



Full wwPDB NMR Structure Validation Report ⓘ

Apr 26, 2016 – 09:32 PM BST

PDB ID : 2JRB
Title : C-terminal domain of ORF1p from mouse LINE-1
Authors : Januszyk, K.; Clubb, R.
Deposited on : 2007-06-21

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

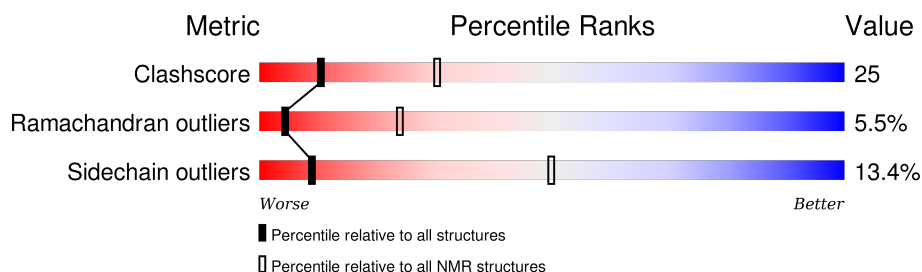
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

The overall completeness of chemical shifts assignment is 87%.

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	88	

2 Ensemble composition and analysis ⓘ

This entry contains 40 models. Model 24 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:289-A:353 (65)	0.29	24

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 6 clusters and 4 single-model clusters were found.

Cluster number	Models
1	8, 9, 10, 11, 12, 14, 22, 24, 30, 31, 34, 35, 38, 40
2	2, 7, 16, 18, 19, 21, 32, 37
3	1, 4, 15, 17, 23, 39
4	13, 20, 28, 36
5	3, 26
6	25, 33
Single-model clusters	5; 6; 27; 29

3 Entry composition

There is only 1 type of molecule in this entry. The entry contains 1092 atoms, of which 555 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called ORF 1 protein.

Mol	Chain	Residues	Atoms							Trace
1	A	65	Total	C	H	N	O	S		0
			1092	344	555	96	95	2		

There is a discrepancy between the modelled and reference sequences:

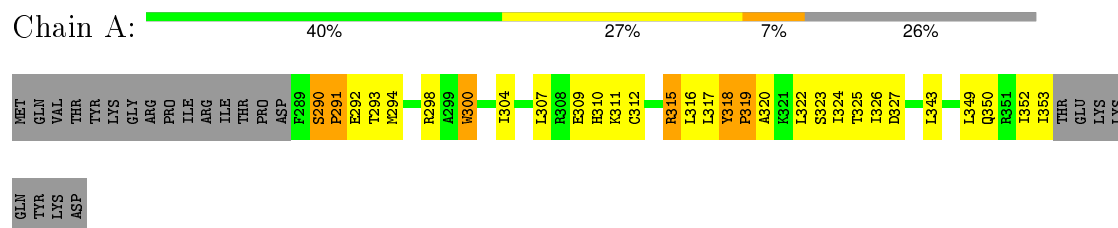
Chain	Residue	Modelled	Actual	Comment	Reference
A	274	MET	-	cloning artifact	UNP Q60712

4 Residue-property plots [i](#)

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: ORF 1 protein

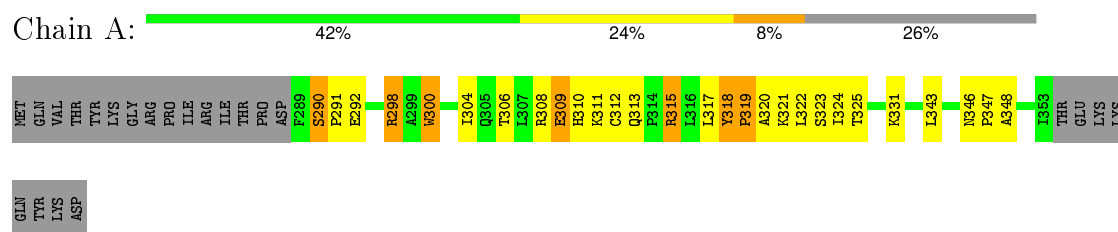


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

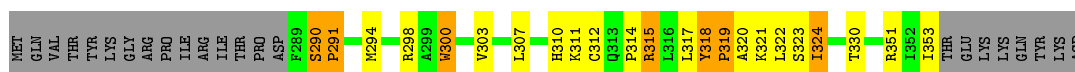
- Molecule 1: ORF 1 protein



4.2.2 Score per residue for model 2

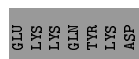
- Molecule 1: ORF 1 protein





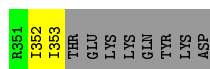
4.2.3 Score per residue for model 3

- Molecule 1: ORF 1 protein



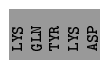
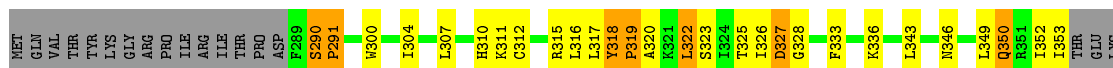
4.2.4 Score per residue for model 4

- Molecule 1: ORF 1 protein



4.2.5 Score per residue for model 5

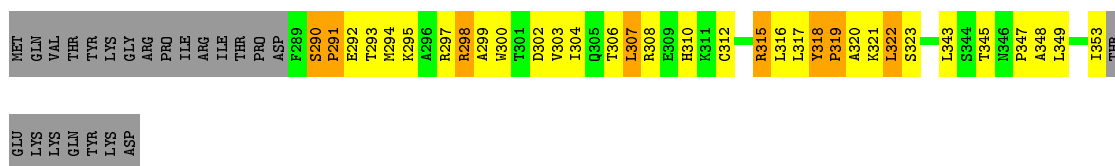
- Molecule 1: ORF 1 protein



4.2.6 Score per residue for model 6

- Molecule 1: ORF 1 protein

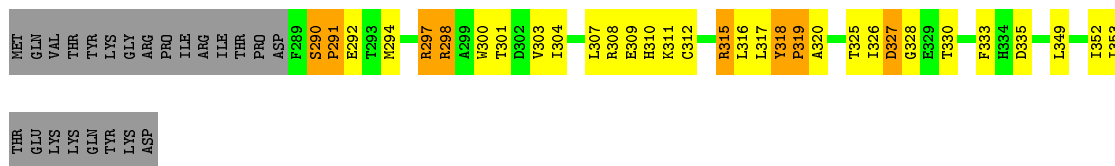




4.2.7 Score per residue for model 7

- Molecule 1: ORF 1 protein

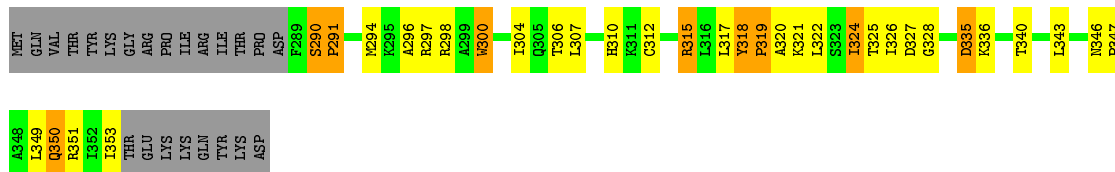
Chain A:



4.2.8 Score per residue for model 8

- Molecule 1: ORF 1 protein

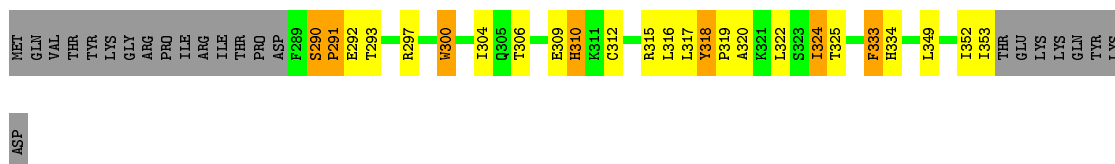
Chain A:



4.2.9 Score per residue for model 9

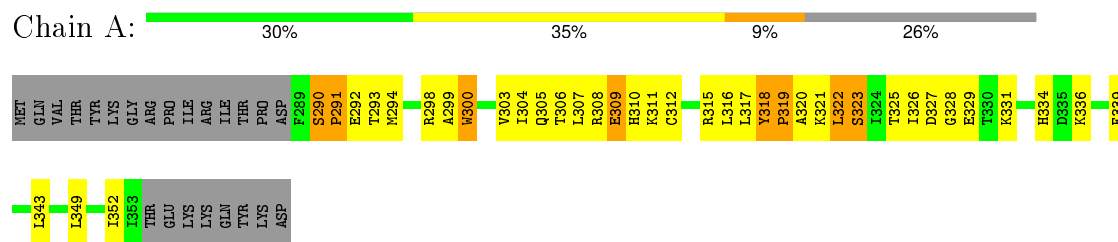
- Molecule 1: ORF 1 protein

Chain A:



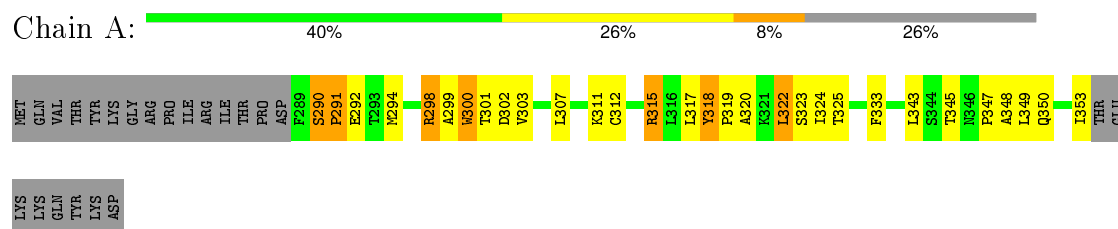
4.2.10 Score per residue for model 10

- Molecule 1: ORF 1 protein



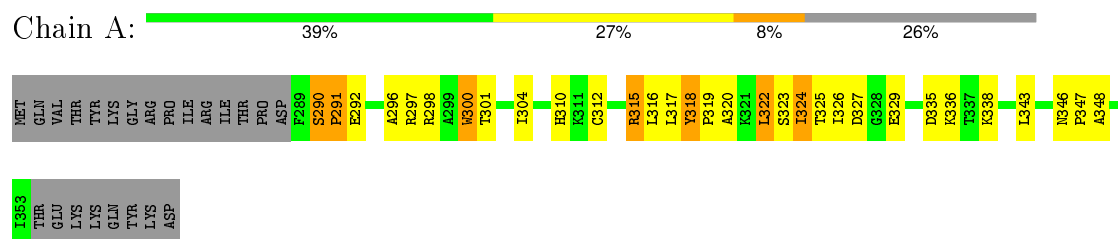
4.2.11 Score per residue for model 11

- Molecule 1: ORF 1 protein



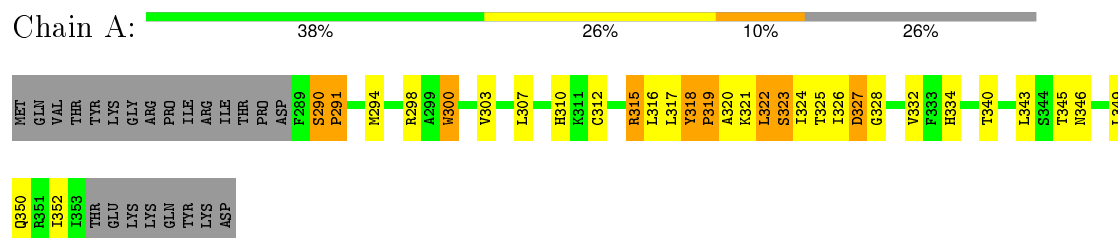
4.2.12 Score per residue for model 12

- Molecule 1: ORF 1 protein



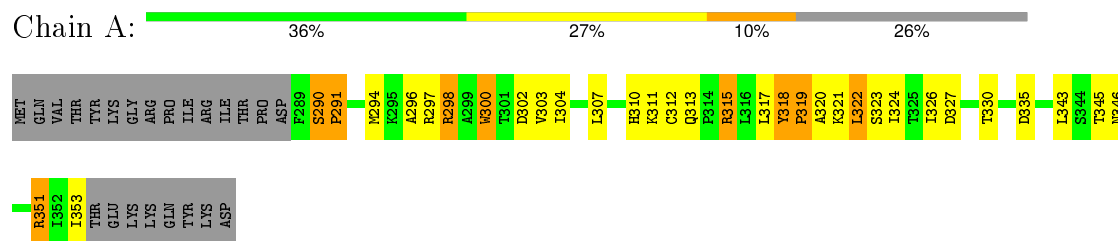
4.2.13 Score per residue for model 13

- Molecule 1: ORF 1 protein



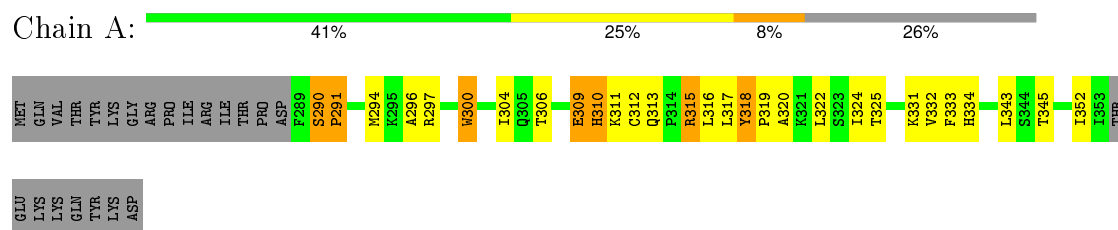
4.2.14 Score per residue for model 14

- Molecule 1: ORF 1 protein



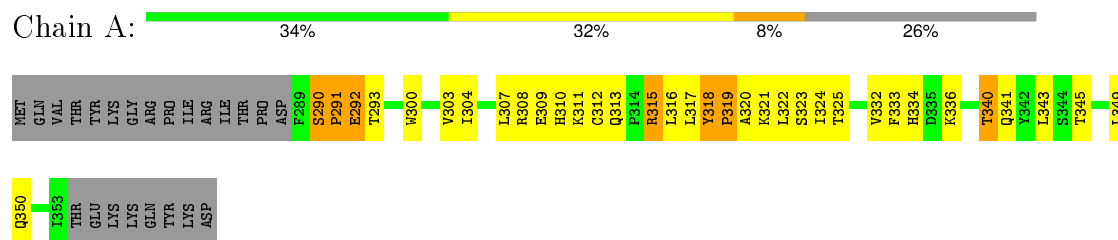
4.2.15 Score per residue for model 15

- Molecule 1: ORF 1 protein



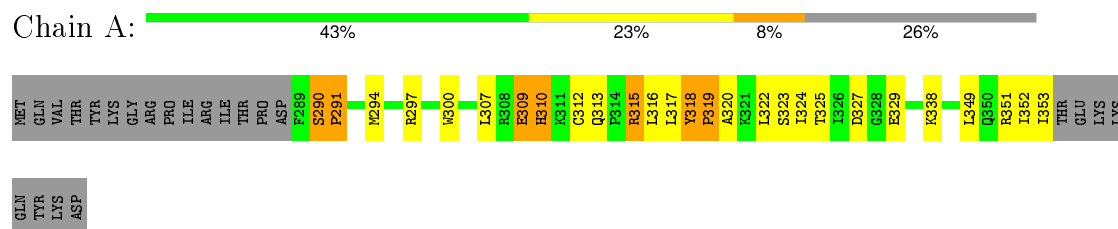
4.2.16 Score per residue for model 16

- Molecule 1: ORF 1 protein



