



Full wwPDB NMR Structure Validation Report ⓘ

Feb 12, 2017 – 08:40 pm GMT

PDB ID : 1XEE
Title : Solution structure of the Chemotaxis Inhibitory Protein of *Staphylococcus aureus*
Authors : Haas, P.J.; de Haas, C.J.; Poppelier, M.J.; van Kessel, K.P.; van Strijp, J.A.; Dijkstra, K.; Scheek, R.M.; Fan, H.; Kruijtzter, J.A.; Liskamp, R.M.; Kemmink, J.
Deposited on : 2004-09-10

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
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
RCI	:	v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV	:	Wang et al. (2010)
ShiftChecker	:	trunk28760
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	recalc28949

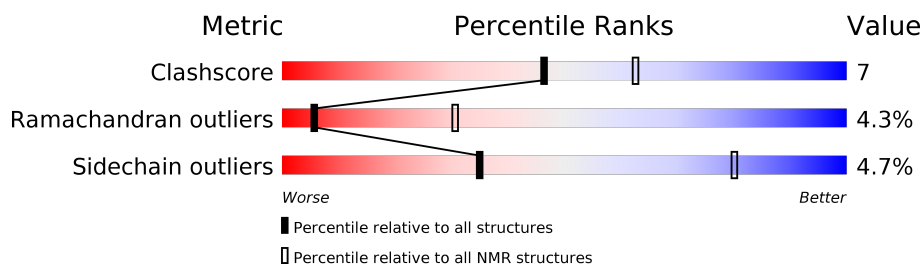
1 Overall quality at a glance

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	125131	11601
Ramachandran outliers	121729	10391
Sidechain outliers	121581	10367

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	91	

2 Ensemble composition and analysis

This entry contains 20 models. Model 17 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:36-A:118 (83)	0.47	17

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 4 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1489 atoms, of which 751 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called chemotaxis-inhibiting protein CHIPS.

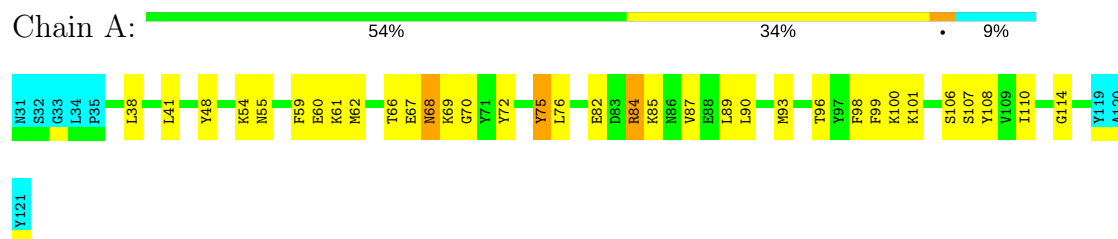
Mol	Chain	Residues	Atoms						Trace
1	A	91	Total	C	H	N	O	S	0
			1489	473	751	122	141	2	

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: chemotaxis-inhibiting protein CHIPS

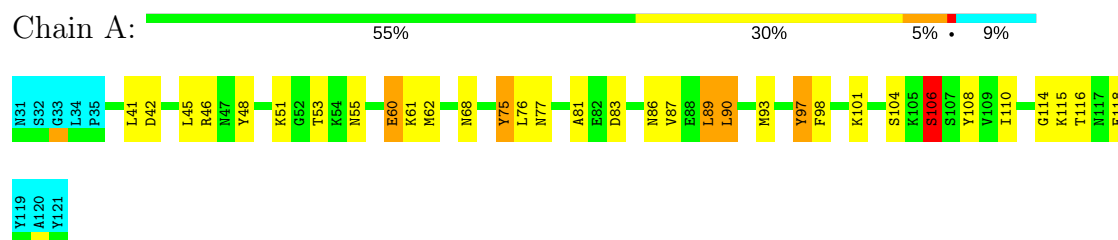


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

4.2.1 Score per residue for model 1

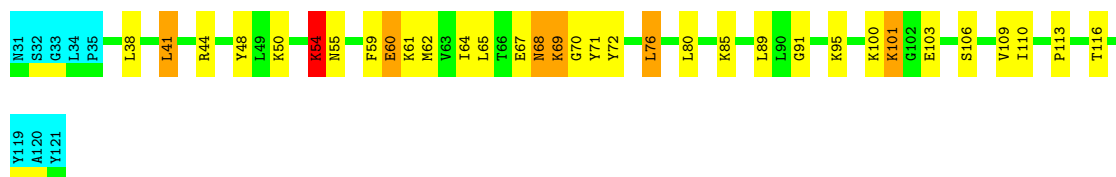
- Molecule 1: chemotaxis-inhibiting protein CHIPS



