



Full wwPDB NMR Structure Validation Report ⓘ

Mar 9, 2026 – 06:24 AM UTC

PDB ID : 1E0H / pdb_00001e0h
Title : Inhibitor Protein Im9 bound to its partner E9 DNase
Authors : Boetzel, R.; Czisch, M.; Kaptein, R.; Hemmings, A.M.; James, R.; Kleanthous, C.; Moore, G.R.
Deposited on : 2000-03-28

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

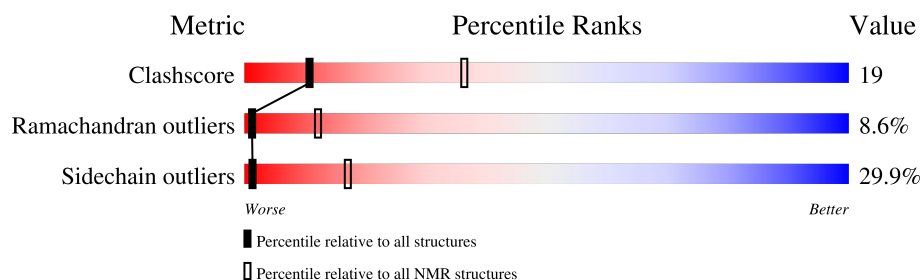
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

SOLUTION NMR

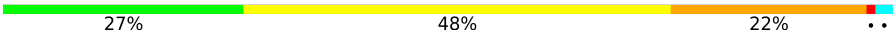
The overall completeness of chemical shifts assignment was not calculated.

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	86	

2 Ensemble composition and analysis

This entry contains 20 models. The atoms present in the NMR models are not consistent. Some calculations may have failed as a result. All residues are included in the validation scores. Model 12 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative.

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:3-A:86 (84)	0.70	12

Ill-defined regions of proteins are excluded from the global statistics.

Ligands and non-protein polymers are included in the analysis.

The models can be grouped into 4 clusters and 3 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1308 atoms, of which 635 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called IMMUNITY PROTEIN FOR COLICIN E9.

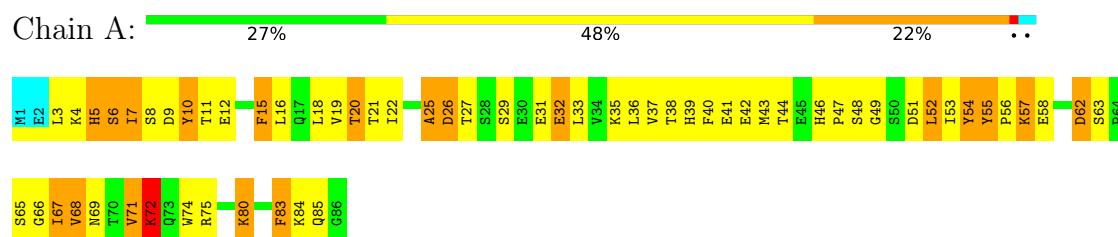
Mol	Chain	Residues	Atoms						Trace
1	A	86	Total	C	H	N	O	S	0
			1308	418	635	108	144	3	

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: IMMUNITY PROTEIN FOR COLICIN E9

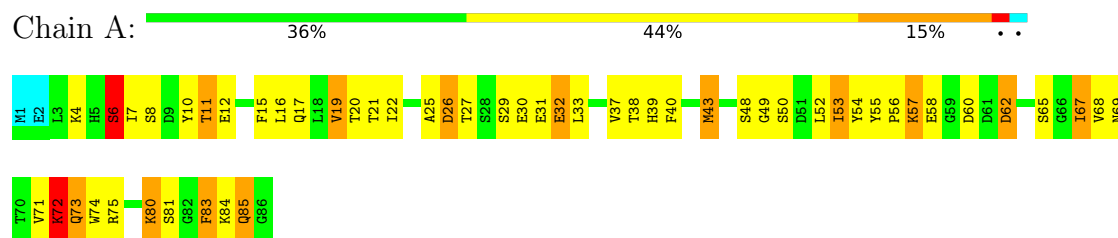


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

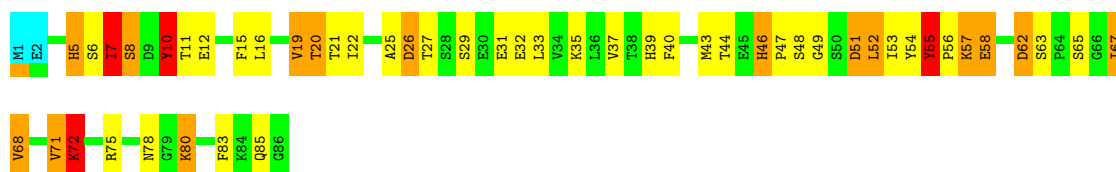
- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



4.2.2 Score per residue for model 2

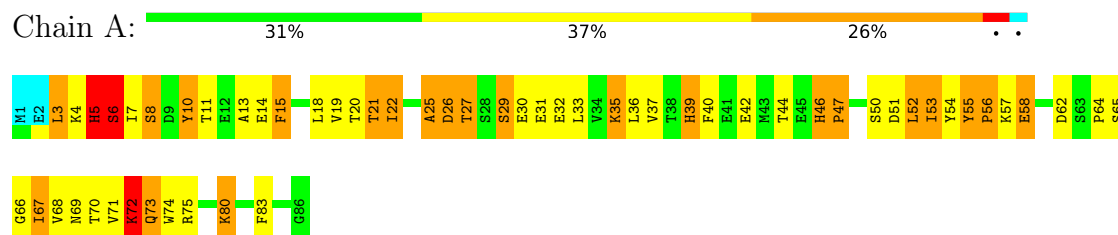
- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9