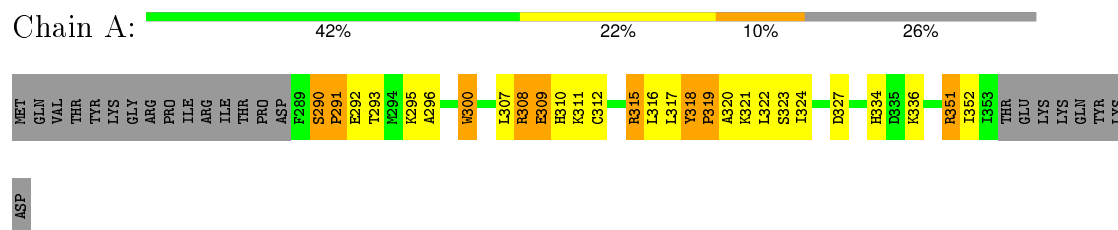
4.2.17 Score per residue for model 17

- Molecule 1: ORF 1 protein



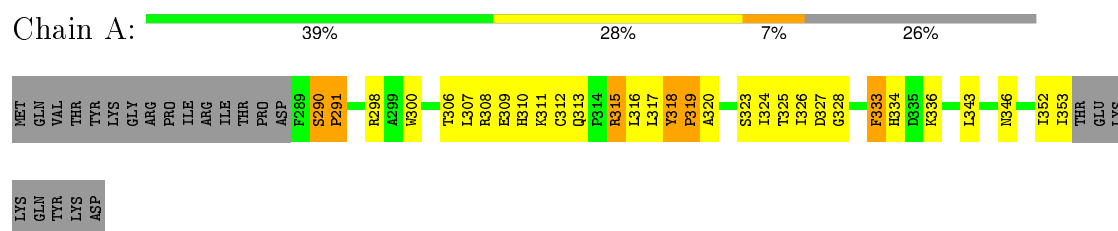
4.2.18 Score per residue for model 18

- Molecule 1: ORF 1 protein



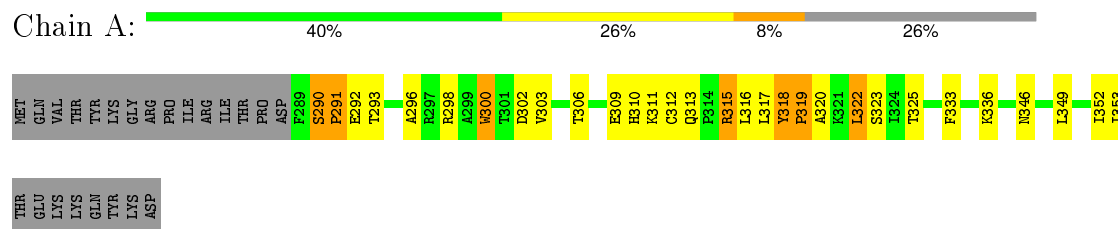
4.2.19 Score per residue for model 19

- Molecule 1: ORF 1 protein



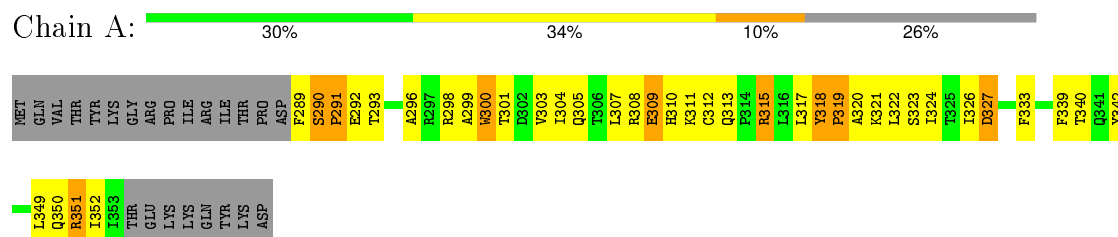
4.2.20 Score per residue for model 20

- Molecule 1: ORF 1 protein



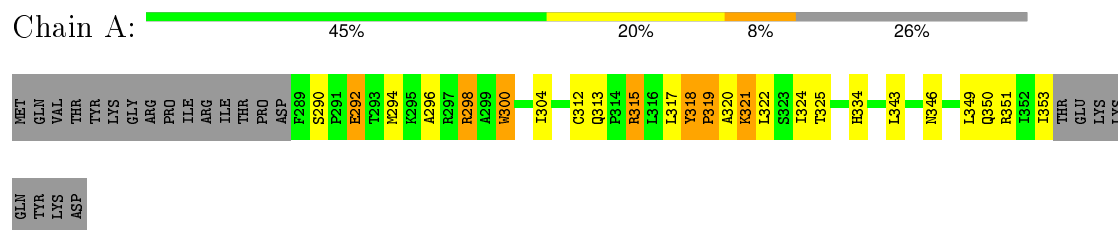
4.2.21 Score per residue for model 21

- Molecule 1: ORF 1 protein



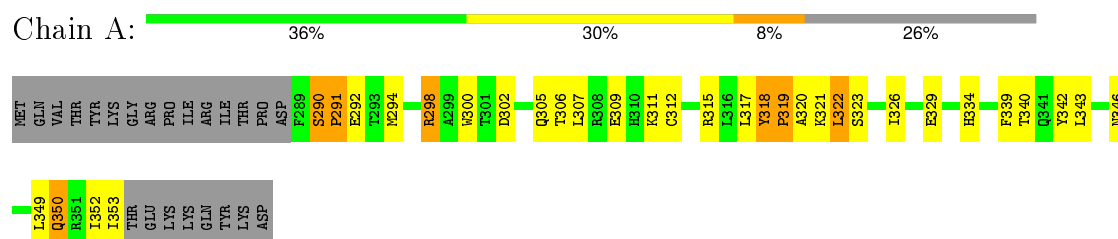
4.2.22 Score per residue for model 22

- Molecule 1: ORF 1 protein



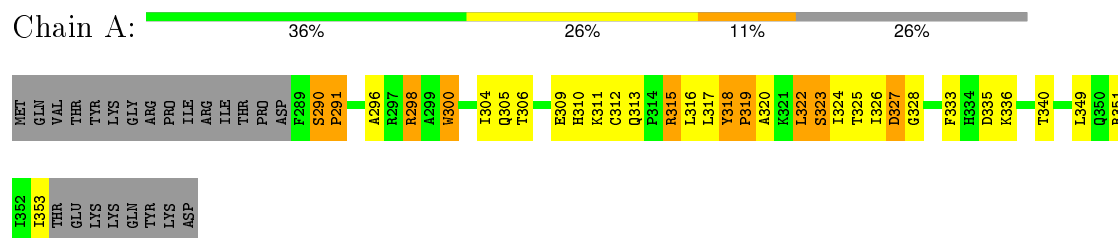
4.2.23 Score per residue for model 23

- Molecule 1: ORF 1 protein



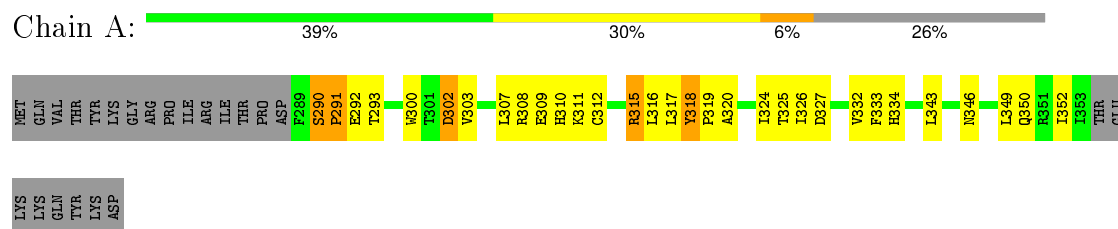
4.2.24 Score per residue for model 24 (medoid)