4.2.2 Score per residue for model 2

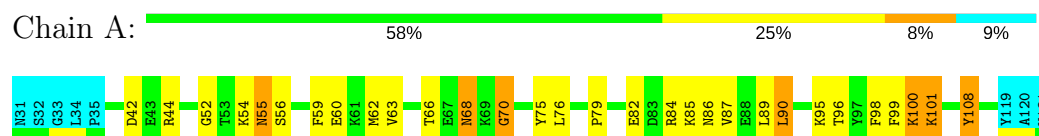
- Molecule 1: chemotaxis-inhibiting protein CHIPS





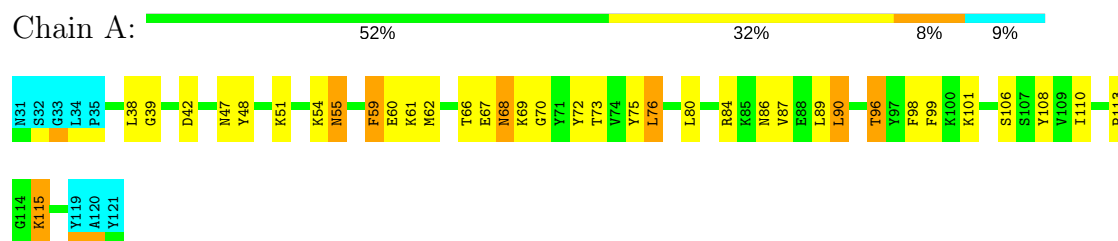
4.2.3 Score per residue for model 3

- Molecule 1: chemotaxis-inhibiting protein CHIPS



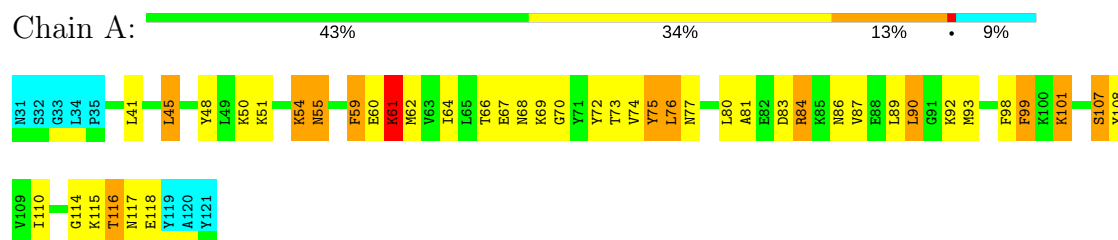
4.2.4 Score per residue for model 4

- Molecule 1: chemotaxis-inhibiting protein CHIPS



4.2.5 Score per residue for model 5

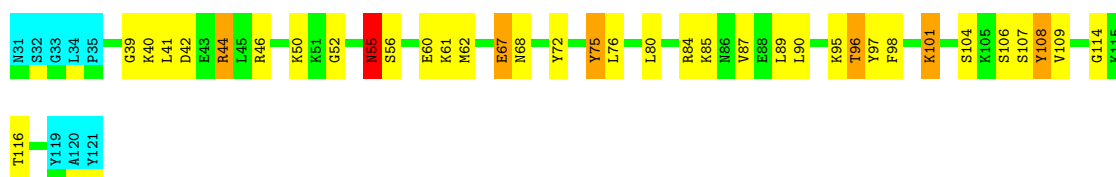
- Molecule 1: chemotaxis-inhibiting protein CHIPS



4.2.6 Score per residue for model 6

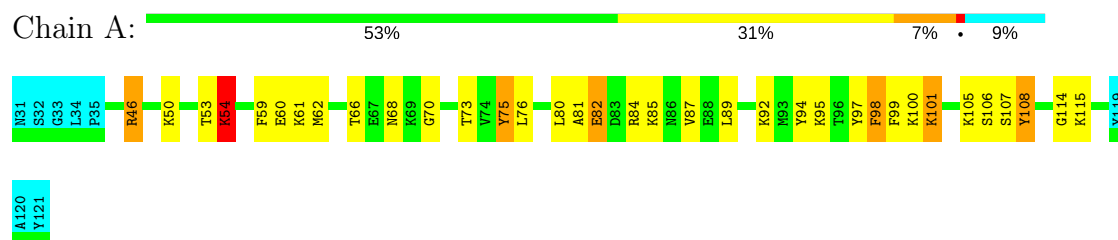
- Molecule 1: chemotaxis-inhibiting protein CHIPS