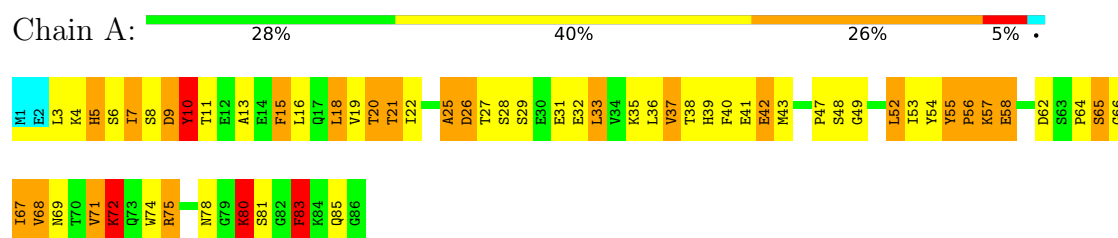
4.2.3 Score per residue for model 3

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



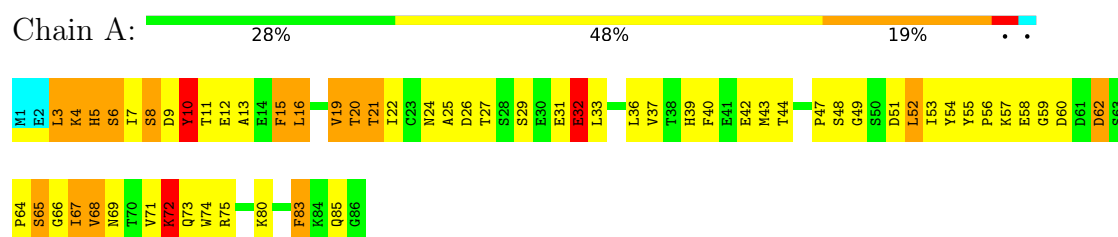
4.2.4 Score per residue for model 4

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



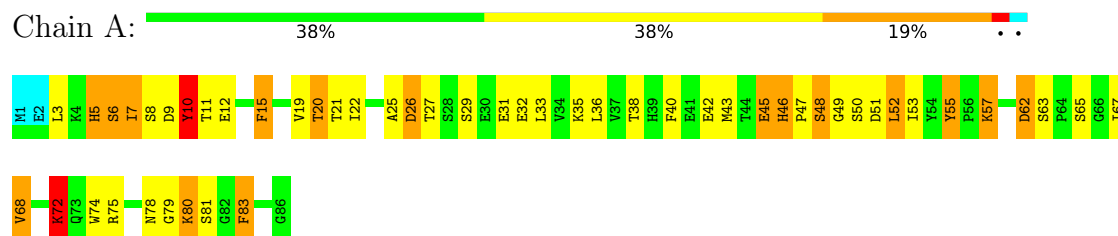
4.2.5 Score per residue for model 5

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



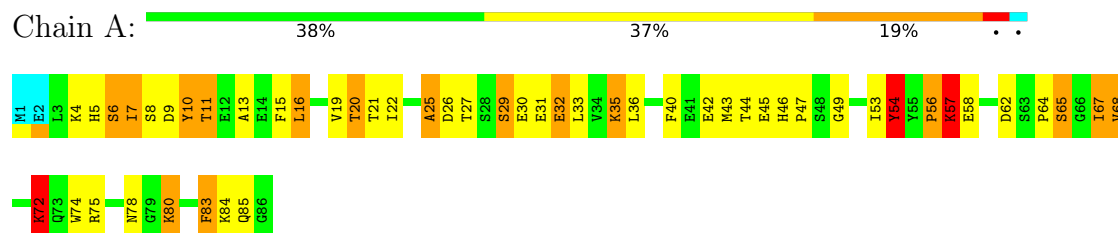
4.2.6 Score per residue for model 6

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



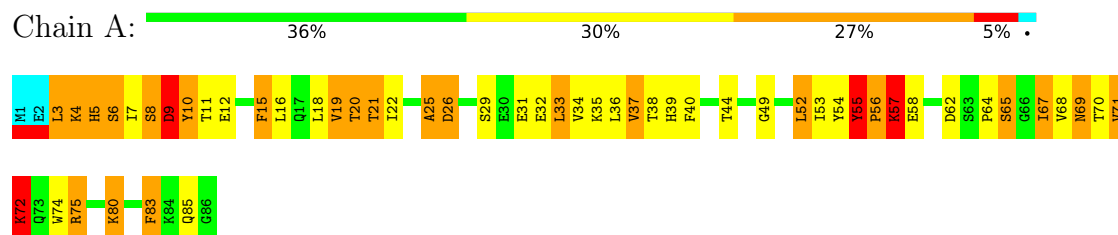
4.2.7 Score per residue for model 7

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



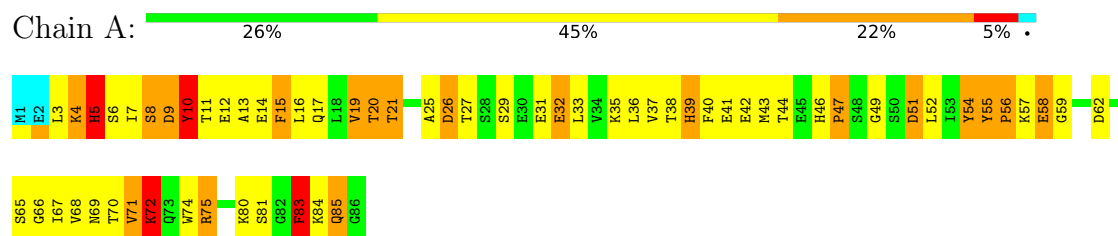
4.2.8 Score per residue for model 8

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



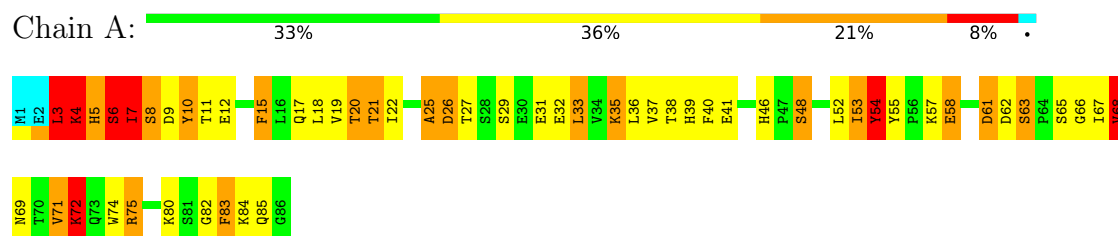
4.2.9 Score per residue for model 9

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



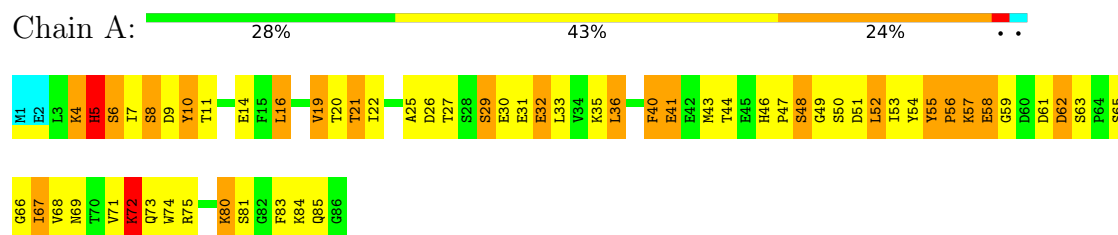
4.2.10 Score per residue for model 10

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



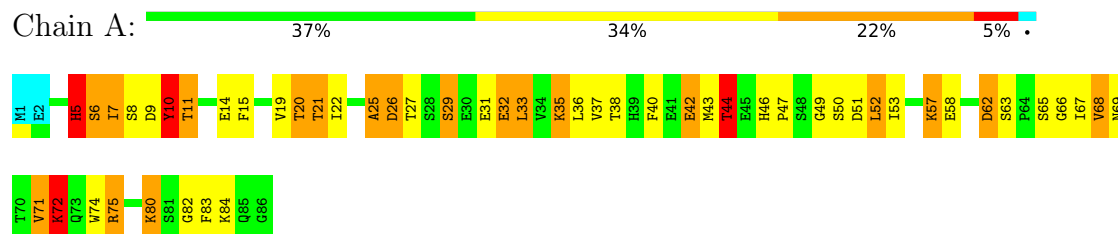
4.2.11 Score per residue for model 11

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



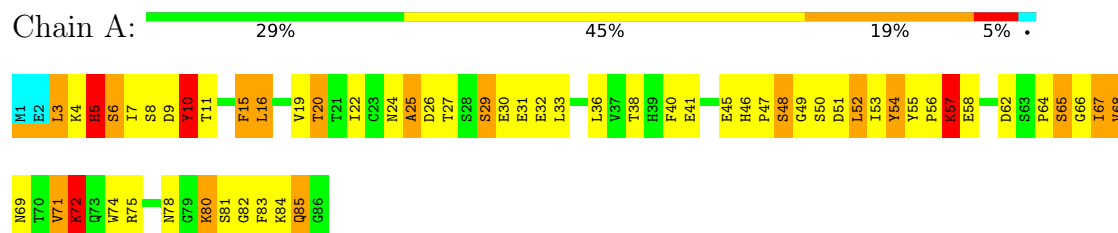
4.2.12 Score per residue for model 12 (medoid)