- Molecule 1: ORF 1 protein



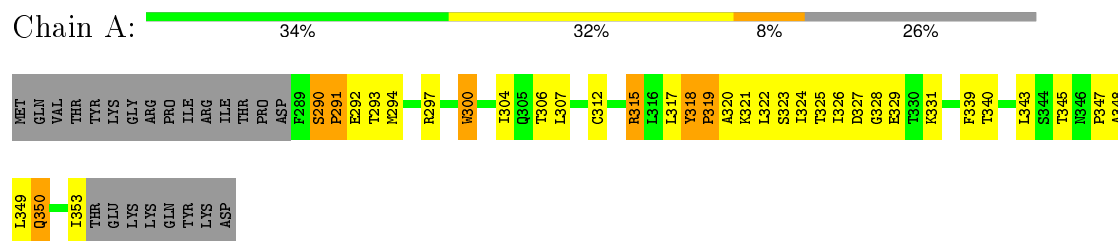
4.2.25 Score per residue for model 25

- Molecule 1: ORF 1 protein



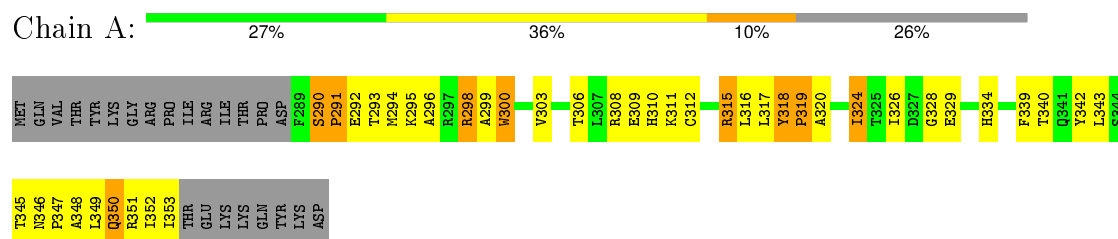
4.2.26 Score per residue for model 26

- Molecule 1: ORF 1 protein



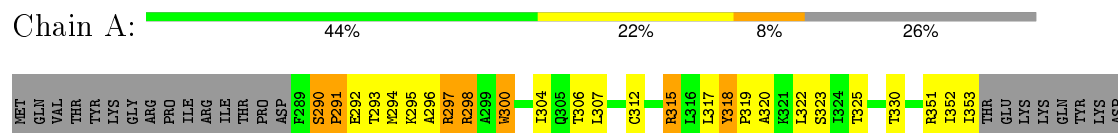
4.2.27 Score per residue for model 27

- Molecule 1: ORF 1 protein



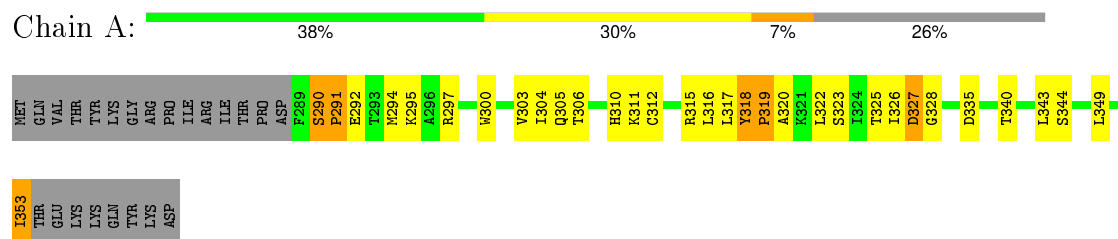
4.2.28 Score per residue for model 28

- Molecule 1: ORF 1 protein



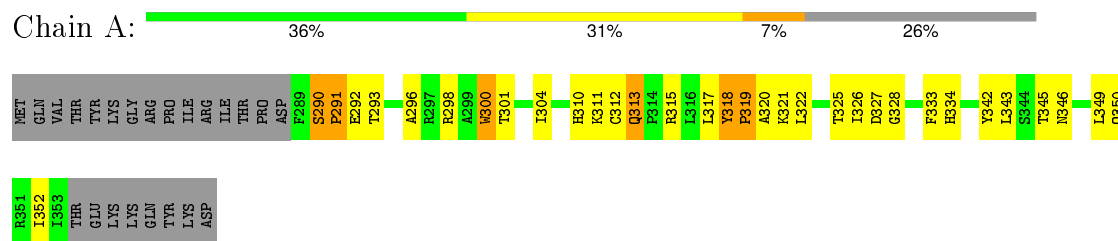
4.2.29 Score per residue for model 29

- Molecule 1: ORF 1 protein



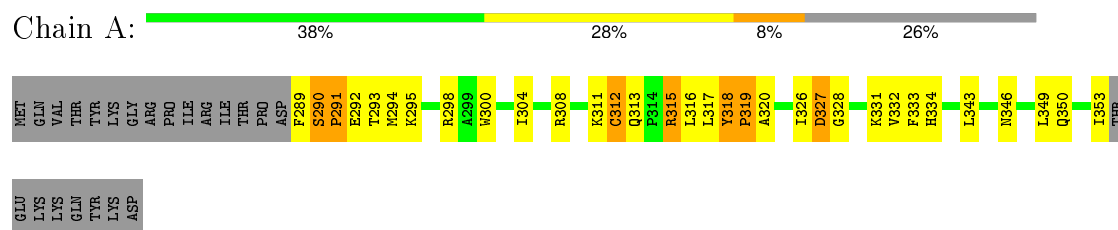
4.2.30 Score per residue for model 30

- Molecule 1: ORF 1 protein



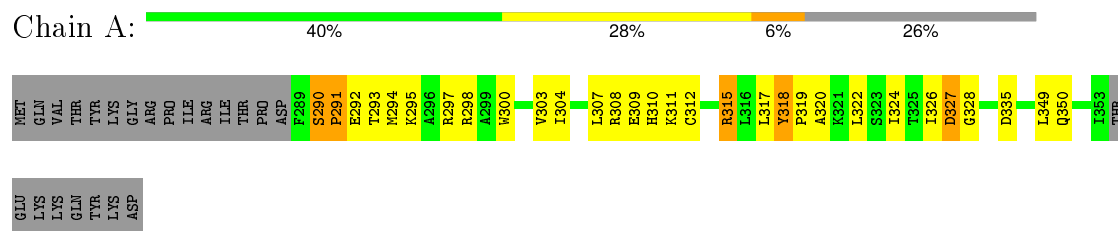
4.2.31 Score per residue for model 31

- Molecule 1: ORF 1 protein



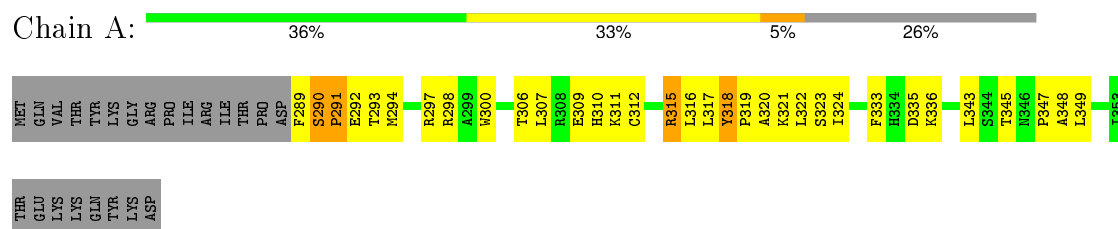
4.2.32 Score per residue for model 32

- Molecule 1: ORF 1 protein



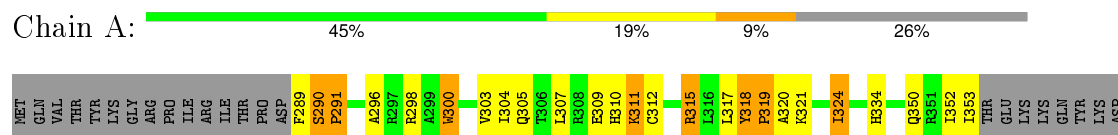
4.2.33 Score per residue for model 33

- Molecule 1: ORF 1 protein



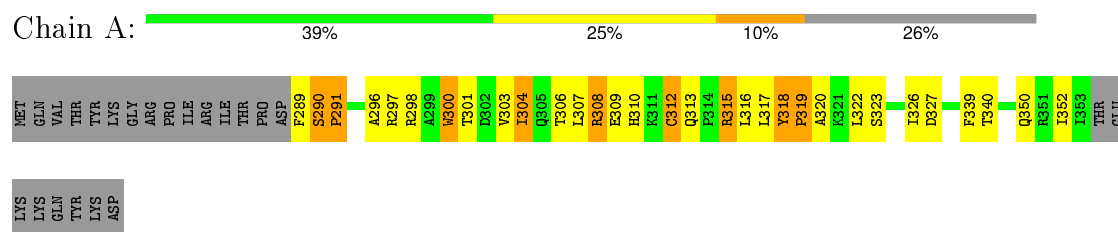
4.2.34 Score per residue for model 34

- Molecule 1: ORF 1 protein



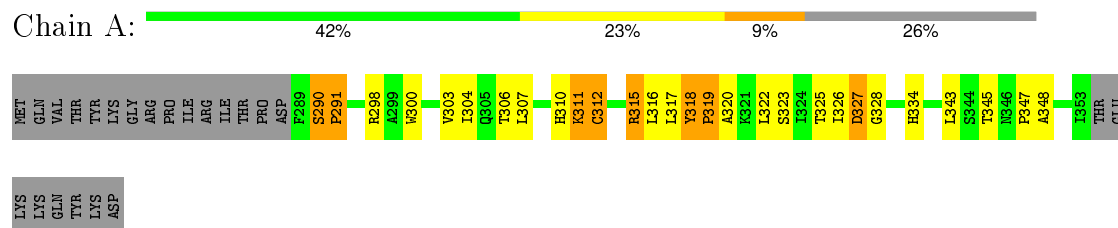
4.2.35 Score per residue for model 35

- Molecule 1: ORF 1 protein



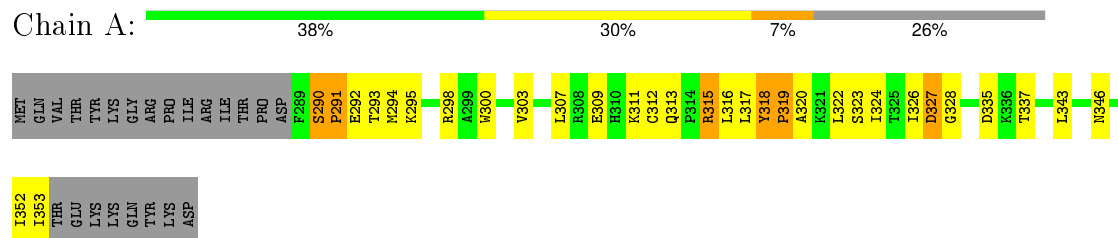
4.2.36 Score per residue for model 36

- Molecule 1: ORF 1 protein



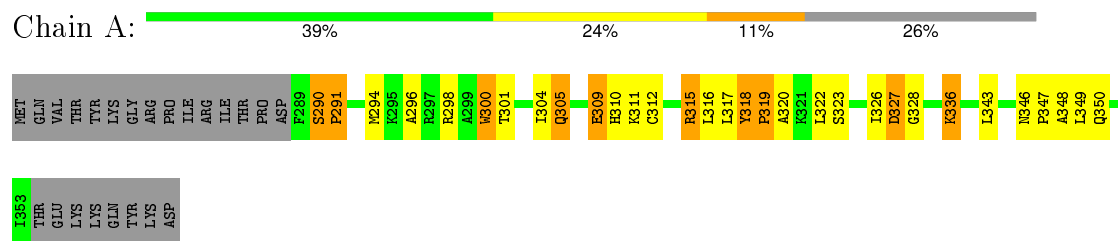
4.2.37 Score per residue for model 37

- Molecule 1: ORF 1 protein



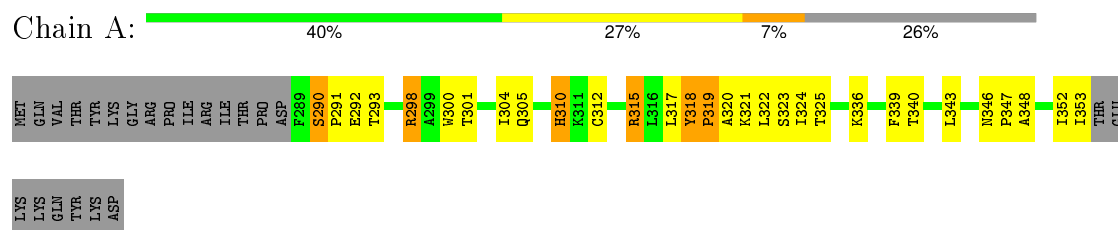
4.2.38 Score per residue for model 38

- Molecule 1: ORF 1 protein