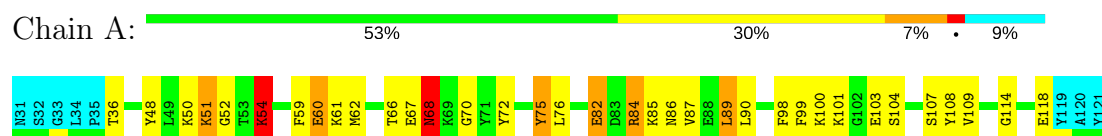
4.2.7 Score per residue for model 7

- Molecule 1: chemotaxis-inhibiting protein CHIPS



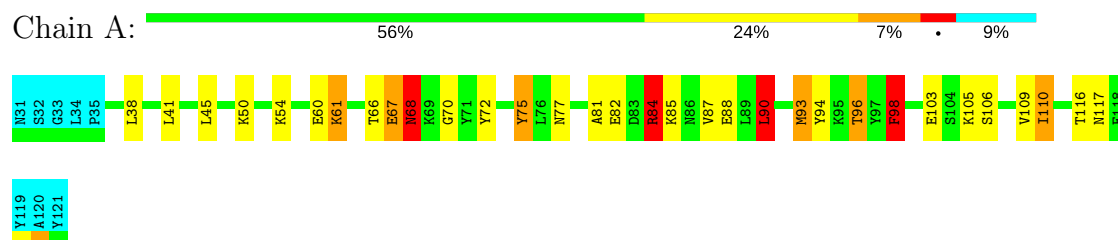
4.2.8 Score per residue for model 8

- Molecule 1: chemotaxis-inhibiting protein CHIPS



4.2.9 Score per residue for model 9

- Molecule 1: chemotaxis-inhibiting protein CHIPS



4.2.10 Score per residue for model 10

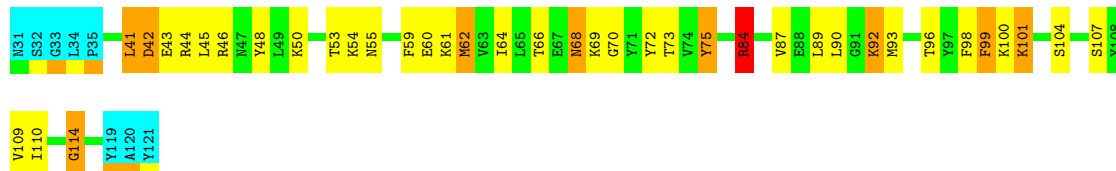
- Molecule 1: chemotaxis-inhibiting protein CHIPS





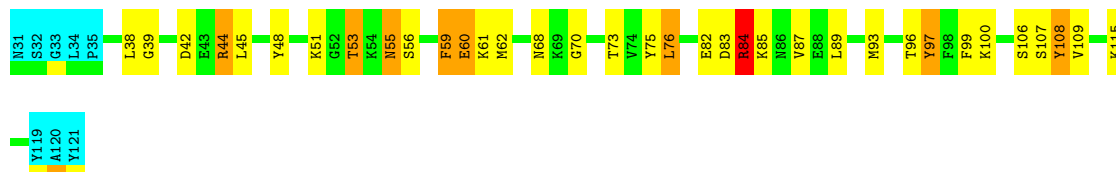
4.2.11 Score per residue for model 11

- Molecule 1: chemotaxis-inhibiting protein CHIPS



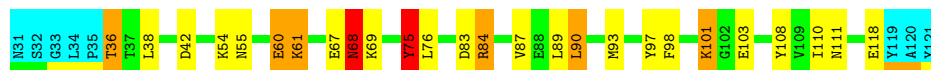
4.2.12 Score per residue for model 12

- Molecule 1: chemotaxis-inhibiting protein CHIPS



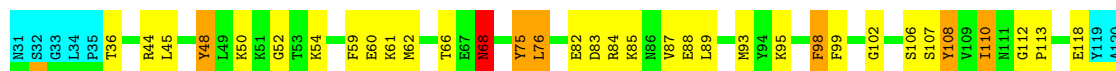
4.2.13 Score per residue for model 13

- Molecule 1: chemotaxis-inhibiting protein CHIPS



4.2.14 Score per residue for model 14

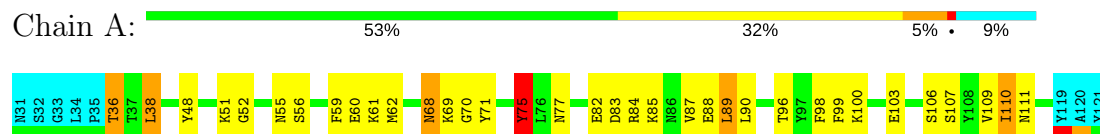
- Molecule 1: chemotaxis-inhibiting protein CHIPS



