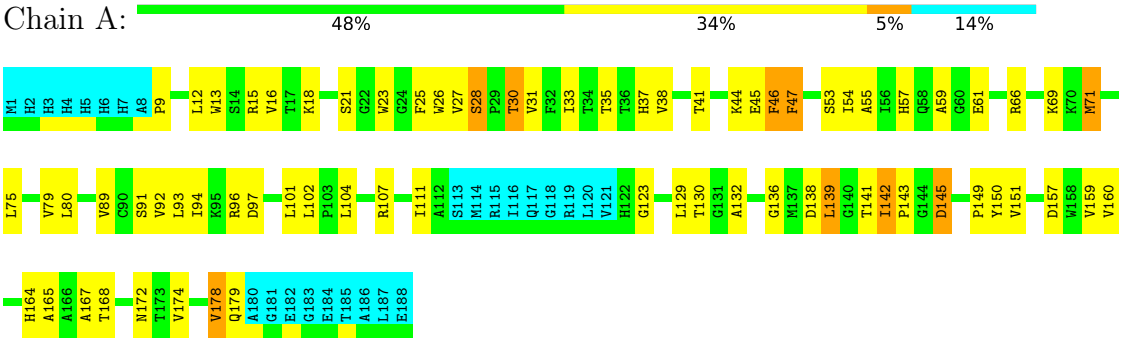
Chain A:



4.2.15 Score per residue for model 15

- Molecule 1: 3C-like protease

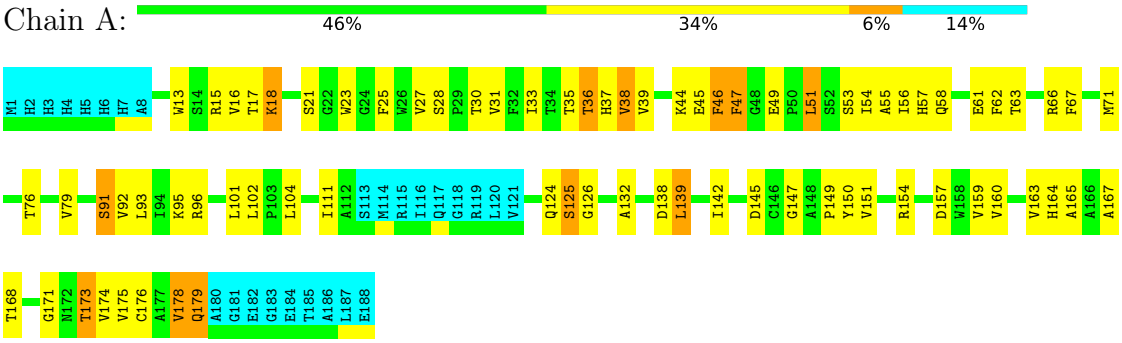
Chain A:



4.2.16 Score per residue for model 16

- Molecule 1: 3C-like protease

Chain A:



4.2.17 Score per residue for model 17

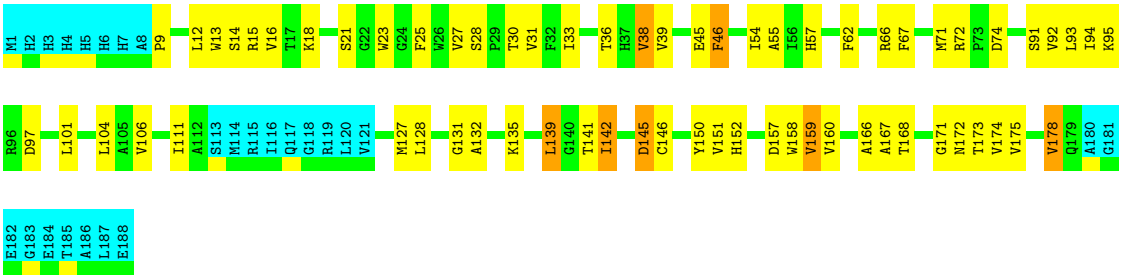
- Molecule 1: 3C-like protease

Chain A: 45% 37% • 14%

4.2.18 Score per residue for model 18

- Molecule 1: 3C-like protease

Chain A: 52% 31% • 14%



4.2.19 Score per residue for model 19

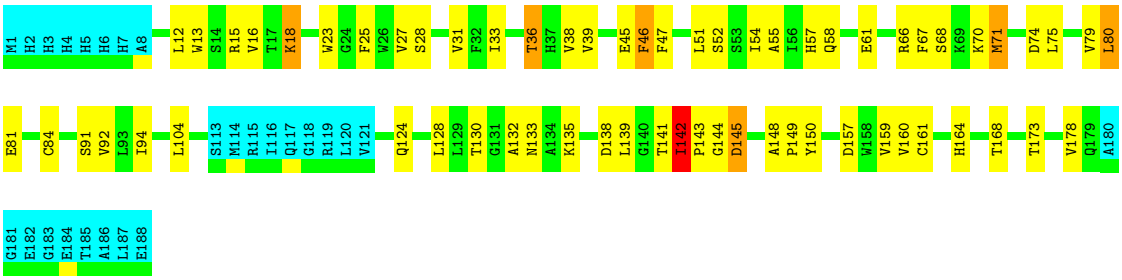
- Molecule 1: 3C-like protease

Chain A: 49% 33% • • 14%

4.2.20 Score per residue for model 20

- Molecule 1: 3C-like protease

Chain A: 53% 30% • • 14%



5 Refinement protocol and experimental data overview (i)

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

Of the 100 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	

The following table shows chemical shift validation statistics as aggregates over all chemical shift files. Detailed validation can be found in section 7 of this report.

Chemical shift file(s)	working_cs.cif
Number of chemical shift lists	1
Total number of shifts	1983
Number of shifts mapped to atoms	1983
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	84%

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	1204	1206	1201	49±6
All	All	24080	24120	24020	989

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 21.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:94:ILE:HD11	1:A:104:LEU:HD11	1.06	1.25	9	9
1:A:128:LEU:HD13	1:A:139:LEU:HD12	0.96	1.32	8	1
1:A:12:LEU:HD21	1:A:151:VAL:HG11	0.89	1.43	3	6
1:A:139:LEU:HD22	1:A:164:HIS:CE1	0.84	2.07	7	1
1:A:128:LEU:HD21	1:A:139:LEU:HD11	0.82	1.47	11	1
1:A:104:LEU:HD22	1:A:130:THR:HG21	0.79	1.53	2	2
1:A:151:VAL:HG12	1:A:160:VAL:HG12	0.79	1.54	14	7
1:A:13:TRP:CD1	1:A:93:LEU:HD22	0.78	2.13	2	5
1:A:104:LEU:CD2	1:A:130:THR:HG21	0.78	2.09	7	1
1:A:13:TRP:O	1:A:16:VAL:HG12	0.77	1.80	16	19
1:A:36:THR:O	1:A:39:VAL:HG12	0.77	1.78	10	9
1:A:139:LEU:CD2	1:A:174:VAL:HG21	0.77	2.08	12	5
1:A:150:TYR:O	1:A:160:VAL:HG23	0.76	1.80	4	12
1:A:94:ILE:HD11	1:A:104:LEU:CD1	0.76	2.09	15	12