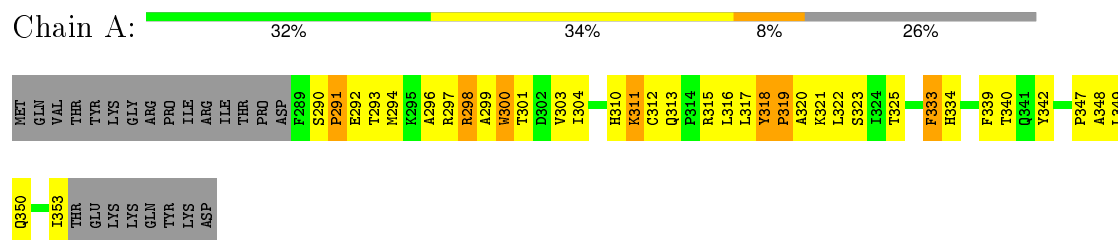
4.2.39 Score per residue for model 39

- Molecule 1: ORF 1 protein



4.2.40 Score per residue for model 40

- Molecule 1: ORF 1 protein



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 40 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
X-PLOR NIH	structure solution	
X-PLOR NIH	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)	BMRB entry 15325
Number of chemical shift lists	1
Total number of shifts	1127
Number of shifts mapped to atoms	1127
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Assignment completeness (well-defined parts)	87%

No validations of the models with respect to experimental NMR restraints is performed at this time.

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	537	555	554	27±5
All	All	21480	22200	22160	1072

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 25.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:318:TYR:O	1:A:320:ALA:N	0.86	2.09	5	40
1:A:317:LEU:O	1:A:318:TYR:O	0.84	1.96	38	40
1:A:310:HIS:CE1	1:A:312:CYS:HG	0.79	1.95	19	3
1:A:349:LEU:HD22	1:A:353:ILE:HD12	0.76	1.58	4	7
1:A:317:LEU:HD22	1:A:317:LEU:N	0.73	1.97	15	11
1:A:324:ILE:O	1:A:324:ILE:HD12	0.72	1.84	19	8
1:A:317:LEU:N	1:A:317:LEU:HD22	0.70	2.02	40	12
1:A:324:ILE:HD12	1:A:324:ILE:O	0.70	1.86	4	5
1:A:307:LEU:HD13	1:A:310:HIS:NE2	0.64	2.07	25	2
1:A:353:ILE:HD12	1:A:353:ILE:C	0.64	2.13	34	3
1:A:307:LEU:HD12	1:A:312:CYS:SG	0.64	2.32	26	6
1:A:315:ARG:CD	1:A:315:ARG:N	0.63	2.61	21	5
1:A:310:HIS:NE2	1:A:312:CYS:SG	0.63	2.69	18	6
1:A:310:HIS:ND1	1:A:311:LYS:N	0.63	2.47	21	11