Y121

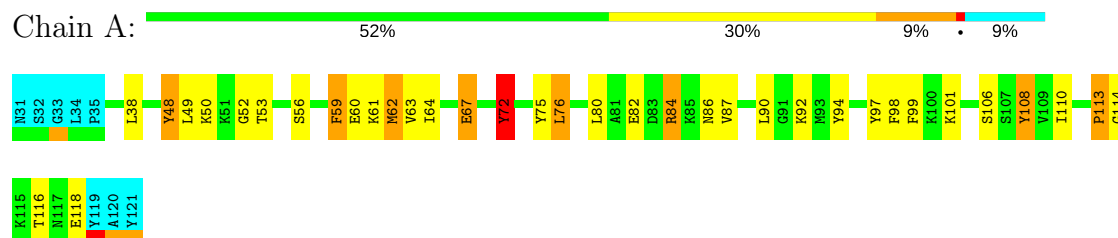
4.2.15 Score per residue for model 15

- Molecule 1: chemotaxis-inhibiting protein CHIPS



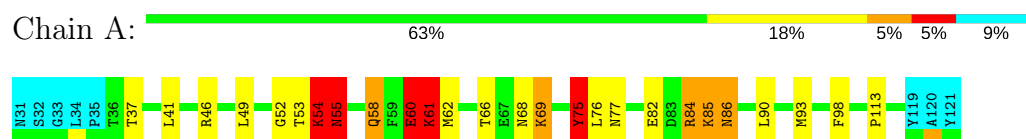
4.2.16 Score per residue for model 16

- Molecule 1: chemotaxis-inhibiting protein CHIPS



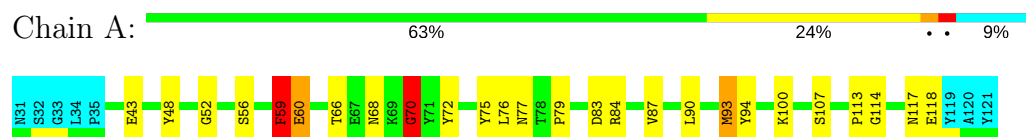
4.2.17 Score per residue for model 17 (medoid)

- Molecule 1: chemotaxis-inhibiting protein CHIPS



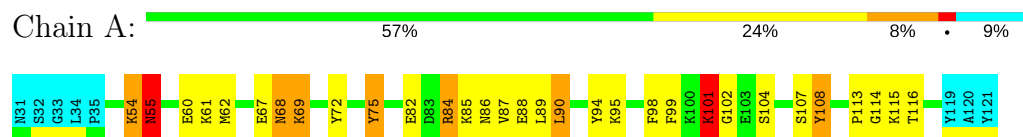
4.2.18 Score per residue for model 18

- Molecule 1: chemotaxis-inhibiting protein CHIPS



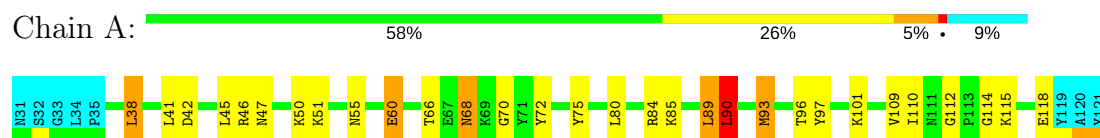
4.2.19 Score per residue for model 19

- Molecule 1: chemotaxis-inhibiting protein CHIPS



4.2.20 Score per residue for model 20

- Molecule 1: chemotaxis-inhibiting protein CHIPS



5 Refinement protocol and experimental data overview

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

Of the 200 calculated structures, 20 were deposited, based on the following criterion: *structures with the lowest energy*.

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

Software name	Classification	Version
CNS	refinement	1.1
ARIA	refinement	1.2

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

6 Model quality i

6.1 Standard geometry i

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

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	#Z>5	RMSZ	#Z>5
1	A	0.54±0.08	0±0/687 (0.0±0.0%)	1.47±0.11	10±3/920 (1.1±0.3%)
All	All	0.55	0/13740 (0.0%)	1.48	196/18400 (1.1%)

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	10.6±2.7
All	All	0	211

There are no bond-length outliers.

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	84	ARG	NE-CZ-NH1	15.71	128.15	120.30	16	2
1	A	84	ARG	NE-CZ-NH2	-12.78	113.91	120.30	16	3
1	A	72	TYR	CB-CG-CD2	-11.33	114.20	121.00	11	9
1	A	84	ARG	CD-NE-CZ	10.60	138.44	123.60	16	1
1	A	97	TYR	CB-CG-CD1	-10.41	114.75	121.00	7	5
1	A	42	ASP	CB-CG-OD2	-10.30	109.03	118.30	12	5
1	A	108	TYR	CB-CG-CD2	-9.99	115.00	121.00	3	4
1	A	101	LYS	CA-C-N	-9.91	96.38	116.20	6	8
1	A	99	PHE	CB-CG-CD1	-9.47	114.17	120.80	12	1
1	A	38	LEU	CB-CG-CD2	9.29	126.78	111.00	15	1
1	A	48	TYR	CB-CG-CD2	-9.10	115.54	121.00	1	4
1	A	72	TYR	CB-CG-CD1	8.98	126.39	121.00	11	4
1	A	48	TYR	CD1-CE1-CZ	8.82	127.74	119.80	14	1
1	A	75	TYR	CB-CG-CD2	-8.60	115.84	121.00	19	6
1	A	62	MET	N-CA-CB	8.31	125.55	110.60	12	16

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	93	MET	CG-SD-CE	-8.23	87.03	100.20	20	3
1	A	108	TYR	CD1-CE1-CZ	8.04	127.03	119.80	14	1
1	A	61	LYS	N-CA-CB	-8.03	96.15	110.60	5	1
1	A	55	ASN	N-CA-CB	-8.02	96.17	110.60	11	5
1	A	54	LYS	CA-C-N	-7.98	99.65	117.20	5	8
1	A	42	ASP	CB-CG-OD1	7.90	125.41	118.30	6	5
1	A	44	ARG	NE-CZ-NH2	-7.75	116.42	120.30	14	2
1	A	61	LYS	CA-C-N	-7.68	100.31	117.20	5	17
1	A	71	TYR	CB-CG-CD2	-7.51	116.49	121.00	2	1
1	A	59	PHE	CB-CG-CD2	-7.49	115.56	120.80	18	3
1	A	75	TYR	CA-C-N	-7.40	100.93	117.20	19	5
1	A	99	PHE	CB-CG-CD2	-7.33	115.67	120.80	5	7
1	A	75	TYR	CB-CG-CD1	-7.18	116.69	121.00	17	5
1	A	53	THR	CA-C-N	-7.16	101.44	117.20	12	1
1	A	98	PHE	CB-CG-CD2	-7.14	115.80	120.80	14	3
1	A	38	LEU	CB-CG-CD1	6.93	122.77	111.00	10	2
1	A	118	GLU	N-CA-CB	-6.76	98.43	110.60	5	4
1	A	55	ASN	N-CA-C	-6.75	92.77	111.00	4	3
1	A	61	LYS	CA-CB-CG	6.65	128.03	113.40	17	1
1	A	97	TYR	CB-CG-CD2	-6.41	117.15	121.00	10	3
1	A	98	PHE	CB-CG-CD1	-6.34	116.36	120.80	9	1
1	A	70	GLY	CA-C-N	-6.32	103.30	117.20	18	2
1	A	56	SER	N-CA-CB	6.26	119.89	110.50	18	1
1	A	112	GLY	N-CA-C	-6.18	97.65	113.10	14	1
1	A	90	LEU	CB-CG-CD1	-6.16	100.54	111.00	10	1
1	A	55	ASN	O-C-N	-6.14	112.87	122.70	17	4
1	A	46	ARG	NE-CZ-NH1	6.14	123.37	120.30	17	2
1	A	48	TYR	CG-CD1-CE1	-6.10	116.42	121.30	14	1
1	A	108	TYR	CB-CG-CD1	5.89	124.53	121.00	3	2
1	A	56	SER	N-CA-C	-5.87	95.16	111.00	3	1
1	A	84	ARG	N-CA-CB	-5.79	100.18	110.60	11	5
1	A	76	LEU	N-CA-CB	-5.78	98.85	110.40	5	5
1	A	108	TYR	CG-CD1-CE1	-5.76	116.69	121.30	14	1
1	A	51	LYS	CA-C-N	5.61	127.41	116.20	12	2
1	A	90	LEU	N-CA-CB	5.59	121.59	110.40	13	1
1	A	90	LEU	CB-CG-CD2	5.51	120.38	111.00	9	1
1	A	110	ILE	CB-CG1-CD1	5.47	129.22	113.90	1	1
1	A	71	TYR	CB-CG-CD1	-5.47	117.72	121.00	10	2
1	A	83	ASP	CB-CG-OD2	-5.43	113.42	118.30	13	1
1	A	72	TYR	N-CA-CB	-5.34	100.98	110.60	8	1
1	A	97	TYR	CG-CD2-CE2	-5.28	117.08	121.30	1	1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	110	ILE	CA-C-N	-5.27	105.60	117.20	9	1
1	A	60	GLU	CG-CD-OE1	5.25	128.81	118.30	1	1
1	A	108	TYR	N-CA-CB	5.21	119.98	110.60	12	2
1	A	44	ARG	N-CA-CB	-5.20	101.24	110.60	11	1
1	A	63	VAL	CG1-CB-CG2	-5.19	102.59	110.90	3	1
1	A	55	ASN	CA-C-N	5.16	128.54	117.20	12	1
1	A	59	PHE	CA-C-N	-5.08	106.02	117.20	4	1
1	A	99	PHE	CA-C-N	-5.05	106.09	117.20	16	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	75	TYR	Mainchain,Sidechain	16
1	A	89	LEU	Mainchain	14
1	A	107	SER	Mainchain	10
1	A	54	LYS	Mainchain	8
1	A	84	ARG	Sidechain	8
1	A	55	ASN	Mainchain	8
1	A	86	ASN	Mainchain	7
1	A	68	ASN	Mainchain	7
1	A	53	THR	Mainchain	6
1	A	114	GLY	Mainchain	6
1	A	115	LYS	Mainchain	6
1	A	59	PHE	Mainchain	6
1	A	113	PRO	Mainchain	6
1	A	52	GLY	Mainchain	5
1	A	70	GLY	Mainchain	5
1	A	108	TYR	Mainchain,Sidechain	5
1	A	101	LYS	Mainchain	5
1	A	73	THR	Mainchain	5
1	A	104	SER	Mainchain	5
1	A	110	ILE	Mainchain	4
1	A	90	LEU	Mainchain	4
1	A	60	GLU	Sidechain,Mainchain	4
1	A	99	PHE	Mainchain	3
1	A	81	ALA	Mainchain	3
1	A	82	GLU	Mainchain	3
1	A	94	TYR	Sidechain	3
1	A	106	SER	Mainchain	3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Group	Models (Total)
1	A	48	TYR	Sidechain	3
1	A	83	ASP	Mainchain	2
1	A	79	PRO	Mainchain	2
1	A	67	GLU	Mainchain	2
1	A	50	LYS	Mainchain	2
1	A	43	GLU	Mainchain	2
1	A	85	LYS	Mainchain	2
1	A	100	LYS	Mainchain	2
1	A	92	LYS	Mainchain	2
1	A	61	LYS	Mainchain	2
1	A	69	LYS	Mainchain	2
1	A	111	ASN	Mainchain	2
1	A	77	ASN	Mainchain	2
1	A	96	THR	Mainchain	2
1	A	36	THR	Mainchain	2
1	A	80	LEU	Mainchain	2
1	A	44	ARG	Mainchain	2
1	A	62	MET	Mainchain	2
1	A	109	VAL	Mainchain	1
1	A	51	LYS	Mainchain	1
1	A	118	GLU	Mainchain	1
1	A	97	TYR	Sidechain	1
1	A	98	PHE	Sidechain	1
1	A	45	LEU	Mainchain	1
1	A	102	GLY	Mainchain	1
1	A	72	TYR	Mainchain	1
1	A	39	GLY	Mainchain	1

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	675	694	694	10±3
All	All	13500	13880	13880	204

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 7.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:82:GLU:HA	1:A:85:LYS:HD3	0.74	1.57	3	4
1:A:98:PHE:HB2	1:A:108:TYR:HB3	0.72	1.59	4	8
1:A:60:GLU:HB2	1:A:101:LYS:HG2	0.70	1.63	16	1
1:A:70:GLY:HA3	1:A:90:LEU:HD11	0.70	1.64	10	1
1:A:84:ARG:HA	1:A:87:VAL:HG23	0.69	1.64	3	10
1:A:82:GLU:HA	1:A:85:LYS:HD2	0.68	1.65	17	2
1:A:92:LYS:HE2	1:A:114:GLY:HA2	0.67	1.66	5	1
1:A:84:ARG:HA	1:A:87:VAL:CG2	0.63	2.23	3	14
1:A:41:LEU:HD12	1:A:64:ILE:HD13	0.63	1.69	11	3
1:A:100:LYS:HE2	1:A:103:GLU:HG3	0.61	1.72	15	1
1:A:59:PHE:HA	1:A:100:LYS:HA	0.61	1.71	18	5
1:A:36:THR:HG22	1:A:89:LEU:HD12	0.60	1.73	15	1
1:A:58:GLN:HA	1:A:58:GLN:HE21	0.59	1.58	17	1
1:A:70:GLY:CA	1:A:90:LEU:HD11	0.58	2.27	10	1
1:A:50:LYS:HE3	1:A:54:LYS:O	0.58	1.98	2	1
1:A:66:THR:OG1	1:A:70:GLY:HA3	0.57	1.98	10	9
1:A:69:LYS:HE3	1:A:90:LEU:HD13	0.57	1.76	19	1
1:A:80:LEU:O	1:A:85:LYS:HE3	0.56	2.00	6	2
1:A:116:THR:OG1	1:A:118:GLU:HG2	0.55	2.01	1	1
1:A:41:LEU:O	1:A:45:LEU:HG	0.55	2.02	20	4
1:A:67:GLU:HG2	1:A:116:THR:O	0.55	2.02	6	5
1:A:54:LYS:H	1:A:54:LYS:HD2	0.54	1.62	7	1
1:A:96:THR:O	1:A:109:VAL:HA	0.53	2.03	9	6
1:A:68:ASN:OD1	1:A:90:LEU:HB2	0.52	2.04	20	2
1:A:60:GLU:HB2	1:A:101:LYS:HA	0.52	1.80	13	2
1:A:46:ARG:O	1:A:50:LYS:HD3	0.52	2.03	7	1
1:A:93:MET:O	1:A:112:GLY:HA3	0.52	2.05	20	1
1:A:38:LEU:HG	1:A:80:LEU:HD11	0.52	1.82	4	1
1:A:100:LYS:HE3	1:A:103:GLU:OE2	0.51	2.05	2	1
1:A:60:GLU:HG2	1:A:61:LYS:HD2	0.50	1.83	17	1
1:A:38:LEU:HG	1:A:80:LEU:HD21	0.50	1.84	2	1
1:A:41:LEU:HG	1:A:89:LEU:HD11	0.50	1.83	6	1
1:A:75:TYR:HB3	1:A:77:ASN:OD1	0.50	2.07	15	2
1:A:61:LYS:O	1:A:99:PHE:HB2	0.50	2.07	5	1
1:A:38:LEU:HB3	1:A:84:ARG:O	0.49	2.07	12	6
1:A:100:LYS:HE3	1:A:103:GLU:HG3	0.49	1.84	8	1
1:A:48:TYR:HA	1:A:51:LYS:HE2	0.49	1.84	5	1
1:A:67:GLU:O	1:A:90:LEU:HD13	0.48	2.08	10	1
1:A:84:ARG:O	1:A:87:VAL:HB	0.48	2.08	9	3
1:A:39:GLY:HA2	1:A:80:LEU:CD2	0.48	2.39	10	1
1:A:60:GLU:HB3	1:A:101:LYS:HA	0.47	1.85	2	2
1:A:67:GLU:HA	1:A:116:THR:O	0.47	2.08	2	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:59:PHE:HB2	1:A:76:LEU:HD12	0.47	1.86	5	2
1:A:67:GLU:O	1:A:68:ASN:HB2	0.47	2.07	13	3
1:A:98:PHE:HE2	1:A:110:ILE:HG13	0.47	1.69	14	2
1:A:65:LEU:HA	1:A:70:GLY:O	0.47	2.10	2	1
1:A:92:LYS:HD2	1:A:113:PRO:HB2	0.47	1.87	16	1
1:A:60:GLU:OE1	1:A:101:LYS:HG3	0.47	2.10	8	1
1:A:82:GLU:HA	1:A:85:LYS:HG2	0.47	1.87	8	1
1:A:39:GLY:HA2	1:A:80:LEU:HD13	0.47	1.87	4	1
1:A:95:LYS:HE2	1:A:109:VAL:HG21	0.46	1.87	2	2
1:A:90:LEU:H	1:A:90:LEU:HD12	0.46	1.70	5	1
1:A:98:PHE:HE1	1:A:110:ILE:HG13	0.46	1.71	9	2
1:A:66:THR:HG22	1:A:93:MET:HA	0.46	1.88	14	6
1:A:94:TYR:CZ	1:A:95:LYS:HE2	0.46	2.45	7	1
1:A:67:GLU:HB2	1:A:91:GLY:HA3	0.45	1.87	2	1
1:A:45:LEU:HD21	1:A:93:MET:SD	0.45	2.51	1	2
1:A:98:PHE:HE1	1:A:110:ILE:HG12	0.45	1.70	11	1
1:A:36:THR:HG23	1:A:89:LEU:HD12	0.45	1.88	10	1
1:A:68:ASN:HA	1:A:118:GLU:O	0.45	2.12	20	1
1:A:92:LYS:HG3	1:A:114:GLY:CA	0.45	2.42	11	1
1:A:82:GLU:HA	1:A:85:LYS:CD	0.45	2.40	17	1
1:A:47:ASN:O	1:A:51:LYS:HG2	0.45	2.11	20	2
1:A:68:ASN:HB3	1:A:69:LYS:HD3	0.45	1.89	19	1
1:A:59:PHE:HE1	1:A:107:SER:HB2	0.44	1.72	15	1
1:A:48:TYR:CD2	1:A:110:ILE:HD13	0.44	2.47	16	2
1:A:49:LEU:HD12	1:A:50:LYS:N	0.44	2.27	16	1
1:A:39:GLY:HA2	1:A:80:LEU:HD21	0.44	1.89	10	1
1:A:46:ARG:O	1:A:50:LYS:HG2	0.44	2.12	11	2
1:A:64:ILE:HB	1:A:72:TYR:HB2	0.44	1.89	16	1
1:A:103:GLU:OE2	1:A:105:LYS:HB2	0.44	2.11	9	1
1:A:97:TYR:HB3	1:A:106:SER:HB3	0.44	1.89	1	1
1:A:61:LYS:HA	1:A:75:TYR:HA	0.44	1.90	13	1
1:A:94:TYR:CD2	1:A:95:LYS:HG2	0.44	2.48	19	1
1:A:98:PHE:CE1	1:A:110:ILE:HG12	0.44	2.47	11	1
1:A:81:ALA:O	1:A:85:LYS:HG3	0.43	2.13	7	1
1:A:41:LEU:HD12	1:A:89:LEU:CD1	0.43	2.43	1	1
1:A:74:VAL:HG13	1:A:80:LEU:HD13	0.43	1.89	5	1
1:A:98:PHE:CE2	1:A:110:ILE:HG13	0.43	2.47	13	1
1:A:96:THR:HB	1:A:110:ILE:HB	0.43	1.90	4	2
1:A:42:ASP:O	1:A:46:ARG:HG3	0.43	2.14	20	3
1:A:72:TYR:OH	1:A:89:LEU:HA	0.43	2.14	20	1
1:A:48:TYR:HA	1:A:51:LYS:HD3	0.43	1.91	8	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:54:LYS:HD2	1:A:54:LYS:N	0.42	2.29	8	1
1:A:83:ASP:O	1:A:87:VAL:HG23	0.42	2.14	12	2
1:A:59:PHE:HE1	1:A:107:SER:HB3	0.42	1.74	5	1
1:A:94:TYR:HA	1:A:114:GLY:HA3	0.42	1.90	16	1
1:A:59:PHE:HB3	1:A:76:LEU:HD12	0.42	1.90	14	1
1:A:97:TYR:HB3	1:A:106:SER:OG	0.42	2.15	12	1
1:A:60:GLU:HG3	1:A:77:ASN:HB2	0.42	1.90	18	1
1:A:98:PHE:CZ	1:A:110:ILE:HD12	0.42	2.49	16	1
1:A:60:GLU:O	1:A:75:TYR:HA	0.42	2.14	12	1
1:A:82:GLU:O	1:A:85:LYS:HB2	0.42	2.15	9	1
1:A:95:LYS:HB2	1:A:95:LYS:NZ	0.42	2.30	3	1
1:A:105:LYS:HA	1:A:105:LYS:HE2	0.41	1.91	7	1
1:A:39:GLY:HA2	1:A:80:LEU:HD23	0.41	1.90	6	1
1:A:69:LYS:HA	1:A:69:LYS:HD3	0.41	1.75	2	1
1:A:48:TYR:O	1:A:51:LYS:HB2	0.41	2.15	8	1
1:A:75:TYR:C	1:A:77:ASN:N	0.41	2.74	17	1
1:A:48:TYR:CE1	1:A:110:ILE:HG12	0.41	2.50	14	1
1:A:49:LEU:HD21	1:A:98:PHE:CE2	0.41	2.50	17	1
1:A:92:LYS:HG3	1:A:114:GLY:HA2	0.41	1.92	11	1
1:A:61:LYS:HE3	1:A:75:TYR:CE2	0.41	2.51	17	1
1:A:68:ASN:OD1	1:A:90:LEU:CB	0.41	2.69	20	1
1:A:40:LYS:O	1:A:44:ARG:HG2	0.41	2.16	6	1
1:A:48:TYR:CE2	1:A:110:ILE:HD12	0.41	2.51	11	1
1:A:59:PHE:CA	1:A:100:LYS:HA	0.41	2.45	18	1
1:A:60:GLU:OE1	1:A:101:LYS:HG2	0.41	2.15	5	1
1:A:37:THR:HB	1:A:85:LYS:O	0.40	2.16	17	1
1:A:68:ASN:HD21	1:A:90:LEU:C	0.40	2.20	9	1
1:A:98:PHE:O	1:A:106:SER:HA	0.40	2.16	9	1
1:A:81:ALA:HB3	1:A:84:ARG:HE	0.40	1.77	7	1
1:A:89:LEU:HD22	1:A:89:LEU:N	0.40	2.31	8	1
1:A:63:VAL:HA	1:A:72:TYR:O	0.40	2.17	16	1

6.3 Torsion angles ⓘ

6.3.1 Protein backbone ⓘ

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	83/91 (91%)	72±3 (87±3%)	7±3 (9±3%)	4±1 (4±2%)	6	30
All	All	1660/1820 (91%)	1445 (87%)	143 (9%)	72 (4%)	6	30

All 18 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	68	ASN	17
1	A	90	LEU	15
1	A	76	LEU	13
1	A	69	LYS	5
1	A	55	ASN	4
1	A	56	SER	3
1	A	52	GLY	3
1	A	114	GLY	2
1	A	102	GLY	1
1	A	54	LYS	1
1	A	118	GLU	1
1	A	86	ASN	1
1	A	93	MET	1
1	A	115	LYS	1
1	A	113	PRO	1
1	A	51	LYS	1
1	A	80	LEU	1
1	A	67	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	74/80 (92%)	71±2 (95±2%)	4±2 (5±2%)	35	80
All	All	1480/1600 (92%)	1410 (95%)	70 (5%)	35	80

All 32 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	60	GLU	13
1	A	106	SER	6
1	A	88	GLU	4
1	A	117	ASN	4
1	A	50	LYS	3
1	A	41	LEU	3
1	A	36	THR	3
1	A	55	ASN	2
1	A	96	THR	2
1	A	90	LEU	2
1	A	83	ASP	2
1	A	69	LYS	2
1	A	44	ARG	2
1	A	45	LEU	2
1	A	54	LYS	2
1	A	101	LYS	2
1	A	58	GLN	1
1	A	84	ARG	1
1	A	103	GLU	1
1	A	68	ASN	1
1	A	100	LYS	1
1	A	82	GLU	1
1	A	93	MET	1
1	A	95	LYS	1
1	A	59	PHE	1
1	A	115	LYS	1
1	A	38	LEU	1
1	A	116	THR	1
1	A	86	ASN	1
1	A	56	SER	1
1	A	79	PRO	1
1	A	61	LYS	1

6.3.3 RNA ⓘ

There are no RNA molecules in this entry.

6.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

6.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.6 Ligand geometry [i](#)

There are no ligands in this entry.

6.7 Other polymers [i](#)

There are no such molecules in this entry.

6.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

7 Chemical shift validation

No chemical shift data were provided