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:TRP:CZ3	1:A:93:LEU:HD22	0.76	2.14	12	2
1:A:139:LEU:HD23	1:A:167:ALA:HB3	0.76	1.55	14	2
1:A:111:ILE:HD12	1:A:124:GLN:NE2	0.76	1.95	19	2
1:A:92:VAL:HG11	1:A:164:HIS:CE1	0.76	2.16	10	2
1:A:27:VAL:HG21	1:A:33:ILE:HG23	0.74	1.59	1	6
1:A:16:VAL:HG22	1:A:23:TRP:CE3	0.74	2.17	14	4
1:A:92:VAL:HG22	1:A:150:TYR:CE1	0.74	2.16	5	9
1:A:139:LEU:HD23	1:A:174:VAL:CG2	0.73	2.13	1	3
1:A:27:VAL:CG2	1:A:33:ILE:HG23	0.73	2.13	1	5
1:A:139:LEU:HD23	1:A:174:VAL:HG21	0.73	1.58	10	7
1:A:141:THR:HG21	1:A:145:ASP:O	0.73	1.81	14	5
1:A:56:ILE:HD11	1:A:63:THR:HG23	0.73	1.60	5	1
1:A:139:LEU:HD23	1:A:167:ALA:HB2	0.72	1.62	5	2
1:A:15:ARG:NH1	1:A:75:LEU:HD13	0.72	2.00	2	1
1:A:33:ILE:HD13	1:A:80:LEU:CD1	0.72	2.14	11	1
1:A:126:GLY:O	1:A:174:VAL:HG22	0.72	1.84	19	1
1:A:128:LEU:HD11	1:A:139:LEU:HD12	0.71	1.63	14	1
1:A:148:ALA:HB3	1:A:164:HIS:ND1	0.71	2.00	11	1
1:A:35:THR:HG21	1:A:37:HIS:CE1	0.71	2.20	9	5
1:A:80:LEU:HD12	1:A:160:VAL:HG13	0.71	1.60	19	1
1:A:55:ALA:HB3	1:A:66:ARG:HB3	0.70	1.63	5	15
1:A:91:SER:O	1:A:151:VAL:HG22	0.70	1.86	19	12
1:A:128:LEU:HD11	1:A:174:VAL:HG13	0.70	1.64	8	1
1:A:138:ASP:OD1	1:A:139:LEU:HD23	0.70	1.87	7	1
1:A:94:ILE:HG23	1:A:145:ASP:CG	0.69	2.08	12	6
1:A:92:VAL:HG22	1:A:150:TYR:CE2	0.69	2.21	11	7
1:A:128:LEU:CD2	1:A:139:LEU:HD11	0.69	2.17	11	1
1:A:167:ALA:HB2	1:A:174:VAL:HG12	0.69	1.65	19	6
1:A:128:LEU:HD23	1:A:139:LEU:HD13	0.69	1.63	9	2
1:A:128:LEU:HD22	1:A:139:LEU:O	0.69	1.88	8	1
1:A:27:VAL:HG13	1:A:80:LEU:HD11	0.68	1.63	6	1
1:A:126:GLY:O	1:A:173:THR:HG23	0.68	1.88	14	5
1:A:111:ILE:HG23	1:A:124:GLN:OE1	0.68	1.89	5	1
1:A:84:CYS:SG	1:A:88:THR:HG21	0.68	2.29	1	1
1:A:30:THR:HG23	1:A:70:LYS:CG	0.68	2.19	2	2
1:A:92:VAL:HG22	1:A:150:TYR:CZ	0.68	2.24	18	8
1:A:139:LEU:HD22	1:A:174:VAL:HG11	0.68	1.65	6	2
1:A:94:ILE:O	1:A:101:LEU:HD23	0.67	1.89	3	4
1:A:161:CYS:O	1:A:178:VAL:HG11	0.67	1.90	14	2
1:A:25:PHE:HB3	1:A:33:ILE:HD11	0.67	1.66	6	7
1:A:25:PHE:CB	1:A:33:ILE:HD11	0.67	2.19	4	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:35:THR:O	1:A:39:VAL:HG23	0.66	1.90	14	3
1:A:55:ALA:HB3	1:A:66:ARG:HB2	0.66	1.67	4	5
1:A:94:ILE:HD11	1:A:104:LEU:CG	0.66	2.20	5	3
1:A:15:ARG:NE	1:A:75:LEU:HD21	0.66	2.06	12	1
1:A:94:ILE:HG21	1:A:142:ILE:HG13	0.66	1.64	4	1
1:A:93:LEU:HD21	1:A:151:VAL:HG21	0.66	1.67	5	2
1:A:165:ALA:HB3	1:A:175:VAL:O	0.66	1.90	12	3
1:A:128:LEU:HD22	1:A:133:ASN:O	0.66	1.89	20	1
1:A:142:ILE:O	1:A:144:GLY:N	0.66	2.29	4	2
1:A:111:ILE:HG23	1:A:124:GLN:NE2	0.66	2.05	7	1
1:A:145:ASP:CG	1:A:148:ALA:HB2	0.66	2.11	5	1
1:A:163:VAL:CG2	1:A:177:ALA:HB3	0.65	2.21	4	2
1:A:128:LEU:CD1	1:A:139:LEU:HD12	0.65	2.18	8	2
1:A:25:PHE:CE2	1:A:160:VAL:HG11	0.65	2.26	8	2
1:A:80:LEU:HD21	1:A:178:VAL:HG23	0.65	1.68	7	2
1:A:94:ILE:HD13	1:A:141:THR:HA	0.65	1.67	14	3
1:A:105:ALA:HB3	1:A:129:LEU:O	0.65	1.91	2	2
1:A:33:ILE:HD13	1:A:80:LEU:HD12	0.65	1.66	11	1
1:A:139:LEU:CD2	1:A:174:VAL:HG11	0.65	2.22	6	1
1:A:104:LEU:HA	1:A:130:THR:HG21	0.65	1.69	13	1
1:A:15:ARG:NH2	1:A:75:LEU:HD22	0.64	2.07	20	1
1:A:80:LEU:HD12	1:A:160:VAL:HG23	0.64	1.67	9	1
1:A:93:LEU:HD11	1:A:151:VAL:HG13	0.64	1.70	10	1
1:A:16:VAL:HG12	1:A:23:TRP:CE3	0.64	2.26	11	1
1:A:102:LEU:CD2	1:A:142:ILE:HD11	0.64	2.22	4	1
1:A:151:VAL:HG12	1:A:160:VAL:CG1	0.64	2.23	12	6
1:A:106:VAL:HG21	1:A:150:TYR:OH	0.64	1.92	3	3
1:A:104:LEU:HD13	1:A:139:LEU:HB3	0.64	1.68	17	3
1:A:30:THR:HG23	1:A:69:LYS:O	0.63	1.93	15	1
1:A:13:TRP:CE3	1:A:101:LEU:HD23	0.62	2.30	17	3
1:A:104:LEU:HD22	1:A:139:LEU:HD12	0.62	1.71	13	1
1:A:167:ALA:HB2	1:A:174:VAL:HG22	0.62	1.72	16	1
1:A:12:LEU:HD11	1:A:78:MET:HE3	0.61	1.71	14	1
1:A:12:LEU:HD11	1:A:78:MET:CE	0.61	2.25	14	1
1:A:27:VAL:CG1	1:A:33:ILE:HD13	0.61	2.25	17	2
1:A:177:ALA:O	1:A:178:VAL:HG13	0.61	1.95	14	1
1:A:167:ALA:CB	1:A:174:VAL:HG22	0.61	2.26	16	1
1:A:94:ILE:HD11	1:A:104:LEU:HD21	0.61	1.71	19	3
1:A:139:LEU:HD23	1:A:174:VAL:HG22	0.60	1.74	1	1
1:A:17:THR:HG21	1:A:47:PHE:CE2	0.60	2.31	12	1
1:A:81:GLU:HG2	1:A:159:VAL:HG11	0.60	1.73	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:94:ILE:HD13	1:A:141:THR:HG22	0.60	1.71	20	1
1:A:11:THR:HG23	1:A:74:ASP:O	0.60	1.95	3	2
1:A:9:PRO:HD2	1:A:12:LEU:HD13	0.60	1.74	19	8
1:A:27:VAL:HG13	1:A:33:ILE:HG12	0.60	1.74	20	2
1:A:79:VAL:O	1:A:160:VAL:HG22	0.60	1.97	9	2
1:A:137:MET:HA	1:A:167:ALA:HB3	0.60	1.73	17	1
1:A:94:ILE:CD1	1:A:141:THR:HG22	0.59	2.27	20	1
1:A:15:ARG:NH1	1:A:75:LEU:HD22	0.59	2.12	4	1
1:A:16:VAL:HG22	1:A:23:TRP:HE3	0.59	1.57	14	5
1:A:139:LEU:HD23	1:A:167:ALA:CB	0.59	2.27	18	3
1:A:161:CYS:O	1:A:178:VAL:HG22	0.59	1.97	20	1
1:A:166:ALA:O	1:A:175:VAL:HG23	0.59	1.98	18	1
1:A:106:VAL:HG22	1:A:128:LEU:HD23	0.59	1.74	5	3
1:A:92:VAL:HB	1:A:104:LEU:HD12	0.59	1.74	17	2
1:A:94:ILE:HD12	1:A:102:LEU:HB3	0.59	1.73	9	7
1:A:80:LEU:HD13	1:A:81:GLU:N	0.58	2.12	20	2
1:A:94:ILE:HD11	1:A:104:LEU:CD2	0.58	2.28	19	3
1:A:54:ILE:HG21	1:A:65:PHE:CD2	0.58	2.33	6	2
1:A:56:ILE:HG23	1:A:65:PHE:CE1	0.58	2.32	17	1
1:A:128:LEU:CD2	1:A:134:ALA:HB2	0.58	2.28	19	1
1:A:79:VAL:O	1:A:159:VAL:HG13	0.58	1.98	6	12