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:290:SER:N	1:A:291:PRO:CD	0.63	2.61	32	37
1:A:310:HIS:CD2	1:A:312:CYS:HG	0.62	2.12	35	2
1:A:333:PHE:CD1	1:A:333:PHE:N	0.62	2.66	16	7
1:A:312:CYS:SG	1:A:325:THR:N	0.62	2.73	22	6
1:A:353:ILE:C	1:A:353:ILE:HD12	0.62	2.15	22	2
1:A:333:PHE:N	1:A:333:PHE:CD1	0.61	2.67	19	7
1:A:324:ILE:H	1:A:324:ILE:HD13	0.61	1.55	3	2
1:A:310:HIS:CG	1:A:311:LYS:N	0.61	2.67	2	13
1:A:315:ARG:N	1:A:315:ARG:CD	0.61	2.64	38	11
1:A:310:HIS:CE1	1:A:312:CYS:SG	0.60	2.93	19	17
1:A:322:LEU:C	1:A:322:LEU:HD13	0.60	2.17	2	16
1:A:322:LEU:HD13	1:A:322:LEU:C	0.60	2.17	37	8
1:A:346:ASN:ND2	1:A:349:LEU:H	0.60	1.95	20	2
1:A:324:ILE:HD13	1:A:324:ILE:H	0.60	1.56	2	2
1:A:315:ARG:HH12	1:A:325:THR:N	0.58	1.96	36	2
1:A:296:ALA:O	1:A:300:TRP:CG	0.57	2.56	24	17
1:A:317:LEU:N	1:A:317:LEU:CD2	0.57	2.68	27	9
1:A:313:GLN:O	1:A:315:ARG:NH1	0.57	2.37	19	10
1:A:317:LEU:CD2	1:A:317:LEU:N	0.57	2.68	35	13
1:A:307:LEU:O	1:A:310:HIS:CE1	0.56	2.58	36	2
1:A:316:LEU:HD23	1:A:317:LEU:N	0.56	2.16	15	25
1:A:310:HIS:NE2	1:A:352:ILE:HG21	0.56	2.16	39	4
1:A:324:ILE:HD13	1:A:324:ILE:N	0.56	2.16	3	3
1:A:351:ARG:CG	1:A:351:ARG:HH11	0.55	2.14	14	2
1:A:322:LEU:O	1:A:322:LEU:HD13	0.55	2.01	18	3
1:A:322:LEU:HD23	1:A:323:SER:N	0.55	2.16	10	6
1:A:342:TYR:O	1:A:346:ASN:N	0.55	2.40	27	2
1:A:315:ARG:NH2	1:A:325:THR:OG1	0.55	2.39	13	6
1:A:349:LEU:O	1:A:353:ILE:N	0.54	2.40	27	15
1:A:346:ASN:ND2	1:A:346:ASN:O	0.54	2.41	8	2
1:A:310:HIS:CG	1:A:311:LYS:H	0.54	2.21	3	2
1:A:317:LEU:O	1:A:318:TYR:C	0.54	2.46	19	40
1:A:311:LYS:O	1:A:312:CYS:SG	0.54	2.65	31	19
1:A:315:ARG:NH1	1:A:325:THR:OG1	0.54	2.40	19	7
1:A:317:LEU:N	1:A:321:LYS:O	0.54	2.35	8	12
1:A:303:VAL:O	1:A:307:LEU:HD23	0.54	2.03	37	11
1:A:294:MET:O	1:A:297:ARG:N	0.54	2.41	17	9
1:A:312:CYS:SG	1:A:312:CYS:O	0.53	2.66	18	1
1:A:305:GLN:O	1:A:305:GLN:NE2	0.53	2.41	38	1
1:A:308:ARG:CG	1:A:308:ARG:HH11	0.53	2.16	35	2
1:A:311:LYS:O	1:A:313:GLN:NE2	0.53	2.42	15	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:349:LEU:CD2	1:A:353:ILE:HD13	0.53	2.33	26	1
1:A:330:THR:O	1:A:330:THR:HG23	0.53	2.03	7	2
1:A:324:ILE:CD1	1:A:324:ILE:N	0.53	2.71	3	2
1:A:349:LEU:O	1:A:352:ILE:N	0.53	2.42	21	10
1:A:335:ASP:OD1	1:A:336:LYS:N	0.53	2.42	12	3
1:A:292:GLU:OE1	1:A:293:THR:N	0.53	2.41	4	2
1:A:307:LEU:O	1:A:310:HIS:NE2	0.53	2.42	6	1
1:A:294:MET:O	1:A:298:ARG:N	0.53	2.42	2	16
1:A:343:LEU:O	1:A:346:ASN:N	0.52	2.41	8	15
1:A:306:THR:O	1:A:309:GLU:N	0.52	2.41	9	9
1:A:312:CYS:SG	1:A:325:THR:O	0.52	2.67	40	18
1:A:351:ARG:NH1	1:A:351:ARG:CG	0.52	2.70	14	3
1:A:351:ARG:CG	1:A:351:ARG:NH1	0.52	2.72	18	3
1:A:322:LEU:HD13	1:A:323:SER:N	0.52	2.19	35	15
1:A:335:ASP:N	1:A:335:ASP:OD1	0.52	2.42	7	2
1:A:307:LEU:O	1:A:310:HIS:CD2	0.52	2.62	3	4
1:A:315:ARG:HH11	1:A:315:ARG:CG	0.52	2.18	33	2
1:A:349:LEU:HD22	1:A:353:ILE:CD1	0.52	2.33	4	4
1:A:307:LEU:O	1:A:309:GLU:N	0.52	2.43	21	10
1:A:310:HIS:CD2	1:A:312:CYS:SG	0.52	3.03	35	2
1:A:298:ARG:NH1	1:A:302:ASP:OD2	0.52	2.43	6	2
1:A:346:ASN:O	1:A:346:ASN:ND2	0.51	2.42	20	1
1:A:307:LEU:O	1:A:312:CYS:SG	0.51	2.68	19	3
1:A:297:ARG:NH1	1:A:297:ARG:CG	0.51	2.73	28	4
1:A:313:GLN:H	1:A:313:GLN:CD	0.51	2.09	21	1
1:A:307:LEU:H	1:A:307:LEU:HD22	0.51	1.66	5	1
1:A:298:ARG:O	1:A:301:THR:N	0.51	2.42	35	7
1:A:297:ARG:O	1:A:300:TRP:N	0.51	2.44	9	1
1:A:310:HIS:CE1	1:A:349:LEU:HD21	0.51	2.40	29	4
1:A:326:ILE:O	1:A:329:GLU:N	0.51	2.44	10	3
1:A:351:ARG:HH11	1:A:351:ARG:CG	0.50	2.19	18	2
1:A:298:ARG:NH1	1:A:298:ARG:CG	0.50	2.74	27	2
1:A:300:TRP:HE1	1:A:320:ALA:C	0.50	2.10	11	9
1:A:312:CYS:O	1:A:312:CYS:SG	0.50	2.69	19	1
1:A:308:ARG:NH1	1:A:308:ARG:CG	0.50	2.71	35	1
1:A:315:ARG:NH1	1:A:315:ARG:CG	0.50	2.72	33	3
1:A:324:ILE:N	1:A:324:ILE:HD13	0.50	2.22	9	1
1:A:343:LEU:C	1:A:345:THR:N	0.50	2.65	36	11
1:A:347:PRO:O	1:A:350:GLN:N	0.50	2.44	26	2
1:A:324:ILE:N	1:A:324:ILE:CD1	0.50	2.75	2	2
1:A:315:ARG:HH12	1:A:324:ILE:C	0.49	2.10	11	3