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



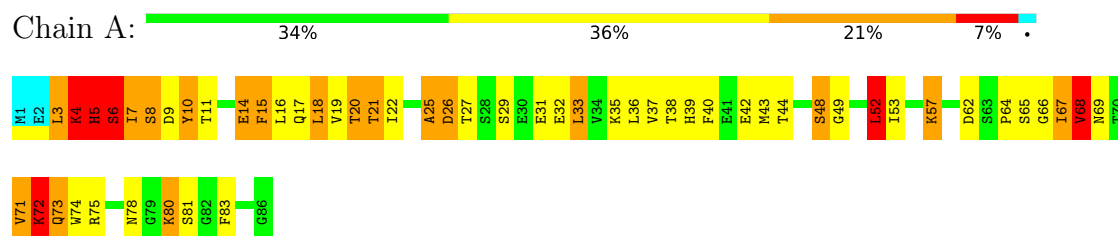
4.2.13 Score per residue for model 13

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



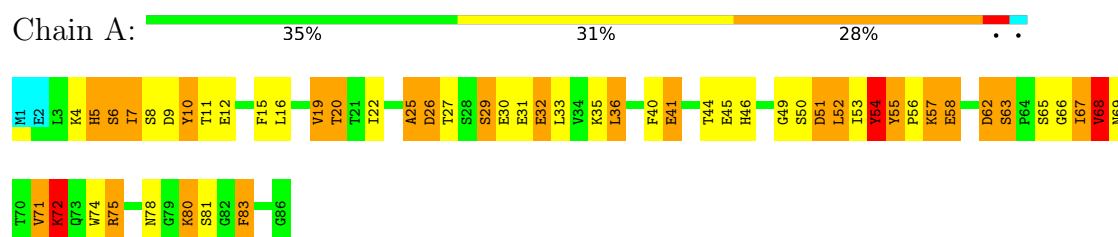
4.2.14 Score per residue for model 14

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



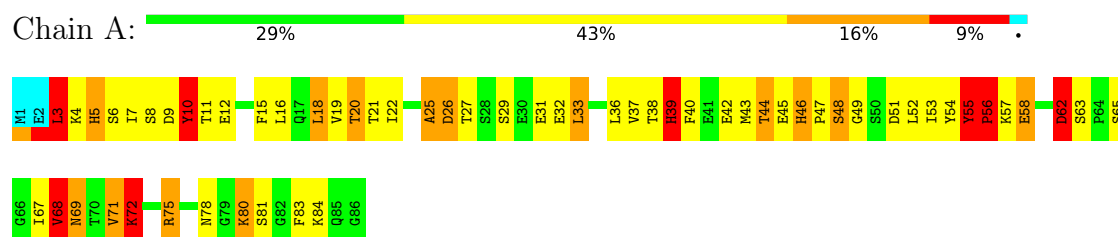
4.2.15 Score per residue for model 15

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



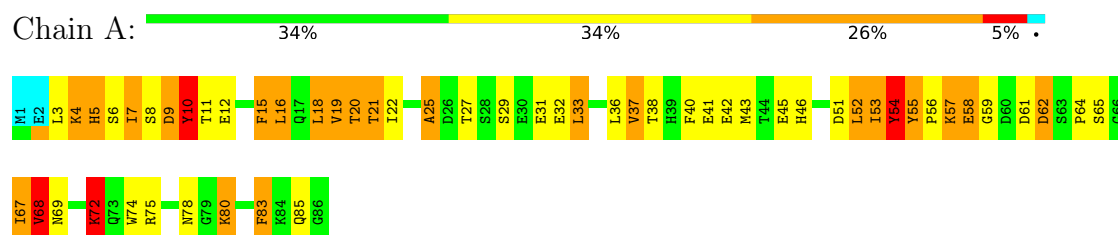
4.2.16 Score per residue for model 16

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



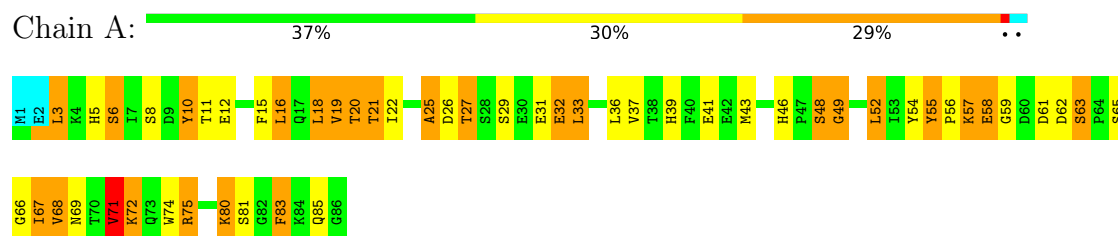
4.2.17 Score per residue for model 17

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



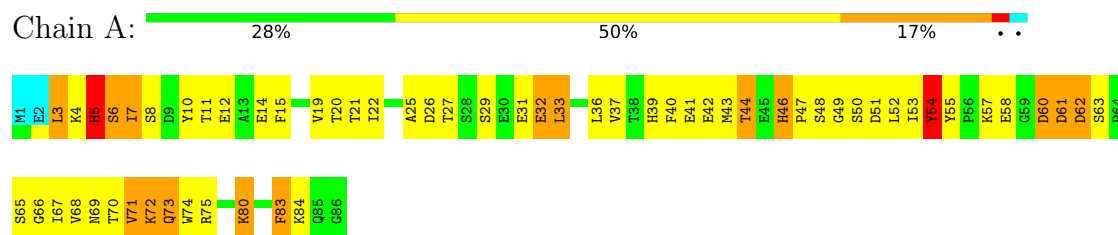
4.2.18 Score per residue for model 18

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



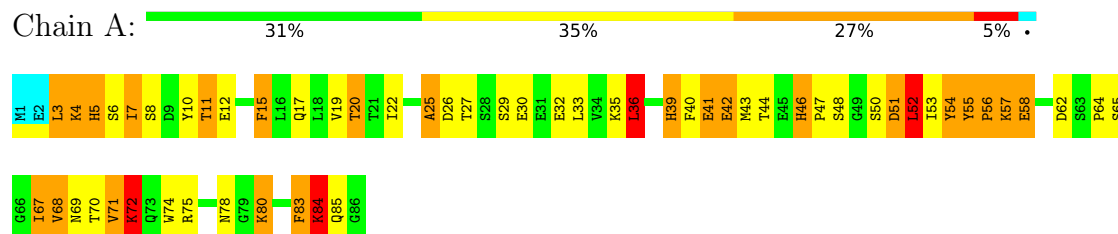
4.2.19 Score per residue for model 19

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



4.2.20 Score per residue for model 20

- Molecule 1: IMMUNITY PROTEIN FOR COLICIN E9



5 Refinement protocol and experimental data overview ⓘ

The models were refined using the following method: *torsion angle dynamics*.

Of the 20 calculated structures, 20 were deposited, based on the following criterion: *LOWEST ENERGY STRUCTURES WITH NO RESTRAINT VIOLATIONS >0.4*.

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

Software name	Classification	Version
DYANA	refinement	
DYANA	structure solution	

No chemical shift data was provided.

6 Model quality

6.1 Standard geometry

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	1.13±0.02	2±1/669 (0.2± 0.2%)	2.25±0.06	33±5/904 (3.6± 0.6%)
All	All	1.13	30/13380 (0.2%)	2.25	658/18080 (3.6%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	Chirality	Planarity
1	A	0.0±0.0	2.4±1.1
All	All	0	48

All unique bond outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	6	SER	N-CA	-8.28	1.35	1.45	15	11
1	A	31	GLU	CA-C	-7.13	1.47	1.52	9	7
1	A	84	LYS	N-CA	-6.15	1.38	1.46	12	2
1	A	53	ILE	N-CA	-5.81	1.41	1.46	20	3
1	A	83	PHE	N-CA	-5.43	1.39	1.46	4	1
1	A	31	GLU	CA-CB	-5.31	1.45	1.53	3	2
1	A	3	LEU	N-CA	-5.16	1.39	1.46	10	1
1	A	17	GLN	N-CA	-5.12	1.40	1.46	1	3

All unique angle outliers are listed below. They are sorted according to the Z-score of the worst occurrence in the ensemble.

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	53	ILE	CB-CA-C	13.31	123.69	110.65	13	15
1	A	83	PHE	CA-C-N	11.82	144.08	122.09	9	19

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	83	PHE	C-N-CA	11.82	144.08	122.09	9	19
1	A	83	PHE	CA-CB-CG	11.76	125.56	113.80	4	12
1	A	51	ASP	CA-CB-CG	11.41	124.01	112.60	20	7
1	A	58	GLU	N-CA-C	10.30	125.21	112.23	10	12
1	A	65	SER	CA-C-N	10.11	131.21	119.98	3	19
1	A	65	SER	C-N-CA	10.11	131.21	119.98	3	19
1	A	41	GLU	CB-CG-CD	10.05	129.69	112.60	15	4
1	A	64	PRO	CA-C-N	9.90	137.76	122.42	13	9
1	A	64	PRO	C-N-CA	9.90	137.76	122.42	13	9
1	A	25	ALA	CA-C-N	9.23	139.16	121.54	16	19
1	A	25	ALA	C-N-CA	9.23	139.16	121.54	16	19
1	A	5	HIS	CB-CG-CD2	-8.82	119.74	131.20	12	18
1	A	84	LYS	CB-CA-C	8.51	127.35	110.42	20	4
1	A	39	HIS	CB-CG-CD2	-8.01	120.79	131.20	16	4
1	A	41	GLU	CA-C-N	7.89	131.06	120.65	4	5
1	A	41	GLU	C-N-CA	7.89	131.06	120.65	4	5
1	A	37	VAL	CA-CB-CG2	7.83	123.72	110.40	4	3
1	A	80	LYS	CA-C-N	7.62	136.10	121.54	15	9
1	A	80	LYS	C-N-CA	7.62	136.10	121.54	15	9
1	A	20	THR	CA-CB-CG2	7.57	123.36	110.50	8	16
1	A	59	GLY	N-CA-C	-7.54	104.63	115.64	18	2
1	A	13	ALA	CA-C-N	7.42	130.82	120.29	9	5
1	A	13	ALA	C-N-CA	7.42	130.82	120.29	9	5
1	A	26	ASP	CA-C-N	7.40	134.07	121.86	3	1
1	A	26	ASP	C-N-CA	7.40	134.07	121.86	3	1
1	A	80	LYS	CA-CB-CG	-7.40	99.30	114.10	7	3
1	A	26	ASP	CA-CB-CG	7.38	119.98	112.60	15	9
1	A	19	VAL	CA-C-N	7.28	130.04	120.28	8	7
1	A	19	VAL	C-N-CA	7.28	130.04	120.28	8	7
1	A	51	ASP	N-CA-C	-7.22	103.78	112.59	12	9
1	A	62	ASP	CB-CA-C	-7.20	98.42	109.29	5	2
1	A	62	ASP	CA-CB-CG	7.16	119.75	112.60	19	6
1	A	73	GLN	CA-CB-CG	-7.10	99.90	114.10	19	4
1	A	42	GLU	CA-C-N	7.01	130.00	120.54	20	3
1	A	42	GLU	C-N-CA	7.01	130.00	120.54	20	3
1	A	68	VAL	CA-C-N	6.92	130.82	120.31	9	12
1	A	68	VAL	C-N-CA	6.92	130.82	120.31	9	12
1	A	16	LEU	CA-C-N	6.89	129.51	120.28	11	9
1	A	16	LEU	C-N-CA	6.89	129.51	120.28	11	9
1	A	71	VAL	CA-CB-CG1	6.88	122.10	110.40	8	13
1	A	85	GLN	CA-C-N	6.70	133.75	121.70	13	4

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	85	GLN	C-N-CA	6.70	133.75	121.70	13	4
1	A	50	SER	CA-C-N	6.64	131.99	121.44	11	5
1	A	50	SER	C-N-CA	6.64	131.99	121.44	11	5
1	A	52	LEU	N-CA-C	-6.63	102.83	111.71	12	7
1	A	31	GLU	N-CA-CB	-6.63	98.91	110.44	4	11
1	A	44	THR	CB-CA-C	6.63	121.15	109.75	12	4
1	A	9	ASP	CA-CB-CG	-6.62	105.98	112.60	8	4
1	A	80	LYS	CG-CD-CE	6.59	126.45	111.30	6	2
1	A	29	SER	CA-C-N	6.57	134.09	121.54	11	1
1	A	29	SER	C-N-CA	6.57	134.09	121.54	11	1
1	A	58	GLU	CA-C-O	6.52	126.22	119.05	7	14
1	A	10	TYR	CA-CB-CG	6.49	125.59	113.90	5	4
1	A	42	GLU	CA-CB-CG	6.44	126.98	114.10	4	2
1	A	8	SER	N-CA-CB	-6.36	102.59	110.98	3	5
1	A	55	TYR	CA-CB-CG	6.28	125.20	113.90	2	1
1	A	83	PHE	CA-C-O	6.24	128.56	122.01	2	3
1	A	72	LYS	CA-CB-CG	-6.23	101.64	114.10	2	18
1	A	45	GLU	N-CA-CB	-6.18	102.90	112.30	15	1
1	A	26	ASP	N-CA-CB	-6.17	100.05	110.49	20	14
1	A	35	LYS	CA-C-N	6.12	131.09	120.68	2	1
1	A	35	LYS	C-N-CA	6.12	131.09	120.68	2	1
1	A	80	LYS	CB-CG-CD	6.09	125.30	111.30	15	9
1	A	71	VAL	CA-CB-CG2	-6.01	100.19	110.40	20	10
1	A	60	ASP	CA-C-N	5.98	132.95	121.54	19	1
1	A	60	ASP	C-N-CA	5.98	132.95	121.54	19	1
1	A	11	THR	CA-CB-OG1	5.96	118.54	109.60	20	2
1	A	37	VAL	CA-CB-CG1	5.95	120.52	110.40	8	2
1	A	75	ARG	NE-CZ-NH2	5.90	124.51	119.20	15	2
1	A	29	SER	N-CA-CB	5.89	120.45	110.49	7	5
1	A	81	SER	CB-CA-C	5.89	122.14	110.42	14	3
1	A	35	LYS	N-CA-CB	-5.89	101.87	110.47	9	5
1	A	46	HIS	CA-C-N	5.89	127.20	119.84	9	9
1	A	46	HIS	C-N-CA	5.89	127.20	119.84	9	9
1	A	32	GLU	N-CA-C	-5.80	104.31	111.33	11	3
1	A	3	LEU	N-CA-C	-5.80	98.44	110.80	6	2
1	A	61	ASP	CA-CB-CG	5.77	118.37	112.60	10	4
1	A	56	PRO	CA-N-CD	-5.75	103.95	112.00	8	2
1	A	6	SER	CA-CB-OG	5.71	122.51	111.10	20	2
1	A	68	VAL	N-CA-C	-5.70	104.96	110.72	18	2
1	A	27	THR	N-CA-C	5.68	118.65	109.79	3	1
1	A	11	THR	CA-CB-CG2	5.66	120.12	110.50	12	3

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	36	LEU	N-CA-CB	-5.65	101.80	110.16	20	2
1	A	67	ILE	N-CA-C	5.62	115.81	110.53	11	2
1	A	68	VAL	CG1-CB-CG2	-5.60	98.48	110.80	9	1
1	A	15	PHE	CA-CB-CG	5.59	119.39	113.80	5	1
1	A	84	LYS	N-CA-CB	-5.54	102.73	110.38	7	2
1	A	48	SER	CA-C-N	5.52	132.23	121.41	6	4
1	A	48	SER	C-N-CA	5.52	132.23	121.41	6	4
1	A	19	VAL	N-CA-C	-5.52	105.12	110.42	5	4
1	A	3	LEU	CD1-CG-CD2	5.50	122.90	110.80	16	1
1	A	4	LYS	CA-C-N	5.47	130.45	122.08	10	3
1	A	4	LYS	C-N-CA	5.47	130.45	122.08	10	3
1	A	20	THR	CA-C-N	5.46	128.61	120.31	6	4
1	A	20	THR	C-N-CA	5.46	128.61	120.31	6	4
1	A	5	HIS	CA-C-N	5.45	131.49	121.85	14	2
1	A	5	HIS	C-N-CA	5.45	131.49	121.85	14	2
1	A	14	GLU	CA-CB-CG	-5.43	103.23	114.10	14	1
1	A	3	LEU	CA-C-N	5.42	131.89	121.54	5	2
1	A	3	LEU	C-N-CA	5.42	131.89	121.54	5	2
1	A	80	LYS	N-CA-CB	5.41	118.59	109.78	13	2
1	A	48	SER	CB-CA-C	5.38	119.78	111.28	6	1
1	A	10	TYR	CB-CA-C	5.37	119.90	109.33	2	3
1	A	8	SER	CA-CB-OG	5.36	121.83	111.10	2	1
1	A	6	SER	CA-C-N	5.36	131.63	121.97	19	1
1	A	6	SER	C-N-CA	5.36	131.63	121.97	19	1
1	A	32	GLU	CB-CG-CD	5.35	121.70	112.60	9	3
1	A	79	GLY	CA-C-N	5.35	128.85	120.82	6	1
1	A	79	GLY	C-N-CA	5.35	128.85	120.82	6	1
1	A	4	LYS	CB-CA-C	5.35	121.06	110.42	20	1
1	A	57	LYS	N-CA-CB	-5.32	101.49	110.49	18	1
1	A	70	THR	N-CA-C	-5.32	105.56	111.36	3	5
1	A	5	HIS	CA-C-O	5.31	124.60	118.55	10	1
1	A	8	SER	CB-CA-C	5.30	116.00	109.16	9	1
1	A	45	GLU	CA-CB-CG	5.28	124.67	114.10	15	2
1	A	53	ILE	N-CA-C	-5.28	108.36	113.53	13	1
1	A	40	PHE	CA-C-N	5.27	127.61	120.38	11	1
1	A	40	PHE	C-N-CA	5.27	127.61	120.38	11	1
1	A	85	GLN	O-C-N	5.27	127.71	122.12	20	1
1	A	52	LEU	N-CA-CB	5.26	118.14	110.25	8	1
1	A	14	GLU	N-CA-CB	-5.21	102.45	110.16	9	1
1	A	35	LYS	CG-CD-CE	5.20	123.25	111.30	3	1
1	A	27	THR	N-CA-CB	-5.19	102.98	110.45	3	1

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	58	GLU	O-C-N	5.14	128.09	122.64	4	1
1	A	56	PRO	CA-C-N	5.14	131.36	121.54	5	1
1	A	56	PRO	C-N-CA	5.14	131.36	121.54	5	1
1	A	75	ARG	CD-NE-CZ	5.12	131.57	124.40	12	1
1	A	36	LEU	N-CA-C	-5.09	105.81	112.23	6	1
1	A	9	ASP	N-CA-CB	5.08	118.66	110.42	8	1
1	A	4	LYS	CG-CD-CE	5.08	122.97	111.30	17	1
1	A	55	TYR	CB-CA-C	-5.06	104.80	113.04	15	1
1	A	17	GLN	N-CA-CB	5.05	118.11	110.28	20	1
1	A	72	LYS	CA-C-N	5.04	131.54	122.46	20	1
1	A	72	LYS	C-N-CA	5.04	131.54	122.46	20	1
1	A	62	ASP	N-CA-C	-5.04	100.07	110.80	16	1
1	A	30	GLU	CA-C-O	5.02	124.05	118.52	1	1
1	A	84	LYS	CA-C-N	5.01	131.12	121.54	1	1
1	A	84	LYS	C-N-CA	5.01	131.12	121.54	1	1

There are no chirality outliers.

All unique planar outliers are listed below. They are sorted by the frequency of occurrence in the ensemble.

Mol	Chain	Res	Type	Group	Models (Total)
1	A	10	TYR	Sidechain	13
1	A	15	PHE	Sidechain	10
1	A	55	TYR	Sidechain	8
1	A	5	HIS	Sidechain	8
1	A	54	TYR	Sidechain	4
1	A	83	PHE	Sidechain	3
1	A	75	ARG	Sidechain	2

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	656	617	618	24±4
All	All	13120	12348	12360	474

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 19.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:3:LEU:HD22	1:A:39:HIS:CD2	0.87	2.05	18	9
1:A:3:LEU:HD21	1:A:36:LEU:CD2	0.83	2.04	9	6
1:A:48:SER:C	1:A:52:LEU:HD23	0.80	2.02	6	1
1:A:19:VAL:HG21	1:A:68:VAL:HG22	0.78	1.53	13	18
1:A:62:ASP:HA	1:A:67:ILE:HG23	0.78	1.56	10	20
1:A:18:LEU:HD21	1:A:36:LEU:HD22	0.76	1.56	14	7
1:A:74:TRP:CZ3	1:A:80:LYS:HE2	0.70	2.21	19	3
1:A:75:ARG:HA	1:A:80:LYS:HG3	0.69	1.65	7	8
1:A:46:HIS:CE1	1:A:52:LEU:HD22	0.64	2.27	6	1
1:A:30:GLU:HA	1:A:33:LEU:HD12	0.64	1.70	20	5
1:A:27:THR:HB	1:A:32:GLU:HB2	0.63	1.70	13	12
1:A:40:PHE:CG	1:A:53:ILE:HD11	0.63	2.28	19	1
1:A:39:HIS:CE1	1:A:43:MET:HE3	0.62	2.29	5	5
1:A:62:ASP:CA	1:A:67:ILE:HG23	0.62	2.25	6	19
1:A:7:ILE:HA	1:A:10:TYR:CE1	0.61	2.30	2	13
1:A:3:LEU:HD21	1:A:36:LEU:HD22	0.60	1.73	9	5
1:A:75:ARG:HA	1:A:80:LYS:CG	0.59	2.27	3	16
1:A:66:GLY:HA2	1:A:69:ASN:HB2	0.59	1.74	15	12
1:A:3:LEU:HD22	1:A:39:HIS:CG	0.59	2.32	20	1
1:A:21:THR:CG2	1:A:36:LEU:HD13	0.58	2.28	3	7
1:A:46:HIS:ND1	1:A:52:LEU:HD22	0.58	2.13	6	1
1:A:40:PHE:CE1	1:A:44:THR:HG21	0.57	2.34	20	5
1:A:4:LYS:CG	1:A:9:ASP:HB3	0.57	2.30	10	4
1:A:15:PHE:CZ	1:A:40:PHE:CD2	0.56	2.93	14	14
1:A:15:PHE:CE1	1:A:40:PHE:CD2	0.56	2.93	8	3
1:A:68:VAL:HG12	1:A:72:LYS:NZ	0.56	2.16	17	3
1:A:46:HIS:CE1	1:A:52:LEU:HD21	0.56	2.34	15	1
1:A:84:LYS:HA	1:A:84:LYS:HE3	0.56	1.77	20	1
1:A:44:THR:HG23	1:A:46:HIS:HB3	0.56	1.78	19	1
1:A:3:LEU:HD21	1:A:36:LEU:HD23	0.55	1.78	17	2
1:A:27:THR:HB	1:A:32:GLU:CB	0.54	2.33	12	15
1:A:42:GLU:OE2	1:A:43:MET:HE2	0.54	2.02	19	1
1:A:33:LEU:O	1:A:37:VAL:HG13	0.53	2.02	4	2
1:A:45:GLU:CD	1:A:80:LYS:HZ1	0.53	2.11	17	1
1:A:15:PHE:CZ	1:A:40:PHE:CE2	0.53	2.97	3	3
1:A:12:GLU:CD	1:A:72:LYS:HE3	0.53	2.29	2	3
1:A:4:LYS:CG	1:A:9:ASP:HB2	0.53	2.34	7	1
1:A:69:ASN:HA	1:A:72:LYS:HB2	0.53	1.81	18	16

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:4:LYS:HG2	1:A:9:ASP:HB2	0.52	1.81	7	1
1:A:62:ASP:CG	1:A:63:SER:H	0.52	2.12	18	1
1:A:3:LEU:CD2	1:A:39:HIS:CD2	0.52	2.92	16	3
1:A:62:ASP:HA	1:A:67:ILE:CG2	0.52	2.30	19	1
1:A:12:GLU:HG3	1:A:83:PHE:CD2	0.51	2.40	1	1
1:A:12:GLU:HG3	1:A:83:PHE:CE2	0.51	2.41	17	3
1:A:68:VAL:HG12	1:A:72:LYS:HZ3	0.51	1.66	17	2
1:A:25:ALA:HA	1:A:33:LEU:HD21	0.51	1.80	8	7
1:A:12:GLU:CD	1:A:72:LYS:HE2	0.51	2.31	8	1
1:A:74:TRP:CE3	1:A:80:LYS:HE2	0.51	2.40	19	1
1:A:54:TYR:CD1	1:A:54:TYR:N	0.51	2.78	7	5
1:A:18:LEU:HD21	1:A:36:LEU:CD2	0.50	2.36	18	2
1:A:7:ILE:HD11	1:A:83:PHE:CZ	0.50	2.42	20	2
1:A:18:LEU:HD12	1:A:39:HIS:CE1	0.50	2.41	3	1
1:A:12:GLU:HA	1:A:83:PHE:CZ	0.50	2.42	5	2
1:A:74:TRP:CZ3	1:A:80:LYS:HD3	0.50	2.42	10	8
1:A:7:ILE:HD11	1:A:75:ARG:CZ	0.49	2.37	5	1
1:A:54:TYR:C	1:A:56:PRO:HD2	0.49	2.33	11	7
1:A:55:TYR:N	1:A:56:PRO:HD3	0.49	2.23	8	2
1:A:66:GLY:CA	1:A:69:ASN:HB2	0.49	2.38	13	10
1:A:40:PHE:O	1:A:44:THR:HG22	0.49	2.07	2	4
1:A:16:LEU:HD11	1:A:65:SER:HA	0.48	1.84	5	4
1:A:48:SER:O	1:A:52:LEU:HD23	0.48	2.08	6	1
1:A:12:GLU:HG3	1:A:83:PHE:CE1	0.48	2.43	18	3
1:A:75:ARG:HA	1:A:80:LYS:HG2	0.47	1.86	20	8
1:A:4:LYS:HG3	1:A:9:ASP:HB3	0.47	1.85	10	1
1:A:40:PHE:CZ	1:A:71:VAL:HG21	0.47	2.44	5	1
1:A:12:GLU:CG	1:A:72:LYS:HE2	0.47	2.40	10	2
1:A:75:ARG:HG2	1:A:80:LYS:HG3	0.47	1.86	5	3
1:A:40:PHE:CE2	1:A:53:ILE:HD11	0.47	2.45	11	1
1:A:7:ILE:HA	1:A:10:TYR:CE2	0.46	2.45	1	2
1:A:6:SER:HB2	1:A:9:ASP:H	0.46	1.70	7	2
1:A:12:GLU:CD	1:A:72:LYS:HZ3	0.46	2.17	15	1
1:A:25:ALA:CB	1:A:33:LEU:HD11	0.46	2.41	20	6
1:A:7:ILE:HD13	1:A:83:PHE:CE2	0.46	2.44	15	1
1:A:84:LYS:HA	1:A:84:LYS:CE	0.46	2.41	20	1
1:A:25:ALA:C	1:A:27:THR:H	0.46	2.18	3	2
1:A:71:VAL:HG13	1:A:75:ARG:CD	0.46	2.41	18	1
1:A:46:HIS:CD2	1:A:47:PRO:HD2	0.45	2.47	7	8
1:A:18:LEU:C	1:A:18:LEU:HD13	0.45	2.37	3	3
1:A:27:THR:HG21	1:A:33:LEU:HG	0.45	1.89	13	4

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:19:VAL:HG21	1:A:68:VAL:CG2	0.45	2.37	4	4
1:A:25:ALA:HA	1:A:33:LEU:HD11	0.45	1.89	19	3
1:A:55:TYR:N	1:A:56:PRO:CD	0.45	2.79	13	8
1:A:56:PRO:O	1:A:57:LYS:CB	0.45	2.65	13	3
1:A:5:HIS:C	1:A:43:MET:HE1	0.45	2.37	19	1
1:A:45:GLU:CD	1:A:80:LYS:HZ2	0.45	2.20	7	1
1:A:19:VAL:HG11	1:A:67:ILE:HG13	0.45	1.89	11	1
1:A:3:LEU:HD13	1:A:39:HIS:NE2	0.45	2.26	16	1
1:A:6:SER:HB2	1:A:8:SER:H	0.44	1.72	1	1
1:A:55:TYR:N	1:A:56:PRO:HD2	0.44	2.27	17	3
1:A:15:PHE:CE1	1:A:40:PHE:CE2	0.44	3.05	3	1
1:A:6:SER:C	1:A:8:SER:H	0.44	2.19	14	6
1:A:40:PHE:CD1	1:A:53:ILE:HD11	0.44	2.47	19	1
1:A:74:TRP:HZ3	1:A:80:LYS:HE2	0.44	1.72	4	10
1:A:16:LEU:CD1	1:A:68:VAL:HG21	0.44	2.43	1	3
1:A:74:TRP:CZ3	1:A:80:LYS:CE	0.44	2.99	19	3
1:A:52:LEU:C	1:A:53:ILE:HG12	0.43	2.38	17	2
1:A:75:ARG:NH2	1:A:83:PHE:CZ	0.43	2.84	5	1
1:A:9:ASP:O	1:A:84:LYS:HE2	0.43	2.14	13	3
1:A:10:TYR:C	1:A:84:LYS:HB3	0.43	2.38	20	1
1:A:12:GLU:HG3	1:A:83:PHE:CD1	0.43	2.49	20	2
1:A:71:VAL:C	1:A:73:GLN:H	0.43	2.22	3	4
1:A:52:LEU:CD2	1:A:71:VAL:HG23	0.43	2.44	5	1
1:A:25:ALA:CA	1:A:33:LEU:HD11	0.43	2.44	19	2
1:A:54:TYR:C	1:A:56:PRO:CD	0.42	2.92	8	1
1:A:12:GLU:HG2	1:A:72:LYS:HE2	0.42	1.91	1	1
1:A:71:VAL:CG1	1:A:75:ARG:HE	0.42	2.27	5	1
1:A:41:GLU:CD	1:A:49:GLY:HA2	0.42	2.39	18	2
1:A:75:ARG:HG2	1:A:80:LYS:HE3	0.42	1.91	19	1
1:A:46:HIS:CE1	1:A:48:SER:H	0.42	2.33	13	4
1:A:16:LEU:CD1	1:A:65:SER:HA	0.42	2.45	7	1
1:A:46:HIS:CE1	1:A:52:LEU:CD2	0.42	3.02	13	2
1:A:53:ILE:HG22	1:A:54:TYR:CE2	0.42	2.50	1	1
1:A:48:SER:O	1:A:52:LEU:N	0.42	2.53	20	2
1:A:21:THR:CG2	1:A:36:LEU:CD1	0.42	2.97	9	3
1:A:44:THR:HA	1:A:75:ARG:CZ	0.41	2.45	12	1
1:A:4:LYS:HE2	1:A:9:ASP:O	0.41	2.15	15	1
1:A:3:LEU:HD11	1:A:36:LEU:CD2	0.41	2.45	16	1
1:A:22:ILE:HG23	1:A:33:LEU:HD23	0.41	1.92	3	1
1:A:34:VAL:O	1:A:37:VAL:HG22	0.41	2.16	8	1
1:A:32:GLU:CD	1:A:35:LYS:CE	0.41	2.94	6	1

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Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:SER:C	1:A:43:MET:HE1	0.41	2.41	5	1
1:A:32:GLU:HA	1:A:35:LYS:HB3	0.41	1.91	14	2
1:A:72:LYS:C	1:A:73:GLN:HG2	0.41	2.39	14	2
1:A:39:HIS:CE1	1:A:43:MET:SD	0.41	3.14	1	1
1:A:45:GLU:HB2	1:A:80:LYS:NZ	0.41	2.31	6	1
1:A:53:ILE:HB	1:A:54:TYR:CZ	0.41	2.50	10	2
1:A:21:THR:HG22	1:A:36:LEU:HD12	0.41	1.92	11	1
1:A:32:GLU:CD	1:A:35:LYS:HZ2	0.41	2.23	20	1
1:A:47:PRO:HG2	1:A:74:TRP:CD1	0.40	2.51	5	1
1:A:54:TYR:C	1:A:56:PRO:HD3	0.40	2.41	8	1
1:A:7:ILE:HD11	1:A:75:ARG:NH1	0.40	2.31	9	1
1:A:39:HIS:CD2	1:A:43:MET:SD	0.40	3.15	9	1
1:A:71:VAL:HG13	1:A:75:ARG:HG3	0.40	1.93	3	1
1:A:3:LEU:HD13	1:A:39:HIS:CD2	0.40	2.51	16	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	83/86 (97%)	57±2 (69±3%)	19±2 (22±3%)	7±2 (9±3%)	1	12
All	All	1660/1720 (97%)	1145 (69%)	372 (22%)	143 (9%)	1	12

All 23 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	29	SER	20
1	A	57	LYS	19
1	A	49	GLY	15
1	A	26	ASP	14
1	A	4	LYS	9
1	A	63	SER	9
1	A	56	PRO	8
1	A	3	LEU	7

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Mol	Chain	Res	Type	Models (Total)
1	A	55	TYR	6
1	A	54	TYR	6
1	A	7	ILE	5
1	A	47	PRO	5
1	A	59	GLY	3
1	A	61	ASP	3
1	A	82	GLY	3
1	A	50	SER	3
1	A	83	PHE	2
1	A	28	SER	1
1	A	80	LYS	1
1	A	72	LYS	1
1	A	30	GLU	1
1	A	62	ASP	1
1	A	58	GLU	1

6.3.2 Protein sidechains ⓘ

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all PDB entries followed by that with respect to all NMR entries. The Analysed column shows the number of residues for which the sidechain conformation was analysed and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	74/76 (97%)	52±3 (70±5%)	22±3 (30±5%)	1	17
All	All	1480/1520 (97%)	1037 (70%)	443 (30%)	1	17

All 56 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	72	LYS	20
1	A	11	THR	19
1	A	20	THR	19
1	A	22	ILE	19
1	A	52	LEU	19
1	A	6	SER	17
1	A	21	THR	17
1	A	10	TYR	17
1	A	33	LEU	15
1	A	5	HIS	15

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Mol	Chain	Res	Type	Models (Total)
1	A	57	LYS	14
1	A	8	SER	14
1	A	71	VAL	13
1	A	67	ILE	12
1	A	85	GLN	12
1	A	58	GLU	12
1	A	37	VAL	11
1	A	38	THR	11
1	A	7	ILE	10
1	A	78	ASN	10
1	A	43	MET	9
1	A	48	SER	9
1	A	54	TYR	9
1	A	42	GLU	9
1	A	68	VAL	8
1	A	4	LYS	8
1	A	35	LYS	7
1	A	9	ASP	7
1	A	81	SER	7
1	A	18	LEU	6
1	A	55	TYR	5
1	A	14	GLU	5
1	A	32	GLU	5
1	A	44	THR	5
1	A	36	LEU	5
1	A	51	ASP	4
1	A	3	LEU	4
1	A	75	ARG	4
1	A	60	ASP	3
1	A	16	LEU	3
1	A	41	GLU	3
1	A	62	ASP	2
1	A	39	HIS	2
1	A	24	ASN	2
1	A	69	ASN	2
1	A	63	SER	2
1	A	45	GLU	2
1	A	27	THR	2
1	A	65	SER	1
1	A	50	SER	1
1	A	31	GLU	1
1	A	17	GLN	1

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Mol	Chain	Res	Type	Models (Total)
1	A	19	VAL	1
1	A	47	PRO	1
1	A	15	PHE	1
1	A	84	LYS	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