1:A:80:LEU:HD21	1:A:178:VAL:HG12	0.58	1.76	8	1
1:A:13:TRP:CZ3	1:A:101:LEU:HD23	0.58	2.32	17	2
1:A:72:ARG:HG2	1:A:75:LEU:HD12	0.58	1.75	12	2
1:A:107:ARG:HB2	1:A:129:LEU:HD12	0.58	1.75	13	1
1:A:56:ILE:HG23	1:A:63:THR:CG2	0.58	2.28	1	3
1:A:35:THR:HG21	1:A:37:HIS:ND1	0.58	2.14	5	3
1:A:139:LEU:CD2	1:A:167:ALA:HB2	0.58	2.27	5	1
1:A:30:THR:HG23	1:A:69:LYS:C	0.58	2.18	15	3
1:A:30:THR:HG22	1:A:70:LYS:HA	0.58	1.74	17	1
1:A:35:THR:HB	1:A:38:VAL:HG22	0.57	1.74	17	8
1:A:56:ILE:CD1	1:A:63:THR:HG23	0.57	2.28	5	1
1:A:27:VAL:HG13	1:A:80:LEU:CD1	0.57	2.29	6	1
1:A:161:CYS:O	1:A:178:VAL:HG12	0.57	1.99	9	1
1:A:148:ALA:HB1	1:A:149:PRO:HD2	0.57	1.76	13	2
1:A:132:ALA:HB1	1:A:172:ASN:ND2	0.57	2.15	15	1
1:A:92:VAL:CB	1:A:104:LEU:HD12	0.57	2.28	17	2
1:A:33:ILE:HD12	1:A:33:ILE:O	0.57	2.00	18	3
1:A:80:LEU:CD2	1:A:178:VAL:HG23	0.57	2.30	2	1
1:A:27:VAL:HG21	1:A:33:ILE:CG2	0.57	2.30	6	5
1:A:67:PHE:CE2	1:A:71:MET:HE3	0.56	2.35	20	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:141:THR:HG21	1:A:145:ASP:HB3	0.56	1.77	8	7
1:A:128:LEU:HD21	1:A:139:LEU:CD1	0.56	2.25	11	1
1:A:93:LEU:HD21	1:A:151:VAL:CG2	0.56	2.30	5	1
1:A:61:GLU:OE2	1:A:165:ALA:HB1	0.56	2.01	15	1
1:A:16:VAL:HG12	1:A:23:TRP:HE3	0.56	1.60	11	1
1:A:124:GLN:C	1:A:175:VAL:HG13	0.55	2.21	12	1
1:A:145:ASP:OD1	1:A:148:ALA:HB2	0.55	2.01	5	2
1:A:94:ILE:CD1	1:A:104:LEU:HD11	0.55	2.31	7	3
1:A:11:THR:HG23	1:A:75:LEU:HD23	0.55	1.78	13	1
1:A:124:GLN:O	1:A:175:VAL:HG13	0.55	2.00	12	1
1:A:12:LEU:HD23	1:A:93:LEU:HD11	0.55	1.78	19	2
1:A:51:LEU:HD12	1:A:51:LEU:C	0.55	2.23	16	2
1:A:81:GLU:CG	1:A:159:VAL:HG11	0.55	2.32	14	1
1:A:138:ASP:HB2	1:A:141:THR:HG23	0.55	1.79	3	3
1:A:154:ARG:HB2	1:A:159:VAL:HG23	0.55	1.78	3	2
1:A:138:ASP:CG	1:A:139:LEU:HD23	0.55	2.22	7	1
1:A:37:HIS:CD2	1:A:38:VAL:HG13	0.54	2.37	5	4
1:A:36:THR:HG23	1:A:63:THR:OG1	0.54	2.02	3	1
1:A:30:THR:HG23	1:A:70:LYS:HG3	0.54	1.79	2	1
1:A:35:THR:HG23	1:A:61:GLU:CG	0.54	2.32	16	1
1:A:104:LEU:HD22	1:A:139:LEU:O	0.54	2.03	17	1
1:A:111:ILE:HD12	1:A:124:GLN:HE22	0.54	1.61	19	1
1:A:94:ILE:HG23	1:A:145:ASP:OD2	0.54	2.03	12	7
1:A:111:ILE:HD11	1:A:122:HIS:HB3	0.54	1.78	14	1
1:A:80:LEU:HD21	1:A:178:VAL:CG1	0.54	2.32	8	1
1:A:83:GLY:N	1:A:178:VAL:HG11	0.54	2.17	4	1
1:A:163:VAL:HG22	1:A:177:ALA:HB3	0.54	1.79	4	1
1:A:167:ALA:HB2	1:A:174:VAL:CG1	0.54	2.33	9	1
1:A:151:VAL:CG1	1:A:160:VAL:HG12	0.53	2.30	16	4
1:A:167:ALA:CB	1:A:174:VAL:HG12	0.53	2.34	6	1
1:A:93:LEU:HD12	1:A:149:PRO:O	0.53	2.03	10	1
1:A:145:ASP:OD2	1:A:148:ALA:HB2	0.53	2.04	6	2
1:A:38:VAL:HG11	1:A:146:CYS:O	0.53	2.04	17	3
1:A:35:THR:HG22	1:A:37:HIS:H	0.53	1.64	6	7
1:A:12:LEU:CD2	1:A:93:LEU:HD11	0.53	2.33	19	3
1:A:35:THR:HG23	1:A:61:GLU:HG2	0.52	1.81	16	1
1:A:128:LEU:CD2	1:A:139:LEU:HD13	0.52	2.34	2	1
1:A:33:ILE:HD13	1:A:80:LEU:HD11	0.52	1.82	2	1
1:A:13:TRP:CH2	1:A:93:LEU:HD22	0.52	2.40	12	2
1:A:106:VAL:HG11	1:A:174:VAL:HG21	0.52	1.80	14	1
1:A:152:HIS:CD2	1:A:159:VAL:HG23	0.52	2.40	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:21:SER:O	1:A:38:VAL:HG11	0.52	2.04	18	3
1:A:89:VAL:HG22	1:A:129:LEU:HD22	0.52	1.82	6	1
1:A:30:THR:HG22	1:A:70:LYS:CA	0.52	2.34	17	1
1:A:111:ILE:HG22	1:A:122:HIS:NE2	0.51	2.21	12	1
1:A:128:LEU:HD23	1:A:139:LEU:CD1	0.51	2.35	2	1
1:A:104:LEU:HD13	1:A:139:LEU:HD12	0.51	1.82	15	2
1:A:93:LEU:HD12	1:A:149:PRO:HG2	0.51	1.81	16	1
1:A:148:ALA:HB3	1:A:164:HIS:CE1	0.51	2.40	11	1
1:A:36:THR:HG21	1:A:58:GLN:HG3	0.51	1.81	9	1
1:A:16:VAL:HG23	1:A:149:PRO:CD	0.51	2.36	12	1
1:A:105:ALA:HB3	1:A:130:THR:OG1	0.51	2.06	10	1
1:A:39:VAL:O	1:A:39:VAL:HG13	0.50	2.06	13	8
1:A:13:TRP:CE3	1:A:101:LEU:HD22	0.50	2.42	8	1
1:A:128:LEU:HB3	1:A:139:LEU:HD21	0.50	1.83	3	1
1:A:111:ILE:O	1:A:111:ILE:HG23	0.50	2.05	13	8
1:A:72:ARG:CG	1:A:75:LEU:HD12	0.50	2.37	2	2
1:A:56:ILE:C	1:A:56:ILE:HD13	0.50	2.27	5	1
1:A:56:ILE:O	1:A:56:ILE:HG23	0.50	2.06	8	2
1:A:13:TRP:CD2	1:A:101:LEU:HD11	0.49	2.42	5	1
1:A:106:VAL:HG11	1:A:174:VAL:CG2	0.49	2.37	13	3
1:A:80:LEU:HD21	1:A:178:VAL:CG2	0.49	2.36	7	1
1:A:46:PHE:CE1	1:A:54:ILE:HD12	0.49	2.42	12	2
1:A:130:THR:HG21	1:A:133:ASN:HD22	0.49	1.66	17	1
1:A:106:VAL:HG13	1:A:127:MET:O	0.49	2.07	10	4
1:A:31:VAL:HG22	1:A:66:ARG:HD2	0.49	1.84	17	1
1:A:15:ARG:CZ	1:A:75:LEU:HD13	0.49	2.37	2	1
1:A:26:TRP:CD1	1:A:32:PHE:CD1	0.49	3.00	2	1
1:A:93:LEU:HD11	1:A:151:VAL:CG1	0.49	2.37	11	2
1:A:51:LEU:HG	1:A:52:SER:N	0.49	2.22	17	2
1:A:92:VAL:HG21	1:A:164:HIS:NE2	0.49	2.23	4	1
1:A:27:VAL:HG11	1:A:33:ILE:CG2	0.49	2.37	10	5
1:A:139:LEU:HD23	1:A:174:VAL:HG11	0.49	1.84	3	1
1:A:138:ASP:OD2	1:A:141:THR:HG22	0.49	2.08	1	2
1:A:51:LEU:HA	1:A:54:ILE:HD12	0.48	1.85	6	6
1:A:21:SER:O	1:A:38:VAL:HG12	0.48	2.07	7	2
1:A:54:ILE:HD11	1:A:67:PHE:CE2	0.48	2.44	14	1
1:A:27:VAL:CG2	1:A:31:VAL:HG12	0.48	2.38	7	12
1:A:128:LEU:C	1:A:129:LEU:HD12	0.48	2.29	4	1
1:A:94:ILE:CD1	1:A:104:LEU:HD21	0.48	2.38	5	3
1:A:30:THR:HG23	1:A:70:LYS:HD3	0.48	1.86	9	1
1:A:26:TRP:HB3	1:A:75:LEU:HD11	0.48	1.85	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:13:TRP:CD2	1:A:93:LEU:HD22	0.48	2.44	17	1
1:A:13:TRP:CE3	1:A:93:LEU:HD23	0.48	2.43	10	1
1:A:82:GLU:HA	1:A:178:VAL:HG21	0.48	1.85	5	1
1:A:128:LEU:HD23	1:A:173:THR:N	0.48	2.24	12	1
1:A:46:PHE:CD1	1:A:46:PHE:N	0.48	2.82	20	19
1:A:92:VAL:HG22	1:A:150:TYR:CD2	0.48	2.44	11	2
1:A:102:LEU:HD23	1:A:142:ILE:HD11	0.47	1.85	4	1
1:A:128:LEU:HD23	1:A:139:LEU:HD11	0.47	1.86	6	1
1:A:46:PHE:CZ	1:A:65:PHE:CZ	0.47	3.02	13	1
1:A:27:VAL:CG1	1:A:31:VAL:HG12	0.47	2.39	2	1
1:A:30:THR:HG23	1:A:70:LYS:N	0.47	2.24	6	1
1:A:30:THR:HG23	1:A:70:LYS:CD	0.47	2.38	9	1
1:A:94:ILE:HG23	1:A:145:ASP:CB	0.47	2.40	14	1
1:A:56:ILE:HD12	1:A:56:ILE:N	0.47	2.25	2	1
1:A:44:LYS:O	1:A:51:LEU:HD23	0.47	2.10	16	1
1:A:80:LEU:HD23	1:A:160:VAL:HG13	0.47	1.85	17	1
1:A:12:LEU:HD23	1:A:12:LEU:O	0.47	2.09	20	3
1:A:18:LYS:CG	1:A:23:TRP:CE2	0.47	2.98	12	15
1:A:94:ILE:HG23	1:A:145:ASP:OD1	0.47	2.10	4	3
1:A:106:VAL:HG22	1:A:139:LEU:HD21	0.47	1.85	2	1
1:A:128:LEU:HD11	1:A:133:ASN:O	0.47	2.09	11	1
1:A:80:LEU:C	1:A:80:LEU:HD23	0.47	2.30	11	1
1:A:111:ILE:HD12	1:A:123:GLY:O	0.47	2.10	15	1
1:A:15:ARG:CB	1:A:25:PHE:CE1	0.47	2.98	10	17
1:A:89:VAL:HG22	1:A:107:ARG:HG3	0.46	1.87	13	1
1:A:142:ILE:N	1:A:143:PRO:CD	0.46	2.78	7	5
1:A:139:LEU:HD23	1:A:150:TYR:OH	0.46	2.10	15	1
1:A:46:PHE:CE1	1:A:54:ILE:CD1	0.46	2.99	7	11
1:A:13:TRP:CE3	1:A:101:LEU:HD11	0.46	2.45	5	1
1:A:92:VAL:CG2	1:A:150:TYR:CZ	0.46	2.99	6	9
1:A:92:VAL:HG21	1:A:164:HIS:CE1	0.46	2.46	10	1
1:A:80:LEU:HD22	1:A:160:VAL:HG13	0.46	1.87	1	1
1:A:25:PHE:CD1	1:A:149:PRO:CB	0.46	2.99	2	6
1:A:107:ARG:HG3	1:A:129:LEU:HD22	0.46	1.87	15	1
1:A:13:TRP:CD2	1:A:101:LEU:HD13	0.46	2.46	16	1
1:A:142:ILE:HG23	1:A:143:PRO:HD2	0.46	1.86	4	1
1:A:139:LEU:N	1:A:164:HIS:CE1	0.46	2.84	8	3
1:A:27:VAL:HG11	1:A:33:ILE:HG21	0.46	1.88	17	2
1:A:18:LYS:N	1:A:23:TRP:CE3	0.46	2.84	14	1
1:A:172:ASN:O	1:A:173:THR:HG23	0.46	2.10	12	2
1:A:37:HIS:NE2	1:A:38:VAL:HG13	0.46	2.26	14	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:46:PHE:CD1	1:A:54:ILE:CD1	0.46	2.99	20	9
1:A:129:LEU:O	1:A:129:LEU:HD23	0.46	2.11	2	1
1:A:152:HIS:N	1:A:158:TRP:CE3	0.46	2.84	4	4
1:A:128:LEU:HD21	1:A:134:ALA:HB2	0.46	1.88	19	1
1:A:92:VAL:CG2	1:A:150:TYR:CE2	0.46	3.00	7	4
1:A:139:LEU:CD2	1:A:167:ALA:HB3	0.46	2.37	8	1
1:A:16:VAL:HG13	1:A:16:VAL:O	0.46	2.11	14	1
1:A:79:VAL:HB	1:A:159:VAL:HG13	0.46	1.87	14	1
1:A:92:VAL:CG2	1:A:150:TYR:CE1	0.45	3.00	10	5
1:A:26:TRP:CB	1:A:75:LEU:HD13	0.45	2.41	5	1
1:A:26:TRP:HB3	1:A:75:LEU:HD13	0.45	1.87	11	3
1:A:164:HIS:CE1	1:A:174:VAL:CG1	0.45	2.99	16	1
1:A:132:ALA:HB2	1:A:172:ASN:OD1	0.45	2.10	4	1
1:A:142:ILE:HB	1:A:143:PRO:HD3	0.45	1.89	6	5
1:A:142:ILE:HD12	1:A:142:ILE:N	0.45	2.27	10	4
1:A:15:ARG:CD	1:A:25:PHE:CZ	0.45	3.00	20	2
1:A:35:THR:CG2	1:A:37:HIS:CD2	0.45	2.99	7	1
1:A:13:TRP:CE3	1:A:101:LEU:CD2	0.45	3.00	8	3
1:A:72:ARG:HG3	1:A:75:LEU:HD12	0.45	1.89	9	1
1:A:26:TRP:CE2	1:A:72:ARG:NE	0.45	2.85	7	1
1:A:13:TRP:CD2	1:A:101:LEU:CD2	0.45	3.00	8	1
1:A:28:SER:OG	1:A:31:VAL:HG23	0.45	2.11	10	2
1:A:54:ILE:CD1	1:A:67:PHE:CE2	0.45	3.00	16	4
1:A:22:GLY:HA3	1:A:38:VAL:HG11	0.45	1.88	4	1
1:A:33:ILE:HD12	1:A:33:ILE:C	0.45	2.31	16	3
1:A:25:PHE:CD2	1:A:160:VAL:HG21	0.45	2.47	15	1
1:A:26:TRP:CH2	1:A:71:MET:CB	0.45	3.00	17	1
1:A:15:ARG:CB	1:A:25:PHE:CZ	0.45	3.00	17	1
1:A:128:LEU:HD21	1:A:174:VAL:HG11	0.45	1.88	4	1
1:A:62:PHE:CE1	1:A:179:GLN:CG	0.45	3.00	7	1
1:A:54:ILE:HG22	1:A:55:ALA:N	0.44	2.27	2	18
1:A:106:VAL:CG2	1:A:139:LEU:HD21	0.44	2.41	2	1
1:A:138:ASP:HA	1:A:164:HIS:CE1	0.44	2.47	6	8
1:A:147:GLY:O	1:A:163:VAL:HG12	0.44	2.13	14	2
1:A:139:LEU:HD13	1:A:139:LEU:O	0.44	2.12	1	1
1:A:92:VAL:HG11	1:A:164:HIS:NE2	0.44	2.27	11	1
1:A:26:TRP:CD2	1:A:75:LEU:HD11	0.44	2.47	6	1
1:A:37:HIS:CD2	1:A:38:VAL:HG22	0.44	2.48	7	1
1:A:36:THR:HG21	1:A:58:GLN:NE2	0.44	2.28	10	1
1:A:13:TRP:CD2	1:A:101:LEU:CD1	0.44	3.00	16	1
1:A:47:PHE:CE1	1:A:71:MET:CE	0.44	3.00	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:128:LEU:CD2	1:A:139:LEU:HD12	0.44	2.43	18	1
1:A:49:GLU:O	1:A:54:ILE:HD11	0.44	2.12	1	2
1:A:13:TRP:CE2	1:A:101:LEU:CD2	0.44	3.00	11	1
1:A:16:VAL:HG23	1:A:149:PRO:CG	0.44	2.43	12	1
1:A:17:THR:HG21	1:A:47:PHE:CD2	0.44	2.48	16	1
1:A:13:TRP:CZ3	1:A:93:LEU:CD2	0.44	3.00	18	1
1:A:67:PHE:CE2	1:A:71:MET:CE	0.44	3.00	20	1
1:A:30:THR:HG23	1:A:70:LYS:HB3	0.44	1.89	8	2
1:A:27:VAL:CG1	1:A:33:ILE:HG23	0.44	2.43	10	1
1:A:13:TRP:CZ3	1:A:101:LEU:HD13	0.44	2.47	15	1
1:A:138:ASP:HB3	1:A:141:THR:HG22	0.44	1.89	1	2
1:A:30:THR:HG22	1:A:69:LYS:C	0.44	2.32	9	1
1:A:139:LEU:HD21	1:A:174:VAL:HG21	0.44	1.87	12	1
1:A:128:LEU:HD21	1:A:174:VAL:HG22	0.44	1.89	12	1
1:A:79:VAL:CB	1:A:159:VAL:HG13	0.43	2.43	14	1
1:A:128:LEU:HD11	1:A:139:LEU:CD1	0.43	2.40	14	1
1:A:89:VAL:HG22	1:A:107:ARG:HG2	0.43	1.89	15	1
1:A:92:VAL:HG11	1:A:164:HIS:HE1	0.43	1.69	10	1
1:A:80:LEU:CD2	1:A:160:VAL:HG13	0.43	2.43	1	1
1:A:25:PHE:CD1	1:A:149:PRO:HB3	0.43	2.48	20	3
1:A:94:ILE:HD11	1:A:104:LEU:HG	0.43	1.90	5	2
1:A:62:PHE:CD1	1:A:177:ALA:HB1	0.43	2.48	9	1
1:A:79:VAL:C	1:A:159:VAL:HG13	0.43	2.34	10	1
1:A:94:ILE:HD12	1:A:104:LEU:CD1	0.43	2.44	10	1
1:A:72:ARG:CB	1:A:75:LEU:HD12	0.43	2.44	7	1
1:A:94:ILE:HG23	1:A:145:ASP:HB2	0.43	1.89	14	1
1:A:41:THR:HG22	1:A:41:THR:O	0.43	2.14	3	1
1:A:178:VAL:HG22	1:A:179:GLN:N	0.43	2.29	6	3
1:A:79:VAL:CG1	1:A:159:VAL:HG13	0.43	2.44	14	1
1:A:106:VAL:HG22	1:A:128:LEU:HB3	0.43	1.90	14	1
1:A:94:ILE:HD12	1:A:104:LEU:HG	0.43	1.90	8	1
1:A:12:LEU:CD2	1:A:93:LEU:HD21	0.43	2.44	10	2
1:A:148:ALA:HB3	1:A:164:HIS:CG	0.43	2.47	11	1
1:A:11:THR:HG23	1:A:75:LEU:CD2	0.43	2.41	13	1
1:A:178:VAL:HG13	1:A:179:GLN:N	0.43	2.28	15	2
1:A:94:ILE:HD13	1:A:142:ILE:HG13	0.43	1.91	4	1
1:A:154:ARG:CB	1:A:159:VAL:HG23	0.43	2.43	8	1
1:A:26:TRP:CG	1:A:75:LEU:CD1	0.43	3.01	13	1
1:A:80:LEU:HD23	1:A:160:VAL:O	0.43	2.14	15	1
1:A:25:PHE:CD1	1:A:149:PRO:CG	0.43	3.02	4	1
1:A:150:TYR:OH	1:A:174:VAL:HG11	0.43	2.14	18	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:9:PRO:CG	1:A:12:LEU:HD13	0.43	2.43	15	2
1:A:13:TRP:CE2	1:A:101:LEU:HD22	0.43	2.48	11	1
1:A:125:SER:HA	1:A:175:VAL:HG22	0.43	1.90	12	1
1:A:9:PRO:HG2	1:A:12:LEU:HD13	0.43	1.91	15	2
1:A:158:TRP:CD1	1:A:158:TRP:N	0.43	2.87	13	1
1:A:72:ARG:N	1:A:73:PRO:HD3	0.42	2.29	6	1
1:A:25:PHE:CE1	1:A:93:LEU:HD12	0.42	2.49	19	1
1:A:92:VAL:HG12	1:A:93:LEU:N	0.42	2.29	13	8
1:A:139:LEU:HD22	1:A:164:HIS:ND1	0.42	2.27	7	1
1:A:154:ARG:HB3	1:A:159:VAL:HG23	0.42	1.90	16	2
1:A:164:HIS:CE1	1:A:174:VAL:HG11	0.42	2.50	16	1
1:A:142:ILE:CB	1:A:143:PRO:HD3	0.42	2.44	13	1
1:A:16:VAL:O	1:A:16:VAL:HG13	0.42	2.15	2	3
1:A:139:LEU:HD21	1:A:141:THR:HG23	0.42	1.92	7	1
1:A:46:PHE:O	1:A:49:GLU:N	0.42	2.53	16	1
1:A:107:ARG:HG3	1:A:129:LEU:HD12	0.42	1.92	3	1
1:A:102:LEU:HD22	1:A:142:ILE:HD11	0.42	1.89	4	1
1:A:106:VAL:HG12	1:A:107:ARG:N	0.42	2.29	17	2
1:A:37:HIS:CD2	1:A:38:VAL:CG1	0.42	3.01	14	1
1:A:139:LEU:HD21	1:A:171:GLY:O	0.42	2.14	18	1
1:A:15:ARG:HB2	1:A:25:PHE:CE1	0.42	2.50	19	8
1:A:78:MET:CE	1:A:160:VAL:HG13	0.42	2.44	5	1
1:A:141:THR:OG1	1:A:145:ASP:N	0.42	2.52	10	1
1:A:26:TRP:CD2	1:A:32:PHE:CD1	0.42	3.08	11	1
1:A:19:PHE:CE1	1:A:43:VAL:HG21	0.42	2.49	3	1
1:A:25:PHE:HE2	1:A:160:VAL:HG11	0.42	1.73	5	2
1:A:93:LEU:HD11	1:A:151:VAL:CG2	0.42	2.44	11	2
1:A:125:SER:OG	1:A:173:THR:HG22	0.42	2.14	16	1
1:A:178:VAL:HG12	1:A:179:GLN:N	0.42	2.30	1	1
1:A:136:GLY:O	1:A:167:ALA:HB3	0.42	2.15	15	1
1:A:128:LEU:HD12	1:A:134:ALA:HB2	0.41	1.91	1	1
1:A:35:THR:CG2	1:A:37:HIS:ND1	0.41	2.83	5	1
1:A:106:VAL:HG13	1:A:127:MET:C	0.41	2.35	11	1
1:A:27:VAL:HG21	1:A:31:VAL:HG12	0.41	1.92	19	1
1:A:23:TRP:CD1	1:A:144:GLY:O	0.41	2.74	6	3
1:A:26:TRP:HB2	1:A:75:LEU:HD22	0.41	1.91	11	1
1:A:37:HIS:CD2	1:A:37:HIS:O	0.41	2.74	12	3
1:A:27:VAL:HG13	1:A:33:ILE:CG1	0.41	2.44	20	1
1:A:104:LEU:HD22	1:A:130:THR:CG2	0.41	2.36	7	1
1:A:80:LEU:HD11	1:A:161:CYS:O	0.41	2.16	3	1
1:A:138:ASP:CG	1:A:141:THR:HG22	0.41	2.36	10	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:93:LEU:HD11	1:A:151:VAL:HG22	0.41	1.91	13	1
1:A:102:LEU:HD23	1:A:104:LEU:HD21	0.41	1.92	16	1
1:A:128:LEU:HD23	1:A:139:LEU:HD12	0.41	1.91	18	1
1:A:67:PHE:CD2	1:A:71:MET:CE	0.41	3.03	20	1
1:A:139:LEU:CB	1:A:164:HIS:NE2	0.41	2.83	10	2
1:A:106:VAL:HG11	1:A:174:VAL:HG22	0.41	1.92	18	1
1:A:128:LEU:HD23	1:A:172:ASN:C	0.41	2.36	12	1
1:A:96:ARG:NH2	1:A:142:ILE:HD13	0.41	2.30	19	1
1:A:18:LYS:HG3	1:A:23:TRP:CE2	0.41	2.51	1	4
1:A:56:ILE:HD13	1:A:57:HIS:N	0.41	2.30	5	1
1:A:80:LEU:HD13	1:A:80:LEU:C	0.41	2.36	1	1
1:A:37:HIS:O	1:A:37:HIS:CD2	0.41	2.74	2	1
1:A:152:HIS:CE1	1:A:159:VAL:O	0.41	2.74	7	5
1:A:22:GLY:CA	1:A:146:CYS:O	0.41	2.68	7	1
1:A:25:PHE:CD1	1:A:149:PRO:HG3	0.41	2.50	7	1
1:A:150:TYR:OH	1:A:164:HIS:CD2	0.41	2.74	7	3
1:A:27:VAL:HG23	1:A:33:ILE:HG12	0.41	1.93	9	1
1:A:18:LYS:CE	1:A:23:TRP:NE1	0.41	2.84	15	1
1:A:96:ARG:HH22	1:A:102:LEU:HD22	0.41	1.75	16	1
1:A:15:ARG:HD3	1:A:25:PHE:CZ	0.41	2.51	20	1
1:A:62:PHE:CE1	1:A:179:GLN:HG2	0.41	2.51	7	1
1:A:151:VAL:HG12	1:A:160:VAL:HB	0.41	1.93	13	1
1:A:62:PHE:CG	1:A:178:VAL:O	0.40	2.75	18	2
1:A:25:PHE:O	1:A:32:PHE:CD1	0.40	2.74	9	1
1:A:62:PHE:CE2	1:A:178:VAL:O	0.40	2.75	16	1
1:A:49:GLU:OE1	1:A:67:PHE:CE2	0.40	2.75	1	1
1:A:27:VAL:CG1	1:A:31:VAL:CG1	0.40	2.99	2	1
1:A:62:PHE:CD2	1:A:178:VAL:O	0.40	2.75	4	1
1:A:30:THR:HG23	1:A:70:LYS:CA	0.40	2.45	5	1
1:A:54:ILE:HD13	1:A:67:PHE:CZ	0.40	2.51	16	1
1:A:18:LYS:HB3	1:A:23:TRP:CE2	0.40	2.51	19	1
1:A:16:VAL:HG23	1:A:149:PRO:HD3	0.40	1.92	20	1
1:A:111:ILE:HG23	1:A:111:ILE:O	0.40	2.16	1	1
1:A:25:PHE:O	1:A:32:PHE:CE1	0.40	2.74	4	1
1:A:28:SER:C	1:A:75:LEU:HD13	0.40	2.37	15	1
1:A:94:ILE:HD11	1:A:104:LEU:HD12	0.40	1.92	20	1
1:A:28:SER:CB	1:A:29:PRO:CD	0.40	2.99	1	1
1:A:25:PHE:CZ	1:A:160:VAL:HG11	0.40	2.51	2	1
1:A:49:GLU:OE1	1:A:67:PHE:CD2	0.40	2.74	4	1
1:A:13:TRP:CE2	1:A:93:LEU:CD2	0.40	3.05	17	1
1:A:23:TRP:CH2	1:A:95:LYS:O	0.40	2.74	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:83:GLY:HA2	1:A:111:ILE:HD11	0.40	1.93	6	1
1:A:27:VAL:HG22	1:A:33:ILE:HD13	0.40	1.94	9	1
1:A:139:LEU:O	1:A:139:LEU:HD13	0.40	2.17	13	1
1:A:30:THR:HG22	1:A:69:LYS:O	0.40	2.16	14	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	162/188 (86%)	136±3 (84±2%)	22±3 (14±2%)	4±2 (2±1%)	9	48
All	All	3240/3760 (86%)	2723 (84%)	444 (14%)	73 (2%)	9	48

All 19 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	142	ILE	13
1	A	59	ALA	12
1	A	132	ALA	9
1	A	131	GLY	8
1	A	74	ASP	5
1	A	178	VAL	5
1	A	60	GLY	4
1	A	179	GLN	4
1	A	143	PRO	2
1	A	146	CYS	2
1	A	76	THR	1
1	A	140	GLY	1
1	A	161	CYS	1
1	A	20	GLY	1
1	A	77	GLY	1
1	A	9	PRO	1
1	A	172	ASN	1
1	A	171	GLY	1

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Mol	Chain	Res	Type	Models (Total)
1	A	130	THR	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	129/149 (87%)	105±4 (81±3%)	24±4 (19±3%)	4 37
All	All	2580/2980 (87%)	2099 (81%)	481 (19%)	4 37

All 76 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	45	GLU	20
1	A	46	PHE	20
1	A	168	THR	20
1	A	139	LEU	19
1	A	157	ASP	19
1	A	57	HIS	17
1	A	30	THR	17
1	A	91	SER	16
1	A	145	ASP	16
1	A	28	SER	15
1	A	47	PHE	15
1	A	142	ILE	14
1	A	18	LYS	12
1	A	135	LYS	10
1	A	154	ARG	10
1	A	38	VAL	10
1	A	53	SER	10
1	A	95	LYS	9
1	A	36	THR	9
1	A	41	THR	8
1	A	124	GLN	8
1	A	130	THR	8
1	A	97	ASP	8
1	A	58	GLN	8

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Mol	Chain	Res	Type	Models (Total)
1	A	71	MET	8
1	A	125	SER	7
1	A	128	LEU	7
1	A	176	CYS	7
1	A	64	GLN	6
1	A	70	LYS	6
1	A	49	GLU	6
1	A	14	SER	6
1	A	44	LYS	5
1	A	169	LYS	5
1	A	76	THR	5
1	A	72	ARG	5
1	A	170	SER	5
1	A	69	LYS	4
1	A	80	LEU	4
1	A	96	ARG	4
1	A	74	ASP	4
1	A	101	LEU	4
1	A	179	GLN	4
1	A	78	MET	4
1	A	107	ARG	3
1	A	108	MET	3
1	A	68	SER	3
1	A	98	SER	3
1	A	173	THR	3
1	A	61	GLU	3
1	A	158	TRP	3
1	A	51	LEU	3
1	A	37	HIS	2
1	A	65	PHE	2
1	A	81	GLU	2
1	A	21	SER	2
1	A	164	HIS	2
1	A	100	GLU	2
1	A	141	THR	2
1	A	52	SER	2
1	A	84	CYS	2
1	A	35	THR	1
1	A	86	GLU	1
1	A	146	CYS	1
1	A	143	PRO	1
1	A	161	CYS	1

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Mol	Chain	Res	Type	Models (Total)
1	A	56	ILE	1
1	A	62	PHE	1
1	A	90	CYS	1
1	A	82	GLU	1
1	A	93	LEU	1
1	A	15	ARG	1
1	A	75	LEU	1
1	A	178	VAL	1
1	A	159	VAL	1
1	A	66	ARG	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)

The completeness of assignment taking into account all chemical shift lists is 84% for the well-defined parts and 81% for the entire structure.

7.1 Chemical shift list 1

File name: working_cs.cif

Chemical shift list name: *assigned_chem_shift_list_1*

7.1.1 Bookkeeping (i)

The following table shows the results of parsing the chemical shift list and reports the number of nuclei with statistically unusual chemical shifts.

Total number of shifts	1983
Number of shifts mapped to atoms	1983
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	4

7.1.2 Chemical shift referencing (i)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction ± precision, *ppm*	Suggested action
$^{13}C_{\alpha}$	179	-0.02 ± 0.12	None needed (< 0.5 ppm)
$^{13}C_{\beta}$	155	0.22 ± 0.14	None needed (< 0.5 ppm)
$^{13}C'$	176	0.23 ± 0.08	None needed (< 0.5 ppm)
^{15}N	167	-0.42 ± 0.45	None needed (< 0.5 ppm)

7.1.3 Completeness of resonance assignments (i)

The following table shows the completeness of the chemical shift assignments for the well-defined regions of the structure. The overall completeness is 84%, i.e. 1757 atoms were assigned a chemical shift out of a possible 2092. 0 out of 28 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	785/811 (97%)	325/335 (97%)	313/324 (97%)	147/152 (97%)
Sidechain	930/1104 (84%)	635/729 (87%)	290/342 (85%)	5/33 (15%)

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	Total	^{1}H	^{13}C	^{15}N
Aromatic	42/177 (24%)	37/88 (42%)	1/75 (1%)	4/14 (29%)
Overall	1757/2092 (84%)	997/1152 (87%)	604/741 (82%)	156/199 (78%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 81%, i.e. 1983 atoms were assigned a chemical shift out of a possible 2448. 0 out of 31 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^{1}H	^{13}C	^{15}N
Backbone	891/944 (94%)	369/390 (95%)	355/376 (94%)	167/178 (94%)
Sidechain	1048/1279 (82%)	715/844 (85%)	327/395 (83%)	6/40 (15%)
Aromatic	44/225 (20%)	39/112 (35%)	1/87 (1%)	4/26 (15%)
Overall	1983/2448 (81%)	1123/1346 (83%)	683/858 (80%)	177/244 (73%)

7.1.4 Statistically unusual chemical shifts (i)

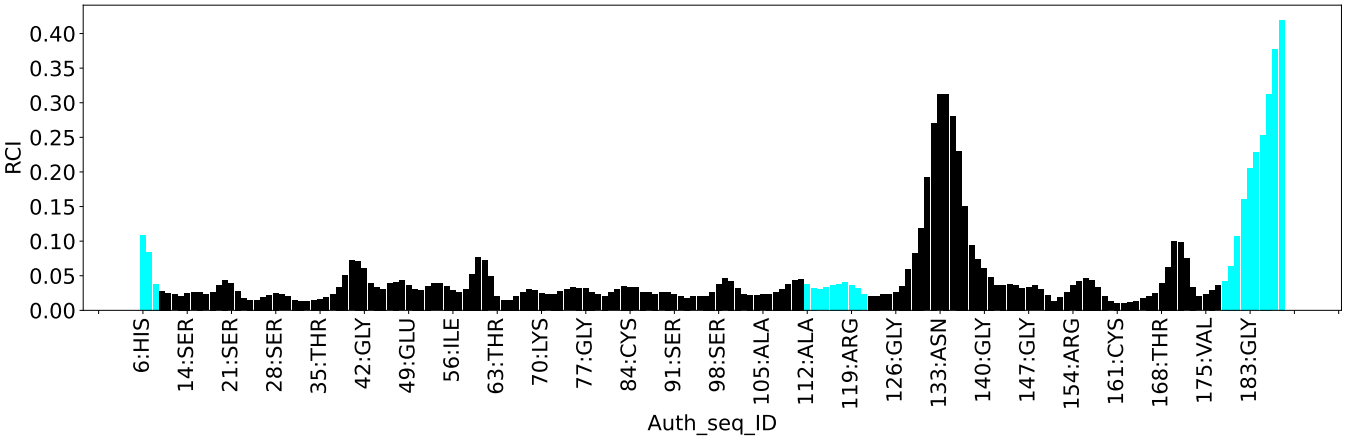
The following table lists the statistically unusual chemical shifts. These are statistical measures, and large deviations from the mean do not necessarily imply incorrect assignments. Molecules containing paramagnetic centres or hemes are expected to give rise to anomalous chemical shifts.

List Id	Chain	Res	Type	Atom	Shift, *ppm*	Expected range, *ppm*	Z-score
1	A	153	LYS	HB3	-0.35	0.46 – 3.04	-8.1
1	A	153	LYS	HG3	-0.33	0.04 – 2.67	-6.4
1	A	95	LYS	HB3	0.20	0.46 – 3.04	-6.0
1	A	101	LEU	HB3	-0.35	-0.26 – 3.31	-5.3

7.1.5 Random Coil Index (RCI) plots (i)

The image below reports *random coil index* values for the protein chains in the structure. The height of each bar gives a probability of a given residue to be disordered, as predicted from the available chemical shifts and the amino acid sequence. A value above 0.2 is an indication of significant predicted disorder. The colour of the bar shows whether the residue is in the well-defined core (black) or in the ill-defined residue ranges (cyan), as described in section 2 on ensemble composition.If well-defined core and ill-defined regions are not identified then it is shown as gray bars.

Random coil index (RCI) for chain A:


RCI
0.40
0.35
0.30
0.25
0.20
0.15
0.10
0.05
0.00
6:HIS
14:SER
21:SER
28:SER
35:THR
42:GLY
49:GLU
56:ILE
63:THR
70:LYS
77:GLY
84:CYS
91:SER
98:SER
105:ALA
112:ALA
119:ARG
126:GLY
133:ASN
140:GLY
147:GLY
154:ARG
161:CYS
168:THR
175:VAL
183:GLY
Auth_seq_ID