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:315:ARG:NH1	1:A:323:SER:C	0.49	2.66	20	1
1:A:302:ASP:N	1:A:302:ASP:OD1	0.49	2.45	25	1
1:A:298:ARG:CG	1:A:298:ARG:NH1	0.49	2.75	14	5
1:A:313:GLN:CD	1:A:313:GLN:H	0.49	2.10	30	3
1:A:313:GLN:OE1	1:A:313:GLN:N	0.49	2.45	21	2
1:A:349:LEU:O	1:A:351:ARG:N	0.49	2.45	27	4
1:A:315:ARG:CG	1:A:315:ARG:NH1	0.49	2.73	34	1
1:A:297:ARG:CG	1:A:297:ARG:NH1	0.49	2.75	40	1
1:A:308:ARG:CG	1:A:308:ARG:NH1	0.49	2.76	18	2
1:A:292:GLU:CD	1:A:293:THR:N	0.48	2.67	4	2
1:A:297:ARG:HH11	1:A:297:ARG:CG	0.48	2.20	28	1
1:A:298:ARG:HH11	1:A:298:ARG:CG	0.48	2.21	27	3
1:A:339:PHE:CE2	1:A:343:LEU:HD11	0.48	2.42	10	1
1:A:313:GLN:CD	1:A:313:GLN:N	0.48	2.67	3	2
1:A:292:GLU:CG	1:A:293:THR:N	0.48	2.75	26	18
1:A:289:PHE:CD1	1:A:289:PHE:N	0.48	2.82	21	2
1:A:315:ARG:CZ	1:A:323:SER:OG	0.48	2.61	18	3
1:A:291:PRO:O	1:A:295:LYS:CD	0.48	2.62	37	5
1:A:313:GLN:N	1:A:313:GLN:CD	0.48	2.67	20	1
1:A:332:VAL:C	1:A:333:PHE:CD1	0.48	2.88	15	4
1:A:315:ARG:O	1:A:317:LEU:CD2	0.48	2.62	6	3
1:A:292:GLU:N	1:A:292:GLU:CD	0.47	2.67	22	1
1:A:315:ARG:CG	1:A:315:ARG:HH11	0.47	2.22	34	2
1:A:299:ALA:O	1:A:303:VAL:HG22	0.47	2.09	10	6
1:A:315:ARG:HH12	1:A:325:THR:CB	0.47	2.23	22	1
1:A:306:THR:O	1:A:309:GLU:CG	0.47	2.63	10	1
1:A:318:TYR:C	1:A:320:ALA:N	0.46	2.68	24	22
1:A:352:ILE:CD1	1:A:352:ILE:N	0.46	2.78	18	2
1:A:336:LYS:O	1:A:340:THR:HG23	0.46	2.10	16	1
1:A:310:HIS:CD2	1:A:352:ILE:HG21	0.46	2.45	9	2
1:A:297:ARG:O	1:A:301:THR:N	0.46	2.49	7	1
1:A:352:ILE:HD12	1:A:352:ILE:N	0.46	2.26	18	3
1:A:315:ARG:NE	1:A:323:SER:OG	0.46	2.49	17	1
1:A:307:LEU:C	1:A:309:GLU:N	0.46	2.68	37	10
1:A:308:ARG:C	1:A:310:HIS:N	0.46	2.69	6	1
1:A:329:GLU:OE1	1:A:329:GLU:N	0.46	2.49	17	1
1:A:347:PRO:O	1:A:348:ALA:C	0.46	2.54	11	11
1:A:326:ILE:O	1:A:328:GLY:N	0.46	2.49	37	17
1:A:313:GLN:H	1:A:313:GLN:NE2	0.46	2.09	15	1
1:A:343:LEU:C	1:A:345:THR:H	0.46	2.14	36	9
1:A:300:TRP:NE1	1:A:320:ALA:O	0.46	2.38	1	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:307:LEU:HD13	1:A:312:CYS:SG	0.45	2.51	23	1
1:A:311:LYS:C	1:A:312:CYS:SG	0.45	2.95	25	5
1:A:290:SER:CB	1:A:291:PRO:CD	0.45	2.95	39	2
1:A:309:GLU:OE1	1:A:309:GLU:O	0.45	2.35	18	2
1:A:349:LEU:O	1:A:350:GLN:C	0.45	2.55	27	12
1:A:316:LEU:CD2	1:A:317:LEU:O	0.45	2.65	15	6
1:A:292:GLU:OE1	1:A:292:GLU:N	0.45	2.50	29	1
1:A:303:VAL:O	1:A:307:LEU:N	0.45	2.48	6	1
1:A:330:THR:CG2	1:A:330:THR:O	0.45	2.65	28	2
1:A:310:HIS:ND1	1:A:312:CYS:SG	0.45	2.89	40	1
1:A:339:PHE:O	1:A:342:TYR:N	0.45	2.50	23	3
1:A:332:VAL:C	1:A:333:PHE:CG	0.44	2.90	15	1
1:A:336:LYS:H	1:A:336:LYS:CD	0.44	2.25	38	1
1:A:353:ILE:C	1:A:353:ILE:CD1	0.44	2.86	22	2
1:A:289:PHE:N	1:A:289:PHE:CD1	0.44	2.84	33	2
1:A:343:LEU:O	1:A:345:THR:N	0.44	2.51	36	7
1:A:318:TYR:O	1:A:319:PRO:C	0.44	2.56	23	30
1:A:346:ASN:HD21	1:A:349:LEU:H	0.44	1.54	20	1
1:A:298:ARG:NH1	1:A:302:ASP:OD1	0.44	2.50	6	1
1:A:309:GLU:O	1:A:309:GLU:OE2	0.44	2.36	1	2
1:A:297:ARG:CG	1:A:297:ARG:HH11	0.44	2.26	40	1
1:A:353:ILE:CD1	1:A:353:ILE:C	0.44	2.84	34	3
1:A:309:GLU:CD	1:A:309:GLU:O	0.44	2.55	17	2
1:A:316:LEU:C	1:A:316:LEU:HD23	0.44	2.33	5	3
1:A:322:LEU:C	1:A:322:LEU:CD1	0.44	2.86	2	7
1:A:316:LEU:HD23	1:A:316:LEU:C	0.44	2.33	24	2
1:A:292:GLU:OE2	1:A:293:THR:OG1	0.44	2.36	16	2
1:A:322:LEU:CD1	1:A:322:LEU:C	0.43	2.87	21	4
1:A:352:ILE:O	1:A:353:ILE:O	0.43	2.35	7	7
1:A:298:ARG:CG	1:A:298:ARG:HH11	0.43	2.26	14	2
1:A:298:ARG:C	1:A:298:ARG:CD	0.43	2.86	24	1
1:A:340:THR:OG1	1:A:341:GLN:N	0.43	2.51	16	1
1:A:327:ASP:O	1:A:327:ASP:OD1	0.43	2.35	24	2
1:A:307:LEU:C	1:A:309:GLU:H	0.43	2.16	21	5
1:A:305:GLN:NE2	1:A:305:GLN:C	0.43	2.71	38	1
1:A:315:ARG:O	1:A:323:SER:OG	0.43	2.36	33	1
1:A:305:GLN:O	1:A:305:GLN:OE1	0.43	2.36	39	1
1:A:298:ARG:O	1:A:301:THR:OG1	0.43	2.35	11	2
1:A:327:ASP:OD1	1:A:327:ASP:C	0.43	2.57	5	1
1:A:322:LEU:HD13	1:A:322:LEU:O	0.43	2.14	15	1
1:A:292:GLU:OE1	1:A:292:GLU:CA	0.43	2.63	22	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:326:ILE:O	1:A:327:ASP:C	0.43	2.57	31	17
1:A:324:ILE:HD11	1:A:331:LYS:HB3	0.43	1.90	26	1
1:A:312:CYS:HG	1:A:325:THR:N	0.43	2.12	28	1
1:A:350:GLN:O	1:A:350:GLN:OE1	0.43	2.36	35	1
1:A:327:ASP:OD1	1:A:327:ASP:O	0.43	2.37	13	2
1:A:349:LEU:HB3	1:A:353:ILE:HD12	0.42	1.91	20	1
1:A:327:ASP:N	1:A:327:ASP:OD1	0.42	2.52	17	1
1:A:336:LYS:N	1:A:336:LYS:CD	0.42	2.81	38	1
1:A:307:LEU:O	1:A:310:HIS:N	0.42	2.51	17	1
1:A:302:ASP:OD1	1:A:302:ASP:N	0.42	2.52	14	1
1:A:327:ASP:OD1	1:A:327:ASP:N	0.42	2.53	31	2
1:A:307:LEU:N	1:A:307:LEU:HD22	0.42	2.30	5	1
1:A:315:ARG:NH1	1:A:323:SER:OG	0.42	2.53	14	1
1:A:326:ILE:C	1:A:328:GLY:N	0.42	2.73	10	1
1:A:326:ILE:O	1:A:329:GLU:OE2	0.42	2.37	26	1
1:A:308:ARG:O	1:A:310:HIS:N	0.42	2.52	6	1
1:A:339:PHE:O	1:A:340:THR:C	0.42	2.58	23	7
1:A:322:LEU:O	1:A:332:VAL:HG13	0.42	2.14	13	1
1:A:315:ARG:CB	1:A:315:ARG:HH11	0.42	2.28	2	1
1:A:314:PRO:C	1:A:315:ARG:CD	0.42	2.88	2	1
1:A:335:ASP:OD1	1:A:337:THR:N	0.42	2.44	37	1
1:A:347:PRO:O	1:A:351:ARG:N	0.41	2.51	8	1
1:A:303:VAL:HG23	1:A:304:ILE:N	0.41	2.30	35	1
1:A:315:ARG:NH1	1:A:324:ILE:C	0.41	2.74	32	1
1:A:290:SER:H	1:A:291:PRO:CD	0.41	2.28	27	1
1:A:324:ILE:O	1:A:324:ILE:HD13	0.41	2.13	34	1
1:A:309:GLU:O	1:A:309:GLU:CG	0.41	2.68	17	1
1:A:303:VAL:O	1:A:306:THR:N	0.41	2.53	20	4
1:A:294:MET:O	1:A:295:LYS:C	0.41	2.59	6	1
1:A:306:THR:O	1:A:307:LEU:C	0.41	2.58	35	6
1:A:315:ARG:NH1	1:A:325:THR:N	0.41	2.67	36	1
1:A:343:LEU:O	1:A:350:GLN:OE1	0.41	2.38	11	1
1:A:308:ARG:C	1:A:310:HIS:H	0.41	2.19	6	1
1:A:297:ARG:HH11	1:A:297:ARG:HG2	0.41	1.76	40	1
1:A:340:THR:O	1:A:343:LEU:N	0.41	2.54	29	1
1:A:315:ARG:HD2	1:A:315:ARG:N	0.40	2.32	39	1
1:A:310:HIS:NE2	1:A:349:LEU:CD2	0.40	2.85	7	1
1:A:298:ARG:NH1	1:A:302:ASP:CG	0.40	2.74	6	1
1:A:318:TYR:C	1:A:320:ALA:H	0.40	2.19	15	1
1:A:326:ILE:HG22	1:A:326:ILE:O	0.40	2.16	13	1
1:A:341:GLN:O	1:A:342:TYR:C	0.40	2.60	4	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:322:LEU:CD1	1:A:324:ILE:CG2	0.40	3.00	9	1
1:A:332:VAL:O	1:A:333:PHE:CD1	0.40	2.75	3	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	63/88 (72%)	51±2 (81±3%)	8±2 (13±3%)	3±1 (6±1%)	4	24
All	All	2520/3520 (72%)	2051 (81%)	330 (13%)	139 (6%)	4	24

All 7 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	318	TYR	40
1	A	319	PRO	40
1	A	291	PRO	37
1	A	327	ASP	11
1	A	308	ARG	8
1	A	312	CYS	2
1	A	350	GLN	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	60/82 (73%)	52±2 (87±3%)	8±2 (13±3%)	9	50
All	All	2400/3280 (73%)	2079 (87%)	321 (13%)	9	50

All 39 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	300	TRP	40
1	A	315	ARG	40
1	A	290	SER	39
1	A	304	ILE	27
1	A	298	ARG	18
1	A	334	HIS	17
1	A	324	ILE	13
1	A	322	LEU	11
1	A	350	GLN	8
1	A	292	GLU	8
1	A	309	GLU	8
1	A	336	LYS	8
1	A	305	GLN	7
1	A	321	LYS	7
1	A	310	HIS	7
1	A	323	SER	7
1	A	311	LYS	6
1	A	340	THR	5
1	A	335	ASP	4
1	A	331	LYS	4
1	A	295	LYS	3
1	A	333	PHE	3
1	A	308	ARG	3
1	A	297	ARG	3
1	A	330	THR	3
1	A	351	ARG	3
1	A	302	ASP	3
1	A	313	GLN	2
1	A	353	ILE	2
1	A	338	LYS	2
1	A	327	ASP	2
1	A	307	LEU	1
1	A	329	GLU	1
1	A	301	THR	1
1	A	312	CYS	1
1	A	344	SER	1
1	A	319	PRO	1
1	A	289	PHE	1
1	A	306	THR	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 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 [i](#)

The completeness of assignment taking into account all chemical shift lists is 87% for the well-defined parts and 87% for the entire structure.

7.1 Chemical shift list 1

File name: BMRB entry 15325

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	1127
Number of shifts mapped to atoms	1127
Number of unparsed shifts	0
Number of shifts with mapping errors	0
Number of shifts with mapping warnings	0
Number of shift outliers (ShiftChecker)	7

7.1.2 Chemical shift referencing [i](#)

The following table shows the suggested chemical shift referencing corrections.

Nucleus	# values	Correction \pm precision, ppm	Suggested action
$^{13}\text{C}_\alpha$	87	-0.14 ± 0.36	None needed (< 0.5 ppm)
$^{13}\text{C}_\beta$	86	0.21 ± 0.21	None needed (< 0.5 ppm)
$^{13}\text{C}'$	84	-0.14 ± 0.22	None needed (< 0.5 ppm)
^{15}N	79	-0.15 ± 0.32	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 87%, i.e. 756 atoms were assigned a chemical shift out of a possible 865. 7 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	^1H	^{13}C	^{15}N
Backbone	311/317 (98%)	124/126 (98%)	128/130 (98%)	59/61 (97%)
Sidechain	387/479 (81%)	239/283 (84%)	144/170 (85%)	4/26 (15%)

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	Total	¹H	¹³C	¹⁵N
Aromatic	58/69 (84%)	30/37 (81%)	27/29 (93%)	1/3 (33%)
Overall	756/865 (87%)	393/446 (88%)	299/329 (91%)	64/90 (71%)

The following table shows the completeness of the chemical shift assignments for the full structure. The overall completeness is 87%, i.e. 756 atoms were assigned a chemical shift out of a possible 865. 7 out of 8 assigned methyl groups (LEU and VAL) were assigned stereospecifically.

	Total	¹H	¹³C	¹⁵N
Backbone	311/317 (98%)	124/126 (98%)	128/130 (98%)	59/61 (97%)
Sidechain	387/479 (81%)	239/283 (84%)	144/170 (85%)	4/26 (15%)
Aromatic	58/69 (84%)	30/37 (81%)	27/29 (93%)	1/3 (33%)
Overall	756/865 (87%)	393/446 (88%)	299/329 (91%)	64/90 (71%)

7.1.4 Statistically unusual chemical shifts ⓘ

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.

Mol	Chain	Res	Type	Atom	Shift, ppm	Expected range, ppm	Z-score
1	A	278	TYR	CE1	133.41	124.14 – 111.74	12.5
1	A	278	TYR	CE2	133.41	124.68 – 111.18	11.5
1	A	278	TYR	CD1	118.28	139.11 – 126.41	-11.4
1	A	278	TYR	CD2	118.28	140.11 – 125.31	-9.8
1	A	322	LEU	HB3	-0.98	3.34 – -0.26	-7.0
1	A	360	LYS	HE2	1.61	3.87 – 1.97	-6.9
1	A	360	LYS	HD2	3.00	2.76 – 0.46	6.0

7.1.5 Random Coil Index (RCI) plots ⓘ

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.

Random coil index (RCI) for chain A:

