



Full wwPDB NMR Structure Validation Report ⓘ

Aug 6, 2020 – 11:44 PM BST

PDB ID : 2JMV
Title : Solution structure of scytovirin refined against residual dipolar couplings
Authors : McFeeters, R.L.; Byrd, R.A.
Deposited on : 2006-12-07

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 following versions of software and data (see [references ⓘ](#)) 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)
RCI : v_1n_11_5_13_A (Berjanski et al., 2005)
PANAV : Wang et al. (2010)
ShiftChecker : 2.13.1
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

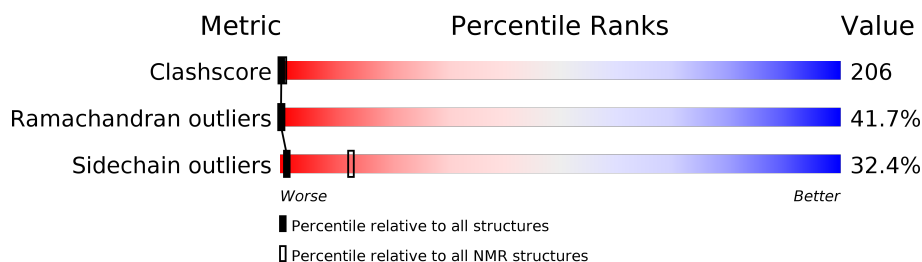
1 Overall quality at a glance

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	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 $\leq 5\%$

Mol	Chain	Length	Quality of chain
1	A	95	

2 Ensemble composition and analysis

This entry contains 20 models. Model 3 is the overall representative, medoid model (most similar to other models). The authors have identified model 1 as representative, based on the following criterion: *closest to the average*.

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:1-A:60, A:65-A:80, A:85-A:94 (86)	0.23	3

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 2 single-model clusters were found.

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

3 Entry composition [i](#)

There is only 1 type of molecule in this entry. The entry contains 1258 atoms, of which 590 are hydrogens and 0 are deuteriums.

- Molecule 1 is a protein called Scytovirin.

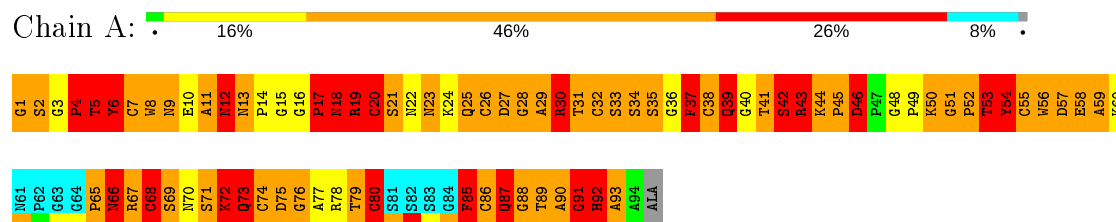
Mol	Chain	Residues	Atoms						Trace
1	A	94	Total	C	H	N	O	S	0
			1258	389	590	131	138	10	

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: Scytovirin

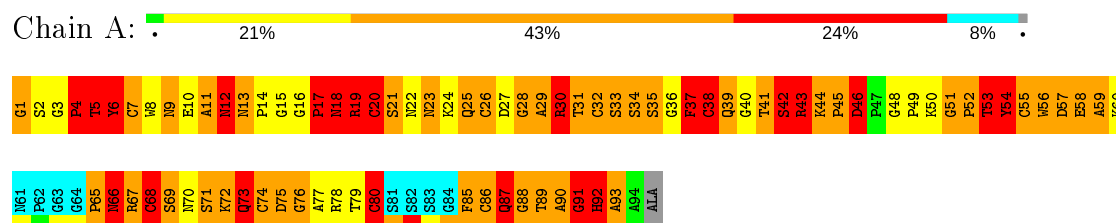


4.2 Scores per residue for each member of the ensemble

Colouring as in section 4.1 above.

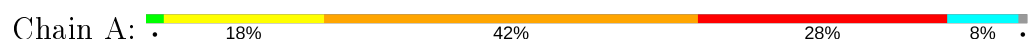
4.2.1 Score per residue for model 1

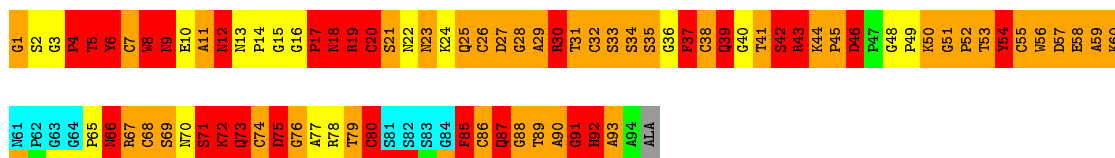
- Molecule 1: Scytovirin



4.2.2 Score per residue for model 2

- Molecule 1: Scytovirin

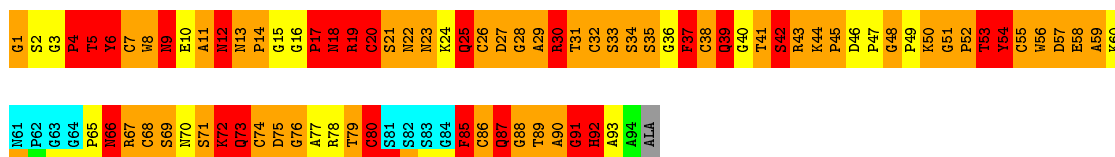




4.2.3 Score per residue for model 3 (medoid)

- Molecule 1: Scytovirin

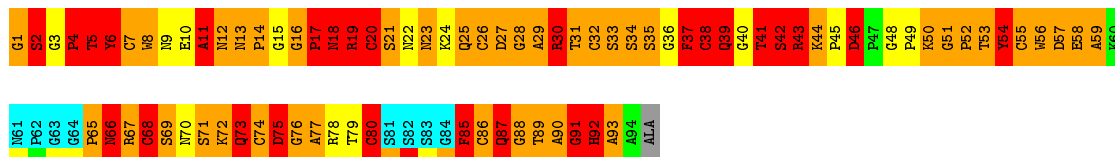
Chain A: . 18% 46% 25% 8% .



4.2.4 Score per residue for model 4

- Molecule 1: Scytovirin

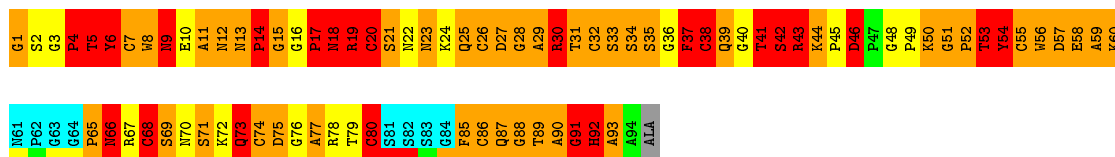
Chain A: . 15% 44% 28% 8% .



4.2.5 Score per residue for model 5

- Molecule 1: Scytovirin

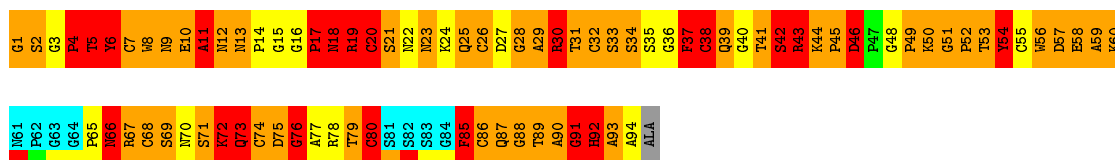
Chain A: . 18% 45% 25% 8% .



4.2.6 Score per residue for model 6

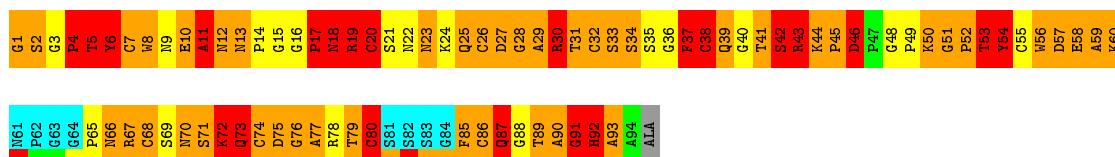
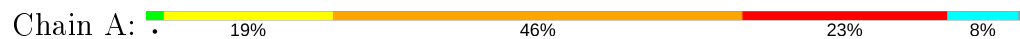
- Molecule 1: Scytovirin

Chain A: . 18% 47% 24% 8% .



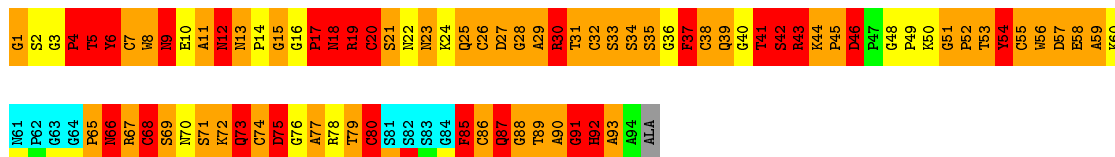
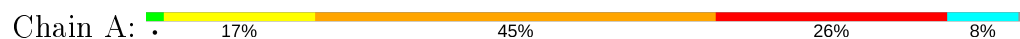
4.2.7 Score per residue for model 7

- Molecule 1: Scytovirin



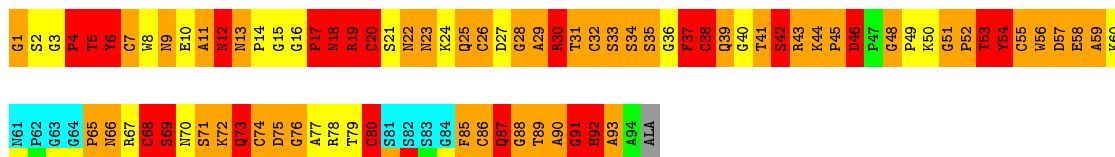
4.2.8 Score per residue for model 8

- Molecule 1: Scytovirin



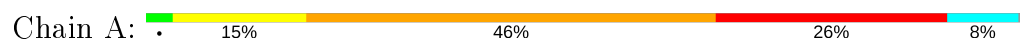
4.2.9 Score per residue for model 9

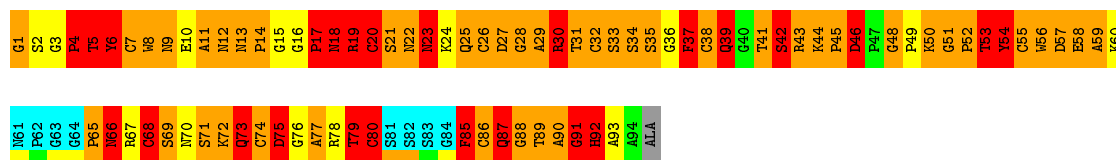
- Molecule 1: Scytovirin



4.2.10 Score per residue for model 10

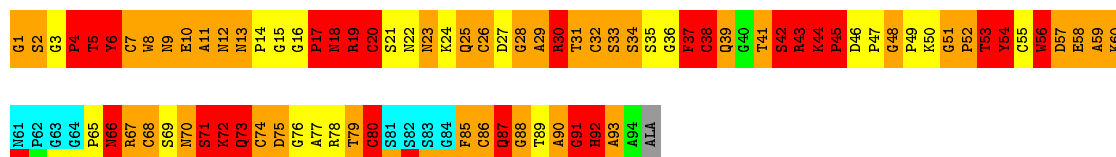
- Molecule 1: Scytovirin





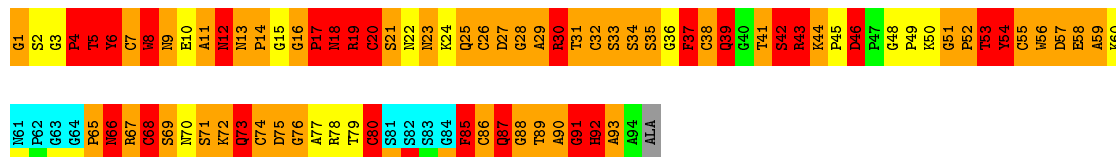
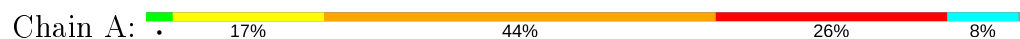
4.2.11 Score per residue for model 11

- Molecule 1: Scytovirin



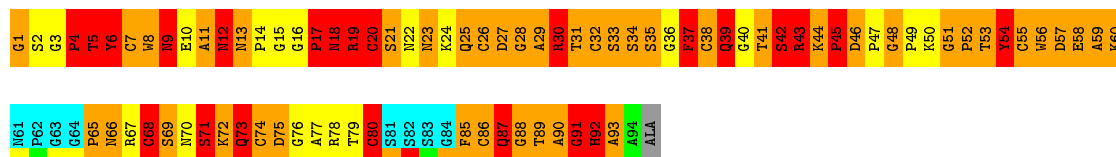
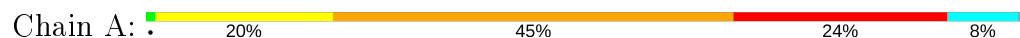
4.2.12 Score per residue for model 12

- Molecule 1: Scytovirin



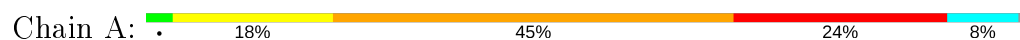
4.2.13 Score per residue for model 13

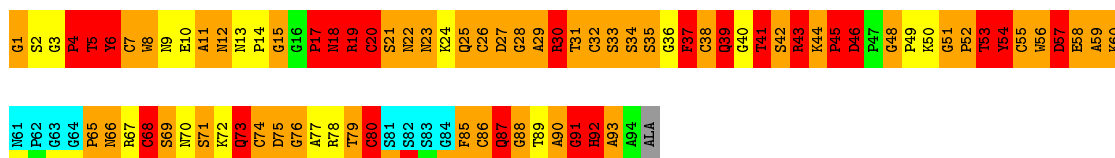
- Molecule 1: Scytovirin



4.2.14 Score per residue for model 14

- Molecule 1: Scytovirin

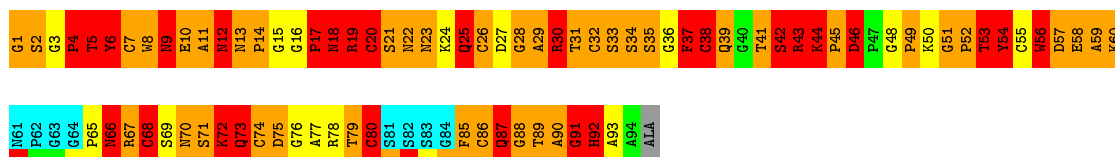




4.2.15 Score per residue for model 15

- Molecule 1: Scytovirin

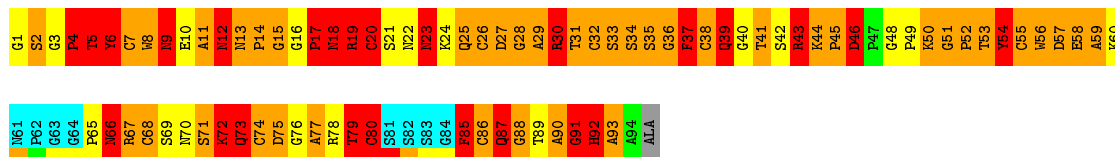
Chain A: . 16% 42% 29% 8% .



4.2.16 Score per residue for model 16

- Molecule 1: Scytovirin

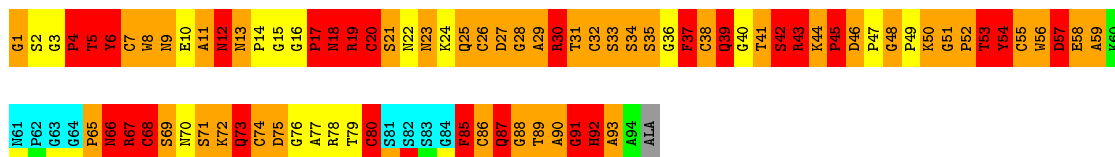
Chain A: . 19% 43% 26% 8% .



4.2.17 Score per residue for model 17

- Molecule 1: Scytovirin

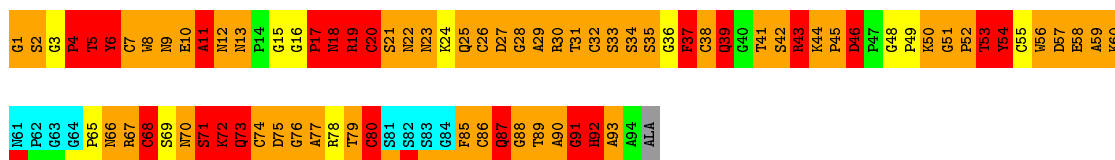
Chain A: . 18% 43% 27% 8% .



4.2.18 Score per residue for model 18

- Molecule 1: Scytovirin

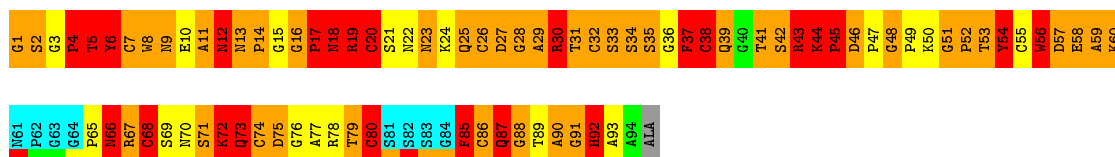
Chain A: . 12% 52% 23% 8% .



4.2.19 Score per residue for model 19

- Molecule 1: Scytovirin

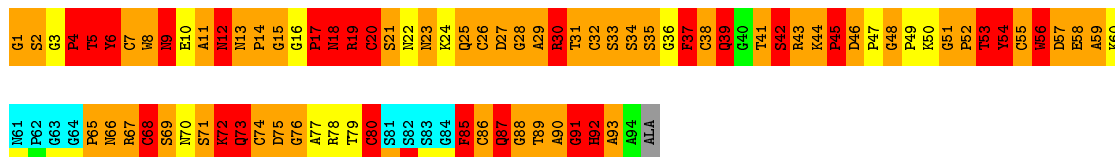
Chain A: . 20% 43% 25% 8% .



4.2.20 Score per residue for model 20

- Molecule 1: Scytovirin

Chain A: . 15% 47% 26% 8% .



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
X-PLOR NIH	structure solution	2.10
X-PLOR NIH	refinement	2.10
X-PLOR NIH	structure solution	2.14
X-PLOR NIH	refinement	2.14

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

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	3.14±0.04	69±4/639 (10.7± 0.6%)	1.34±0.02	2±1/863 (0.2± 0.1%)
All	All	3.14	1371/12780 (10.7%)	1.34	36/17260 (0.2%)

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	TYR	CB-CG	18.25	1.79	1.51	5	20
1	A	91	GLY	CA-C	15.94	1.77	1.51	2	20
1	A	80	CYS	CB-SG	13.75	2.05	1.82	13	15
1	A	1	GLY	N-CA	-12.59	1.27	1.46	13	19
1	A	74	CYS	N-CA	12.32	1.71	1.46	7	20
1	A	51	GLY	N-CA	-12.00	1.28	1.46	7	20
1	A	86	CYS	CB-SG	11.55	2.01	1.82	13	15
1	A	6	TYR	CA-C	-11.38	1.23	1.52	10	20
1	A	74	CYS	CB-SG	11.03	2.01	1.82	13	12
1	A	19	ARG	C-N	10.86	1.59	1.34	17	20
1	A	91	GLY	N-CA	10.73	1.62	1.46	17	20
1	A	28	GLY	CA-C	10.38	1.68	1.51	15	20
1	A	42	SER	CA-CB	9.90	1.67	1.52	15	19
1	A	31	THR	C-O	-9.75	1.04	1.23	16	20
1	A	20	CYS	CB-SG	9.74	1.98	1.82	17	20
1	A	92	HIS	N-CA	9.63	1.65	1.46	2	20
1	A	30	ARG	CA-CB	9.22	1.74	1.53	1	14
1	A	72	LYS	C-N	-9.21	1.12	1.34	2	20
1	A	51	GLY	C-O	-9.19	1.08	1.23	13	20
1	A	7	CYS	N-CA	-9.02	1.28	1.46	2	20
1	A	4	PRO	CA-C	-9.02	1.34	1.52	10	20
1	A	85	PHE	N-CA	-8.99	1.28	1.46	20	20
1	A	19	ARG	CA-C	-8.98	1.29	1.52	13	20
1	A	15	GLY	N-CA	8.56	1.58	1.46	12	4
1	A	75	ASP	N-CA	8.54	1.63	1.46	2	18

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	73	GLN	CA-CB	8.39	1.72	1.53	7	20
1	A	86	CYS	N-CA	8.31	1.62	1.46	17	20
1	A	15	GLY	C-O	-8.19	1.10	1.23	14	1
1	A	8	TRP	CB-CG	8.14	1.65	1.50	5	14
1	A	15	GLY	C-N	-8.12	1.18	1.33	1	13
1	A	34	SER	C-N	8.10	1.52	1.34	16	20
1	A	19	ARG	N-CA	-8.08	1.30	1.46	20	13
1	A	37	PHE	C-N	8.07	1.52	1.34	9	20
1	A	5	THR	C-N	8.04	1.52	1.34	5	20
1	A	85	PHE	C-O	-8.02	1.08	1.23	17	13
1	A	26	CYS	CB-SG	7.76	1.95	1.82	17	20
1	A	75	ASP	CG-OD1	-7.68	1.07	1.25	3	12
1	A	32	CYS	N-CA	7.55	1.61	1.46	19	20
1	A	33	SER	CA-CB	-7.44	1.41	1.52	15	20
1	A	30	ARG	CZ-NH1	-7.34	1.23	1.33	14	2
1	A	37	PHE	N-CA	-7.26	1.31	1.46	16	20
1	A	55	CYS	N-CA	7.20	1.60	1.46	8	5
1	A	17	PRO	CA-C	-7.18	1.38	1.52	20	17
1	A	1	GLY	C-N	7.14	1.50	1.34	9	6
1	A	73	GLN	C-O	-7.13	1.09	1.23	15	13
1	A	11	ALA	N-CA	-7.12	1.32	1.46	10	19
1	A	39	GLN	C-O	-7.10	1.09	1.23	16	11
1	A	16	GLY	CA-C	-7.08	1.40	1.51	12	3
1	A	44	LYS	CA-C	-7.07	1.34	1.52	9	20
1	A	51	GLY	CA-C	-7.02	1.40	1.51	7	20
1	A	54	TYR	C-N	7.00	1.50	1.34	19	13
1	A	87	GLN	N-CA	-6.93	1.32	1.46	19	5
1	A	28	GLY	C-O	-6.92	1.12	1.23	16	7
1	A	46	ASP	CA-CB	6.84	1.69	1.53	9	14
1	A	28	GLY	N-CA	-6.83	1.35	1.46	7	11
1	A	59	ALA	C-O	-6.76	1.10	1.23	15	7
1	A	59	ALA	CA-CB	-6.76	1.38	1.52	14	19
1	A	42	SER	CA-C	-6.75	1.35	1.52	18	6
1	A	45	PRO	CA-C	-6.74	1.39	1.52	19	6
1	A	76	GLY	C-O	-6.72	1.12	1.23	18	3
1	A	14	PRO	N-CD	-6.70	1.38	1.47	9	8
1	A	56	TRP	C-N	6.69	1.49	1.34	14	20
1	A	56	TRP	CG-CD1	-6.65	1.27	1.36	7	19
1	A	86	CYS	CA-CB	-6.62	1.39	1.53	3	11
1	A	17	PRO	N-CD	-6.59	1.38	1.47	15	5
1	A	60	LYS	CA-C	-6.58	1.35	1.52	2	4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	34	SER	N-CA	-6.56	1.33	1.46	16	6
1	A	53	THR	CB-OG1	-6.55	1.30	1.43	12	8
1	A	54	TYR	CB-CG	6.46	1.61	1.51	4	9
1	A	75	ASP	C-N	-6.42	1.21	1.33	8	6
1	A	15	GLY	CA-C	-6.40	1.41	1.51	14	1
1	A	33	SER	C-N	-6.37	1.19	1.34	17	20
1	A	79	THR	C-O	-6.35	1.11	1.23	19	5
1	A	74	CYS	C-N	6.35	1.48	1.34	8	16
1	A	26	CYS	C-N	-6.26	1.19	1.34	18	1
1	A	30	ARG	NE-CZ	6.23	1.41	1.33	9	4
1	A	43	ARG	CB-CG	6.20	1.69	1.52	18	9
1	A	54	TYR	N-CA	6.18	1.58	1.46	19	6
1	A	85	PHE	CB-CG	6.17	1.61	1.51	4	7
1	A	32	CYS	CA-CB	6.12	1.67	1.53	13	14
1	A	80	CYS	C-N	-6.11	1.20	1.34	1	13
1	A	10	GLU	CB-CG	-6.08	1.40	1.52	11	5
1	A	17	PRO	C-N	6.05	1.48	1.34	8	6
1	A	9	ASN	C-N	-6.03	1.20	1.34	10	12
1	A	68	CYS	CA-C	-6.03	1.37	1.52	17	16
1	A	53	THR	C-N	-6.02	1.20	1.34	7	7
1	A	80	CYS	CA-CB	6.01	1.67	1.53	15	4
1	A	72	LYS	CA-CB	6.01	1.67	1.53	5	7
1	A	65	PRO	N-CD	-5.97	1.39	1.47	4	9
1	A	6	TYR	CG-CD2	5.97	1.47	1.39	5	2
1	A	79	THR	CA-C	-5.97	1.37	1.52	16	6
1	A	56	TRP	N-CA	-5.88	1.34	1.46	2	5
1	A	31	THR	N-CA	-5.88	1.34	1.46	11	7
1	A	41	THR	CA-C	5.84	1.68	1.52	8	4
1	A	11	ALA	C-N	-5.80	1.20	1.34	5	7
1	A	12	ASN	CA-C	5.80	1.68	1.52	19	12
1	A	30	ARG	CA-C	5.78	1.68	1.52	17	5
1	A	45	PRO	C-N	-5.77	1.20	1.34	19	1
1	A	2	SER	C-N	-5.75	1.22	1.33	7	6
1	A	35	SER	N-CA	-5.73	1.34	1.46	17	5
1	A	8	TRP	CG-CD2	5.72	1.53	1.43	5	12
1	A	56	TRP	CG-CD2	5.72	1.53	1.43	8	10
1	A	68	CYS	C-N	-5.67	1.21	1.34	10	7
1	A	35	SER	CA-CB	-5.66	1.44	1.52	16	13
1	A	50	LYS	CA-CB	5.65	1.66	1.53	7	9
1	A	93	ALA	N-CA	5.64	1.57	1.46	5	16
1	A	75	ASP	CA-CB	5.60	1.66	1.53	5	3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)	Models	
								Worst	Total
1	A	44	LYS	C-O	-5.58	1.12	1.23	9	1
1	A	30	ARG	C-N	-5.55	1.21	1.34	5	3
1	A	76	GLY	N-CA	5.54	1.54	1.46	6	1
1	A	59	ALA	C-N	5.54	1.46	1.34	3	3
1	A	36	GLY	N-CA	-5.51	1.37	1.46	16	1
1	A	93	ALA	CA-CB	5.51	1.64	1.52	4	2
1	A	5	THR	C-O	-5.49	1.12	1.23	6	10
1	A	5	THR	N-CA	-5.46	1.35	1.46	6	1
1	A	32	CYS	C-N	-5.45	1.21	1.34	10	9
1	A	21	SER	N-CA	5.44	1.57	1.46	18	4
1	A	56	TRP	CD2-CE2	-5.44	1.34	1.41	8	6
1	A	79	THR	C-N	5.43	1.46	1.34	15	1
1	A	23	ASN	N-CA	-5.42	1.35	1.46	16	1
1	A	85	PHE	CG-CD1	5.41	1.46	1.38	4	1
1	A	79	THR	N-CA	-5.40	1.35	1.46	14	1
1	A	18	ASN	C-N	5.31	1.46	1.34	11	1
1	A	34	SER	CA-C	5.30	1.66	1.52	5	1
1	A	70	ASN	CA-C	-5.30	1.39	1.52	11	4
1	A	10	GLU	C-N	-5.29	1.21	1.34	11	3
1	A	44	LYS	C-N	5.26	1.44	1.34	13	2
1	A	22	ASN	CA-C	-5.25	1.39	1.52	18	3
1	A	31	THR	CA-C	-5.24	1.39	1.52	9	2
1	A	1	GLY	CA-C	-5.23	1.43	1.51	4	2
1	A	71	SER	N-CA	5.23	1.56	1.46	2	1
1	A	86	CYS	C-N	5.21	1.46	1.34	5	1
1	A	72	LYS	N-CA	5.20	1.56	1.46	20	1
1	A	43	ARG	CA-C	-5.17	1.39	1.52	7	1
1	A	67	ARG	NE-CZ	5.11	1.39	1.33	17	1
1	A	68	CYS	CA-CB	5.09	1.65	1.53	15	2
1	A	27	ASP	CA-C	-5.08	1.39	1.52	18	1
1	A	71	SER	CA-C	5.04	1.66	1.52	13	1
1	A	8	TRP	CD2-CE3	5.02	1.47	1.40	14	1
1	A	50	LYS	CB-CG	5.01	1.66	1.52	16	1

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	30	ARG	CB-CA-C	-6.45	97.51	110.40	16	1
1	A	80	CYS	N-CA-CB	5.76	120.96	110.60	15	5
1	A	6	TYR	CA-CB-CG	-5.39	103.15	113.40	13	7

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)	Models	
								Worst	Total
1	A	85	PHE	CB-CG-CD2	-5.29	117.10	120.80	4	2
1	A	6	TYR	N-CA-CB	5.24	120.03	110.60	5	14
1	A	86	CYS	CA-CB-SG	-5.24	104.57	114.00	2	2
1	A	31	THR	N-CA-CB	-5.23	100.36	110.30	4	2
1	A	20	CYS	N-CA-C	-5.06	97.33	111.00	17	3

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	623	553	550	242±10
All	All	12460	11060	10981	4838

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 206.

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

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:TYR:CG	1:A:6:TYR:CB	1.66	1.75	13	9
1:A:6:TYR:CB	1:A:6:TYR:CG	1.65	1.75	15	9
1:A:91:GLY:C	1:A:91:GLY:CA	1.55	1.75	13	7
1:A:91:GLY:CA	1:A:91:GLY:C	1.54	1.76	12	8
1:A:74:CYS:N	1:A:74:CYS:CA	1.51	1.70	18	4
1:A:74:CYS:CA	1:A:74:CYS:N	1.49	1.70	19	1
1:A:80:CYS:CB	1:A:80:CYS:SG	1.47	2.03	16	5
1:A:80:CYS:SG	1:A:80:CYS:CB	1.47	2.03	3	4
1:A:86:CYS:CB	1:A:86:CYS:SG	1.46	2.01	13	1
1:A:44:LYS:O	1:A:46:ASP:N	1.07	1.86	9	20
1:A:76:GLY:O	1:A:78:ARG:N	1.01	1.94	7	7
1:A:51:GLY:O	1:A:53:THR:N	1.00	1.94	19	20
1:A:17:PRO:C	1:A:19:ARG:H	0.95	1.65	8	20
1:A:17:PRO:O	1:A:19:ARG:N	0.94	2.01	20	20

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:30:ARG:NE	1:A:42:SER:N	0.93	2.17	18	3
1:A:6:TYR:CG	1:A:6:TYR:CA	0.93	2.52	9	11
1:A:6:TYR:CA	1:A:6:TYR:CG	0.91	2.54	17	7
1:A:59:ALA:O	1:A:68:CYS:N	0.91	2.04	6	20
1:A:17:PRO:C	1:A:19:ARG:N	0.90	2.25	20	20
1:A:80:CYS:SG	1:A:86:CYS:N	0.90	2.44	15	20
1:A:80:CYS:H	1:A:85:PHE:H	0.90	1.04	18	20
1:A:31:THR:O	1:A:39:GLN:O	0.89	1.90	16	20
1:A:1:GLY:H2	1:A:27:ASP:CG	0.89	1.71	9	20
1:A:80:CYS:CA	1:A:86:CYS:H	0.85	1.84	7	20
1:A:80:CYS:N	1:A:85:PHE:H	0.82	1.72	11	19
1:A:1:GLY:N	1:A:27:ASP:HA	0.81	1.89	11	18
1:A:32:CYS:HA	1:A:38:CYS:N	0.80	1.91	16	20
1:A:2:SER:N	1:A:29:ALA:H	0.80	1.74	2	20
1:A:1:GLY:H1	1:A:27:ASP:HA	0.80	1.36	7	20
1:A:31:THR:OG1	1:A:39:GLN:O	0.80	2.00	14	20
1:A:73:GLN:C	1:A:74:CYS:CA	0.80	2.50	11	5
1:A:21:SER:N	1:A:25:GLN:O	0.79	2.16	7	20
1:A:20:CYS:SG	1:A:25:GLN:C	0.79	2.61	7	20
1:A:30:ARG:HE	1:A:42:SER:N	0.79	1.76	19	2
1:A:80:CYS:H	1:A:85:PHE:N	0.78	1.76	18	14
1:A:74:CYS:SG	1:A:85:PHE:HB3	0.78	2.18	6	15
1:A:23:ASN:HA	1:A:38:CYS:HA	0.78	1.53	9	20
1:A:2:SER:H	1:A:29:ALA:N	0.77	1.76	20	10
1:A:31:THR:O	1:A:39:GLN:N	0.77	2.17	5	20
1:A:53:THR:OG1	1:A:76:GLY:O	0.76	2.03	15	13
1:A:22:ASN:N	1:A:25:GLN:HA	0.75	1.97	17	20
1:A:10:GLU:H	1:A:18:ASN:HD21	0.75	1.20	18	15
1:A:2:SER:H	1:A:29:ALA:H	0.75	1.24	14	9
1:A:2:SER:N	1:A:29:ALA:N	0.75	2.34	8	20
1:A:8:TRP:HB2	1:A:27:ASP:CB	0.74	2.12	11	20
1:A:51:GLY:O	1:A:53:THR:O	0.73	2.05	13	20
1:A:53:THR:O	1:A:92:HIS:N	0.73	2.18	19	15
1:A:53:THR:C	1:A:92:HIS:H	0.73	1.87	19	20
1:A:19:ARG:O	1:A:20:CYS:O	0.72	2.06	16	20
1:A:52:PRO:O	1:A:93:ALA:N	0.72	2.22	16	20
1:A:1:GLY:C	1:A:29:ALA:H	0.72	1.88	4	11
1:A:23:ASN:OD1	1:A:26:CYS:O	0.72	2.08	7	20
1:A:30:ARG:NE	1:A:42:SER:CB	0.72	2.53	19	1
1:A:5:THR:O	1:A:7:CYS:N	0.71	2.23	7	20
1:A:7:CYS:O	1:A:8:TRP:C	0.71	2.29	6	20

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:14:PRO:C	1:A:16:GLY:H	0.71	1.88	20	5
1:A:10:GLU:N	1:A:18:ASN:HD21	0.70	1.84	18	10
1:A:22:ASN:ND2	1:A:23:ASN:HD21	0.70	1.84	20	3
1:A:86:CYS:CA	1:A:86:CYS:SG	0.70	2.78	13	1
1:A:55:CYS:N	1:A:75:ASP:OD1	0.70	2.24	20	16
1:A:30:ARG:N	1:A:41:THR:O	0.70	2.25	19	20
1:A:51:GLY:C	1:A:53:THR:H	0.70	1.88	15	19
1:A:1:GLY:N	1:A:23:ASN:CG	0.70	2.45	14	20
1:A:31:THR:N	1:A:39:GLN:O	0.69	2.24	16	20
1:A:59:ALA:HB3	1:A:68:CYS:SG	0.69	2.28	13	12
1:A:80:CYS:HA	1:A:86:CYS:O	0.69	1.87	2	18
1:A:80:CYS:CA	1:A:86:CYS:N	0.69	2.56	6	20
1:A:6:TYR:CD2	1:A:27:ASP:CG	0.69	2.66	2	20
1:A:1:GLY:N	1:A:23:ASN:CB	0.69	2.55	17	19
1:A:32:CYS:CA	1:A:38:CYS:N	0.69	2.55	14	20
1:A:32:CYS:N	1:A:37:PHE:N	0.69	2.40	12	20
1:A:43:ARG:HH21	1:A:54:TYR:H	0.68	1.32	4	2
1:A:30:ARG:HE	1:A:42:SER:CB	0.68	2.00	19	1
1:A:31:THR:C	1:A:38:CYS:H	0.68	1.91	9	20
1:A:53:THR:N	1:A:92:HIS:N	0.68	2.42	13	20
1:A:24:LYS:H	1:A:38:CYS:HA	0.67	1.49	5	11
1:A:19:ARG:O	1:A:20:CYS:C	0.67	2.33	11	20
1:A:23:ASN:O	1:A:30:ARG:NE	0.67	2.28	17	16
1:A:80:CYS:CB	1:A:86:CYS:H	0.67	2.02	3	20
1:A:55:CYS:H	1:A:75:ASP:CG	0.67	1.93	12	16
1:A:30:ARG:NH1	1:A:42:SER:OG	0.67	2.27	14	8
1:A:30:ARG:HA	1:A:41:THR:H	0.67	1.50	16	2
1:A:80:CYS:HA	1:A:86:CYS:N	0.67	2.05	15	20
1:A:32:CYS:SG	1:A:33:SER:N	0.66	2.68	18	20
1:A:22:ASN:O	1:A:26:CYS:N	0.66	2.27	16	20
1:A:89:THR:HG22	1:A:90:ALA:N	0.66	2.05	7	15
1:A:6:TYR:O	1:A:6:TYR:CD2	0.66	2.48	8	10
1:A:59:ALA:CB	1:A:73:GLN:O	0.66	2.44	6	20
1:A:79:THR:O	1:A:87:GLN:HB3	0.66	1.90	19	5
1:A:80:CYS:HA	1:A:86:CYS:H	0.66	1.51	15	6
1:A:4:PRO:O	1:A:5:THR:HG22	0.66	1.91	13	20
1:A:80:CYS:N	1:A:86:CYS:N	0.65	2.44	2	20
1:A:30:ARG:CZ	1:A:42:SER:OG	0.65	2.44	11	13
1:A:80:CYS:H	1:A:86:CYS:N	0.65	1.88	2	15
1:A:6:TYR:CD2	1:A:6:TYR:O	0.65	2.49	5	10
1:A:46:ASP:O	1:A:48:GLY:N	0.65	2.29	11	8

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:32:CYS:H	1:A:37:PHE:N	0.65	1.89	16	20
1:A:32:CYS:HA	1:A:38:CYS:H	0.65	1.50	14	20
1:A:75:ASP:OD1	1:A:76:GLY:N	0.65	2.30	2	10
1:A:65:PRO:O	1:A:67:ARG:N	0.65	2.30	6	20
1:A:92:HIS:CG	1:A:92:HIS:O	0.65	2.50	6	11
1:A:78:ARG:HB2	1:A:85:PHE:O	0.65	1.91	17	18
1:A:15:GLY:O	1:A:19:ARG:CD	0.65	2.45	14	3
1:A:31:THR:O	1:A:39:GLN:HG3	0.64	1.92	16	20
1:A:1:GLY:N	1:A:23:ASN:ND2	0.64	2.45	18	8
1:A:21:SER:O	1:A:22:ASN:ND2	0.64	2.30	4	8
1:A:32:CYS:CB	1:A:37:PHE:H	0.64	2.05	16	20
1:A:30:ARG:HG3	1:A:41:THR:C	0.64	2.13	5	16
1:A:1:GLY:H3	1:A:23:ASN:ND2	0.64	1.91	12	5
1:A:1:GLY:N	1:A:27:ASP:OD1	0.64	2.31	18	13
1:A:39:GLN:NE2	1:A:40:GLY:N	0.64	2.45	14	13
1:A:1:GLY:H3	1:A:23:ASN:CB	0.64	2.06	13	17
1:A:71:SER:HA	1:A:85:PHE:HB2	0.64	1.69	1	5
1:A:23:ASN:N	1:A:23:ASN:ND2	0.64	2.46	5	6
1:A:15:GLY:O	1:A:19:ARG:NE	0.64	2.30	14	1
1:A:92:HIS:O	1:A:92:HIS:CG	0.63	2.51	4	9
1:A:51:GLY:N	1:A:77:ALA:HB1	0.63	2.08	12	19
1:A:15:GLY:O	1:A:19:ARG:HD3	0.63	1.93	15	9
1:A:44:LYS:C	1:A:46:ASP:N	0.63	2.51	19	20
1:A:53:THR:O	1:A:54:TYR:CB	0.63	2.46	19	20
1:A:89:THR:CG2	1:A:90:ALA:N	0.63	2.61	18	15
1:A:24:LYS:HB2	1:A:30:ARG:HE	0.63	1.52	14	1
1:A:66:ASN:ND2	1:A:73:GLN:NE2	0.63	2.46	11	3
1:A:10:GLU:C	1:A:17:PRO:HB3	0.63	2.14	3	20
1:A:59:ALA:O	1:A:68:CYS:SG	0.63	2.57	7	10
1:A:43:ARG:NE	1:A:53:THR:OG1	0.62	2.32	8	11
1:A:6:TYR:O	1:A:6:TYR:CG	0.62	2.52	4	9
1:A:77:ALA:HB3	1:A:90:ALA:H	0.62	1.55	2	18
1:A:51:GLY:O	1:A:92:HIS:N	0.62	2.33	5	20
1:A:72:LYS:N	1:A:85:PHE:CD2	0.62	2.67	11	8
1:A:32:CYS:HB2	1:A:37:PHE:H	0.62	1.54	5	20
1:A:10:GLU:H	1:A:18:ASN:ND2	0.62	1.90	11	3
1:A:74:CYS:N	1:A:74:CYS:C	0.62	2.48	15	5
1:A:1:GLY:N	1:A:27:ASP:CG	0.62	2.53	18	20
1:A:5:THR:O	1:A:7:CYS:HB2	0.62	1.95	20	20
1:A:1:GLY:H3	1:A:23:ASN:CG	0.62	1.99	13	11
1:A:1:GLY:N	1:A:23:ASN:OD1	0.62	2.33	13	9

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:28:GLY:O	1:A:43:ARG:N	0.62	2.33	7	20
1:A:5:THR:C	1:A:7:CYS:N	0.62	2.51	16	20
1:A:71:SER:HA	1:A:85:PHE:CB	0.61	2.24	1	6
1:A:53:THR:OG1	1:A:77:ALA:N	0.61	2.32	5	7
1:A:56:TRP:NE1	1:A:58:GLU:O	0.61	2.34	3	7
1:A:55:CYS:N	1:A:75:ASP:OD2	0.61	2.33	4	3
1:A:6:TYR:CB	1:A:6:TYR:CD1	0.61	2.74	18	9
1:A:23:ASN:HA	1:A:37:PHE:C	0.61	2.15	3	18
1:A:56:TRP:N	1:A:75:ASP:OD1	0.61	2.34	7	4
1:A:1:GLY:CA	1:A:30:ARG:N	0.61	2.64	18	19
1:A:2:SER:N	1:A:27:ASP:OD1	0.60	2.33	11	6
1:A:24:LYS:O	1:A:25:GLN:HB2	0.60	1.95	3	20
1:A:6:TYR:CG	1:A:6:TYR:O	0.60	2.53	19	11
1:A:3:GLY:O	1:A:5:THR:N	0.60	2.35	7	20
1:A:43:ARG:NE	1:A:76:GLY:O	0.60	2.34	19	9
1:A:87:GLN:OE1	1:A:88:GLY:N	0.60	2.35	17	15
1:A:23:ASN:HB2	1:A:30:ARG:HB2	0.60	1.73	18	7
1:A:43:ARG:HE	1:A:53:THR:CB	0.60	2.09	8	5
1:A:51:GLY:N	1:A:77:ALA:CB	0.60	2.65	16	19
1:A:8:TRP:O	1:A:55:CYS:SG	0.60	2.59	2	16
1:A:32:CYS:CA	1:A:38:CYS:H	0.59	2.09	14	20
1:A:56:TRP:N	1:A:75:ASP:OD2	0.59	2.35	15	12
1:A:80:CYS:CA	1:A:80:CYS:SG	0.59	2.89	16	5
1:A:68:CYS:O	1:A:69:SER:CB	0.59	2.50	3	20
1:A:22:ASN:O	1:A:25:GLN:N	0.59	2.35	1	12
1:A:51:GLY:O	1:A:91:GLY:N	0.59	2.35	19	20
1:A:32:CYS:H	1:A:35:SER:C	0.59	2.00	18	19
1:A:8:TRP:O	1:A:9:ASN:C	0.59	2.39	6	20
1:A:20:CYS:C	1:A:25:GLN:O	0.59	2.41	7	20
1:A:4:PRO:O	1:A:5:THR:CB	0.59	2.51	4	20
1:A:4:PRO:C	1:A:5:THR:HG22	0.59	2.18	19	20
1:A:7:CYS:O	1:A:7:CYS:SG	0.59	2.61	1	13
1:A:1:GLY:HA3	1:A:30:ARG:N	0.59	2.12	20	19
1:A:10:GLU:O	1:A:17:PRO:HB3	0.59	1.97	15	4
1:A:56:TRP:NE1	1:A:59:ALA:HB2	0.59	2.13	15	5
1:A:30:ARG:CG	1:A:30:ARG:HH11	0.59	2.11	2	3
1:A:28:GLY:O	1:A:43:ARG:HB3	0.59	1.98	16	4
1:A:91:GLY:O	1:A:92:HIS:ND1	0.59	2.36	10	20
1:A:80:CYS:H	1:A:85:PHE:C	0.59	2.01	13	14
1:A:23:ASN:ND2	1:A:23:ASN:N	0.59	2.47	14	3
1:A:30:ARG:HH11	1:A:42:SER:CB	0.59	2.11	14	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:20:CYS:SG	1:A:25:GLN:CB	0.58	2.92	14	20
1:A:22:ASN:CG	1:A:23:ASN:ND2	0.58	2.56	3	9
1:A:51:GLY:O	1:A:91:GLY:CA	0.58	2.51	14	20
1:A:6:TYR:CD1	1:A:6:TYR:CB	0.58	2.75	17	8
1:A:8:TRP:HB2	1:A:27:ASP:N	0.58	2.14	18	19
1:A:30:ARG:NE	1:A:42:SER:OG	0.58	2.36	19	3
1:A:71:SER:N	1:A:80:CYS:SG	0.58	2.76	3	10
1:A:22:ASN:C	1:A:23:ASN:OD1	0.58	2.42	4	11
1:A:71:SER:O	1:A:72:LYS:HB3	0.58	1.99	11	9
1:A:78:ARG:CB	1:A:85:PHE:O	0.58	2.52	17	20
1:A:30:ARG:HE	1:A:42:SER:CA	0.58	2.12	19	1
1:A:30:ARG:HD2	1:A:42:SER:CA	0.58	2.29	15	15
1:A:59:ALA:HB3	1:A:73:GLN:O	0.58	1.99	18	8
1:A:58:GLU:HG3	1:A:58:GLU:O	0.58	1.98	18	13
1:A:7:CYS:SG	1:A:7:CYS:O	0.58	2.62	9	7
1:A:23:ASN:HA	1:A:38:CYS:CA	0.57	2.29	9	19
1:A:34:SER:C	1:A:36:GLY:H	0.57	2.02	7	20
1:A:37:PHE:CD2	1:A:37:PHE:O	0.57	2.57	1	7
1:A:29:ALA:O	1:A:30:ARG:O	0.57	2.22	16	14
1:A:80:CYS:SG	1:A:80:CYS:CA	0.57	2.90	6	4
1:A:52:PRO:O	1:A:93:ALA:HB2	0.57	1.99	11	4
1:A:22:ASN:ND2	1:A:23:ASN:ND2	0.57	2.53	20	3
1:A:7:CYS:C	1:A:55:CYS:SG	0.57	2.83	2	20
1:A:11:ALA:O	1:A:12:ASN:CB	0.57	2.53	4	20
1:A:70:ASN:C	1:A:80:CYS:SG	0.57	2.83	6	10
1:A:54:TYR:HA	1:A:75:ASP:OD1	0.57	2.00	3	9
1:A:79:THR:N	1:A:87:GLN:OE1	0.57	2.38	17	13
1:A:11:ALA:N	1:A:18:ASN:OD1	0.57	2.36	19	18
1:A:74:CYS:N	1:A:74:CYS:CB	0.57	2.61	15	3
1:A:6:TYR:CD2	1:A:27:ASP:OD2	0.56	2.58	9	16
1:A:5:THR:HG21	1:A:93:ALA:O	0.56	1.99	4	3
1:A:49:PRO:CB	1:A:53:THR:HG23	0.56	2.29	6	1
1:A:7:CYS:O	1:A:9:ASN:N	0.56	2.39	16	20
1:A:43:ARG:O	1:A:44:LYS:C	0.56	2.43	19	16
1:A:80:CYS:N	1:A:86:CYS:H	0.56	1.99	7	4
1:A:80:CYS:HA	1:A:86:CYS:C	0.56	2.20	2	20
1:A:43:ARG:O	1:A:45:PRO:N	0.56	2.39	19	16
1:A:24:LYS:N	1:A:38:CYS:HA	0.56	2.15	19	15
1:A:13:ASN:O	1:A:16:GLY:O	0.56	2.23	12	18
1:A:29:ALA:HB3	1:A:43:ARG:H	0.56	1.61	7	7
1:A:44:LYS:O	1:A:46:ASP:CA	0.56	2.54	17	5

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:TRP:CH2	1:A:22:ASN:ND2	0.56	2.73	18	4
1:A:65:PRO:C	1:A:67:ARG:N	0.56	2.59	10	20
1:A:89:THR:O	1:A:90:ALA:HB3	0.56	2.00	9	20
1:A:53:THR:OG1	1:A:76:GLY:C	0.56	2.44	3	13
1:A:56:TRP:CZ2	1:A:66:ASN:OD1	0.56	2.59	3	17
1:A:6:TYR:CG	1:A:27:ASP:OD1	0.56	2.58	8	14
1:A:28:GLY:O	1:A:29:ALA:CB	0.56	2.53	16	20
1:A:59:ALA:CB	1:A:68:CYS:SG	0.56	2.93	13	7
1:A:75:ASP:CG	1:A:76:GLY:N	0.56	2.60	8	4
1:A:1:GLY:H1	1:A:23:ASN:CG	0.56	2.04	9	10
1:A:58:GLU:O	1:A:58:GLU:HG3	0.55	2.01	15	7
1:A:70:ASN:O	1:A:71:SER:CB	0.55	2.54	17	20
1:A:92:HIS:O	1:A:92:HIS:CD2	0.55	2.59	20	10
1:A:22:ASN:O	1:A:25:GLN:C	0.55	2.44	9	17
1:A:92:HIS:CD2	1:A:92:HIS:O	0.55	2.59	14	7
1:A:8:TRP:O	1:A:10:GLU:N	0.55	2.39	1	16
1:A:71:SER:OG	1:A:71:SER:O	0.55	2.23	14	5
1:A:54:TYR:CD2	1:A:75:ASP:OD2	0.55	2.60	10	8
1:A:1:GLY:O	1:A:30:ARG:O	0.55	2.25	15	10
1:A:23:ASN:O	1:A:26:CYS:N	0.55	2.36	8	4
1:A:66:ASN:ND2	1:A:73:GLN:HE22	0.55	1.99	11	1
1:A:56:TRP:CG	1:A:57:ASP:N	0.55	2.73	8	17
1:A:71:SER:O	1:A:71:SER:OG	0.55	2.25	2	6
1:A:30:ARG:CG	1:A:30:ARG:NH1	0.55	2.70	2	2
1:A:7:CYS:O	1:A:55:CYS:SG	0.55	2.65	11	20
1:A:87:GLN:CD	1:A:88:GLY:N	0.55	2.59	15	18
1:A:51:GLY:HA2	1:A:91:GLY:N	0.55	2.17	15	19
1:A:8:TRP:CG	1:A:26:CYS:O	0.55	2.60	7	1
1:A:54:TYR:CD1	1:A:54:TYR:O	0.55	2.60	13	12
1:A:22:ASN:O	1:A:23:ASN:OD1	0.55	2.24	9	6
1:A:20:CYS:CA	1:A:25:GLN:O	0.55	2.55	14	20
1:A:68:CYS:SG	1:A:69:SER:N	0.55	2.78	12	11
1:A:74:CYS:CB	1:A:74:CYS:N	0.55	2.65	18	2
1:A:6:TYR:C	1:A:6:TYR:CG	0.55	2.80	12	10
1:A:54:TYR:O	1:A:54:TYR:CD1	0.55	2.60	8	8
1:A:30:ARG:NH1	1:A:30:ARG:CG	0.55	2.70	11	2
1:A:42:SER:O	1:A:44:LYS:N	0.54	2.40	11	2
1:A:71:SER:HA	1:A:80:CYS:SG	0.54	2.42	2	2
1:A:6:TYR:CB	1:A:27:ASP:OD1	0.54	2.56	14	20
1:A:30:ARG:HD2	1:A:42:SER:CB	0.54	2.32	7	14
1:A:32:CYS:O	1:A:35:SER:N	0.54	2.33	7	19

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:6:TYR:CG	1:A:6:TYR:C	0.54	2.80	13	8
1:A:10:GLU:N	1:A:18:ASN:ND2	0.54	2.54	11	2
1:A:20:CYS:SG	1:A:25:GLN:O	0.54	2.65	18	20
1:A:59:ALA:C	1:A:68:CYS:SG	0.54	2.85	19	5
1:A:23:ASN:ND2	1:A:27:ASP:OD2	0.54	2.41	7	2
1:A:72:LYS:O	1:A:73:GLN:CB	0.54	2.56	11	17
1:A:54:TYR:CD2	1:A:75:ASP:OD1	0.54	2.61	19	7
1:A:66:ASN:CG	1:A:73:GLN:NE2	0.54	2.61	14	2
1:A:42:SER:O	1:A:43:ARG:NH1	0.54	2.41	19	2
1:A:4:PRO:O	1:A:5:THR:CG2	0.54	2.56	13	20
1:A:77:ALA:HB3	1:A:90:ALA:N	0.53	2.17	6	15
1:A:2:SER:O	1:A:29:ALA:HA	0.53	2.03	4	19
1:A:54:TYR:CA	1:A:75:ASP:OD1	0.53	2.56	6	6
1:A:23:ASN:HB2	1:A:26:CYS:O	0.53	2.02	18	3
1:A:89:THR:O	1:A:90:ALA:CB	0.53	2.56	10	20
1:A:55:CYS:N	1:A:75:ASP:CG	0.53	2.62	3	15
1:A:12:ASN:CG	1:A:12:ASN:O	0.53	2.47	3	12
1:A:30:ARG:NE	1:A:42:SER:H	0.53	1.98	18	1
1:A:60:LYS:O	1:A:69:SER:CB	0.53	2.57	13	9
1:A:53:THR:HG1	1:A:76:GLY:C	0.52	2.05	2	1
1:A:15:GLY:O	1:A:19:ARG:CG	0.52	2.57	14	1
1:A:20:CYS:SG	1:A:26:CYS:N	0.52	2.83	7	12
1:A:1:GLY:O	1:A:29:ALA:C	0.52	2.48	4	5
1:A:37:PHE:O	1:A:37:PHE:CD2	0.52	2.62	15	5
1:A:12:ASN:O	1:A:12:ASN:CG	0.52	2.47	11	8
1:A:56:TRP:NE1	1:A:66:ASN:HB2	0.52	2.20	10	11
1:A:56:TRP:H	1:A:75:ASP:CG	0.52	2.07	11	8
1:A:51:GLY:C	1:A:91:GLY:CA	0.52	2.78	18	20
1:A:6:TYR:CG	1:A:27:ASP:CG	0.52	2.83	9	16
1:A:30:ARG:HD2	1:A:42:SER:N	0.52	2.19	12	6
1:A:12:ASN:ND2	1:A:12:ASN:O	0.52	2.42	10	4
1:A:56:TRP:CD1	1:A:59:ALA:HB2	0.52	2.39	19	5
1:A:23:ASN:CB	1:A:30:ARG:HB2	0.52	2.34	13	8
1:A:24:LYS:HB2	1:A:30:ARG:NH1	0.52	2.20	19	1
1:A:23:ASN:HD22	1:A:37:PHE:HB2	0.52	1.65	12	3
1:A:21:SER:O	1:A:22:ASN:OD1	0.52	2.28	11	2
1:A:68:CYS:SG	1:A:73:GLN:O	0.52	2.67	18	4
1:A:23:ASN:CA	1:A:38:CYS:HA	0.52	2.35	15	19
1:A:28:GLY:O	1:A:43:ARG:CB	0.52	2.58	7	13
1:A:10:GLU:O	1:A:73:GLN:NE2	0.52	2.42	14	1
1:A:74:CYS:SG	1:A:86:CYS:HB3	0.52	2.44	1	6

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:80:CYS:SG	1:A:85:PHE:HB2	0.52	2.44	5	5
1:A:56:TRP:C	1:A:75:ASP:OD2	0.52	2.49	6	12
1:A:1:GLY:C	1:A:29:ALA:N	0.52	2.63	4	8
1:A:59:ALA:O	1:A:67:ARG:CA	0.52	2.58	7	5
1:A:11:ALA:O	1:A:18:ASN:OD1	0.51	2.29	18	5
1:A:30:ARG:HE	1:A:41:THR:C	0.51	2.07	18	1
1:A:23:ASN:HB3	1:A:30:ARG:HB3	0.51	1.82	16	1
1:A:65:PRO:C	1:A:67:ARG:H	0.51	2.09	6	15
1:A:1:GLY:H1	1:A:23:ASN:CB	0.51	2.18	14	9
1:A:30:ARG:CD	1:A:42:SER:N	0.51	2.73	18	1
1:A:56:TRP:CZ2	1:A:66:ASN:CG	0.51	2.84	2	4
1:A:31:THR:O	1:A:39:GLN:C	0.51	2.48	16	10
1:A:71:SER:HA	1:A:85:PHE:CG	0.51	2.40	13	5
1:A:10:GLU:O	1:A:11:ALA:HB2	0.51	2.06	4	5
1:A:22:ASN:O	1:A:25:GLN:CA	0.51	2.57	9	4
1:A:22:ASN:H	1:A:25:GLN:HA	0.51	1.66	17	7
1:A:42:SER:O	1:A:43:ARG:C	0.51	2.49	17	19
1:A:56:TRP:CE2	1:A:66:ASN:HB2	0.51	2.41	8	13
1:A:26:CYS:HB2	1:A:30:ARG:NE	0.51	2.20	8	12
1:A:2:SER:C	1:A:29:ALA:HA	0.51	2.26	18	17
1:A:22:ASN:O	1:A:23:ASN:C	0.51	2.48	9	13
1:A:54:TYR:HB3	1:A:92:HIS:N	0.51	2.21	15	14
1:A:14:PRO:O	1:A:16:GLY:N	0.51	2.39	10	5
1:A:30:ARG:HH11	1:A:30:ARG:CG	0.51	2.19	11	1
1:A:23:ASN:CB	1:A:30:ARG:CB	0.51	2.89	16	1
1:A:22:ASN:OD1	1:A:23:ASN:ND2	0.50	2.44	3	2
1:A:53:THR:C	1:A:92:HIS:N	0.50	2.63	6	12
1:A:26:CYS:O	1:A:27:ASP:HB2	0.50	2.06	7	4
1:A:80:CYS:HA	1:A:86:CYS:CA	0.50	2.37	17	20
1:A:1:GLY:CA	1:A:29:ALA:H	0.50	2.19	7	11
1:A:20:CYS:C	1:A:25:GLN:HB3	0.50	2.26	2	16
1:A:23:ASN:OD1	1:A:27:ASP:CB	0.50	2.60	16	1
1:A:78:ARG:NH1	1:A:88:GLY:C	0.50	2.64	20	1
1:A:19:ARG:C	1:A:20:CYS:O	0.50	2.49	15	20
1:A:44:LYS:O	1:A:46:ASP:CB	0.50	2.60	13	6
1:A:73:GLN:OE1	1:A:73:GLN:O	0.49	2.30	14	1
1:A:8:TRP:HE1	1:A:21:SER:H	0.49	1.49	7	3
1:A:22:ASN:C	1:A:23:ASN:CG	0.49	2.71	5	12
1:A:53:THR:N	1:A:92:HIS:H	0.49	2.06	13	14
1:A:23:ASN:HA	1:A:38:CYS:N	0.49	2.22	14	13
1:A:24:LYS:O	1:A:25:GLN:CB	0.49	2.60	19	8

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:74:CYS:SG	1:A:86:CYS:SG	0.49	3.10	1	6
1:A:52:PRO:O	1:A:93:ALA:CB	0.49	2.59	15	4
1:A:43:ARG:HH21	1:A:54:TYR:N	0.49	2.04	4	1
1:A:4:PRO:C	1:A:5:THR:CG2	0.49	2.81	19	20
1:A:69:SER:C	1:A:86:CYS:SG	0.49	2.91	10	5
1:A:79:THR:H	1:A:88:GLY:H	0.49	1.50	16	3
1:A:20:CYS:SG	1:A:25:GLN:HB3	0.49	2.48	5	19
1:A:31:THR:O	1:A:39:GLN:CA	0.49	2.61	16	20
1:A:58:GLU:CG	1:A:58:GLU:O	0.49	2.60	19	9
1:A:53:THR:CA	1:A:92:HIS:HA	0.49	2.37	13	17
1:A:58:GLU:O	1:A:58:GLU:CG	0.49	2.60	11	4
1:A:79:THR:O	1:A:87:GLN:CB	0.49	2.60	7	4
1:A:1:GLY:CA	1:A:27:ASP:OD1	0.49	2.60	16	1
1:A:71:SER:O	1:A:72:LYS:CB	0.48	2.59	20	8
1:A:30:ARG:NE	1:A:41:THR:C	0.48	2.67	18	1
1:A:23:ASN:O	1:A:30:ARG:CD	0.48	2.60	7	9
1:A:14:PRO:C	1:A:16:GLY:N	0.48	2.64	20	6
1:A:24:LYS:CB	1:A:30:ARG:HE	0.48	2.21	14	1
1:A:20:CYS:CB	1:A:25:GLN:HB3	0.48	2.38	1	18
1:A:34:SER:C	1:A:36:GLY:N	0.48	2.67	6	19
1:A:32:CYS:C	1:A:35:SER:H	0.48	2.11	8	17
1:A:43:ARG:CD	1:A:76:GLY:O	0.48	2.62	13	3
1:A:5:THR:O	1:A:7:CYS:CB	0.48	2.61	13	13
1:A:80:CYS:SG	1:A:85:PHE:CB	0.48	3.01	15	8
1:A:23:ASN:C	1:A:25:GLN:N	0.48	2.65	5	4
1:A:28:GLY:O	1:A:43:ARG:CG	0.48	2.61	19	7
1:A:1:GLY:HA3	1:A:30:ARG:CB	0.48	2.37	16	1
1:A:5:THR:C	1:A:7:CYS:H	0.48	2.12	6	12
1:A:8:TRP:HB2	1:A:27:ASP:HB2	0.48	1.86	11	2
1:A:18:ASN:OD1	1:A:18:ASN:N	0.48	2.41	10	1
1:A:77:ALA:HB3	1:A:90:ALA:CA	0.47	2.39	6	14
1:A:17:PRO:O	1:A:18:ASN:C	0.47	2.53	3	9
1:A:68:CYS:O	1:A:69:SER:OG	0.47	2.33	15	7
1:A:56:TRP:O	1:A:75:ASP:OD2	0.47	2.31	20	8
1:A:43:ARG:CD	1:A:43:ARG:O	0.47	2.62	16	5
1:A:6:TYR:CB	1:A:6:TYR:CD2	0.47	2.78	15	3
1:A:56:TRP:O	1:A:57:ASP:CB	0.47	2.63	3	16
1:A:51:GLY:CA	1:A:91:GLY:N	0.47	2.78	19	3
1:A:67:ARG:O	1:A:73:GLN:CB	0.47	2.62	5	5
1:A:53:THR:OG1	1:A:77:ALA:CA	0.47	2.63	6	1
1:A:78:ARG:HB3	1:A:85:PHE:O	0.47	2.09	7	2

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:78:ARG:NH1	1:A:89:THR:CA	0.47	2.78	4	2
1:A:18:ASN:O	1:A:19:ARG:HB2	0.47	2.10	10	9
1:A:1:GLY:CA	1:A:30:ARG:HB2	0.47	2.39	16	1
1:A:32:CYS:N	1:A:35:SER:C	0.47	2.68	18	12
1:A:73:GLN:O	1:A:74:CYS:CA	0.47	2.61	11	5
1:A:58:GLU:O	1:A:65:PRO:HB3	0.47	2.09	15	9
1:A:56:TRP:H	1:A:75:ASP:HA	0.47	1.69	15	6
1:A:22:ASN:O	1:A:23:ASN:O	0.47	2.33	10	4
1:A:59:ALA:O	1:A:67:ARG:HA	0.47	2.10	11	5
1:A:8:TRP:CZ2	1:A:22:ASN:ND2	0.46	2.83	17	1
1:A:22:ASN:CB	1:A:23:ASN:ND2	0.46	2.79	5	8
1:A:13:ASN:CB	1:A:17:PRO:O	0.46	2.63	4	11
1:A:1:GLY:CA	1:A:27:ASP:HA	0.46	2.41	4	4
1:A:71:SER:CA	1:A:80:CYS:SG	0.46	3.04	6	2
1:A:59:ALA:HA	1:A:65:PRO:HB2	0.46	1.88	5	8
1:A:43:ARG:O	1:A:43:ARG:CD	0.46	2.63	7	3
1:A:16:GLY:O	1:A:17:PRO:O	0.46	2.33	18	6
1:A:31:THR:CA	1:A:39:GLN:O	0.46	2.63	16	1
1:A:8:TRP:CA	1:A:27:ASP:HB3	0.46	2.40	7	6
1:A:45:PRO:HB3	1:A:77:ALA:HA	0.46	1.86	8	1
1:A:78:ARG:NH1	1:A:88:GLY:O	0.46	2.49	20	1
1:A:30:ARG:NH1	1:A:30:ARG:HG2	0.46	2.26	2	1
1:A:51:GLY:N	1:A:77:ALA:HB2	0.46	2.25	4	7
1:A:77:ALA:HB3	1:A:90:ALA:HA	0.46	1.87	17	10
1:A:56:TRP:HE1	1:A:59:ALA:HB2	0.46	1.70	7	5
1:A:1:GLY:HA2	1:A:29:ALA:H	0.46	1.70	8	5
1:A:23:ASN:HA	1:A:37:PHE:O	0.46	2.10	9	3
1:A:32:CYS:N	1:A:38:CYS:H	0.45	2.08	9	13
1:A:30:ARG:HG2	1:A:30:ARG:NH1	0.45	2.25	9	1
1:A:8:TRP:CB	1:A:27:ASP:CB	0.45	2.92	7	10
1:A:32:CYS:HA	1:A:38:CYS:CA	0.45	2.41	16	9
1:A:22:ASN:CB	1:A:23:ASN:OD1	0.45	2.64	12	4
1:A:86:CYS:O	1:A:87:GLN:CB	0.45	2.64	14	13
1:A:11:ALA:C	1:A:18:ASN:OD1	0.45	2.55	15	10
1:A:49:PRO:HB2	1:A:53:THR:HG23	0.45	1.88	6	1
1:A:75:ASP:OD1	1:A:90:ALA:HB2	0.45	2.11	8	2
1:A:67:ARG:HG3	1:A:67:ARG:HH11	0.45	1.72	11	1
1:A:74:CYS:SG	1:A:86:CYS:CB	0.45	3.04	1	4
1:A:74:CYS:HB2	1:A:85:PHE:CA	0.45	2.42	11	4
1:A:87:GLN:C	1:A:87:GLN:CD	0.45	2.75	2	7
1:A:53:THR:OG1	1:A:77:ALA:HB2	0.45	2.11	6	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:24:LYS:O	1:A:30:ARG:NH2	0.45	2.48	10	1
1:A:4:PRO:O	1:A:52:PRO:O	0.45	2.35	18	3
1:A:56:TRP:CB	1:A:74:CYS:O	0.45	2.64	18	3
1:A:32:CYS:N	1:A:37:PHE:CA	0.45	2.80	13	10
1:A:32:CYS:H	1:A:36:GLY:N	0.45	2.10	15	14
1:A:23:ASN:CA	1:A:37:PHE:O	0.45	2.66	5	4
1:A:51:GLY:C	1:A:53:THR:N	0.45	2.65	8	3
1:A:31:THR:OG1	1:A:39:GLN:OE1	0.45	2.35	15	9
1:A:36:GLY:C	1:A:37:PHE:CD2	0.44	2.90	5	2
1:A:1:GLY:HA2	1:A:28:GLY:H	0.44	1.71	16	1
1:A:4:PRO:CB	1:A:53:THR:HG22	0.44	2.43	6	1
1:A:56:TRP:O	1:A:57:ASP:OD1	0.44	2.36	9	3
1:A:51:GLY:H	1:A:77:ALA:HB2	0.44	1.72	10	1
1:A:22:ASN:ND2	1:A:37:PHE:CD1	0.44	2.84	20	1
1:A:69:SER:CA	1:A:86:CYS:SG	0.44	3.05	4	2
1:A:53:THR:HG1	1:A:77:ALA:HA	0.44	1.72	6	1
1:A:78:ARG:NH1	1:A:89:THR:O	0.44	2.50	8	1
1:A:8:TRP:HE1	1:A:21:SER:N	0.44	2.11	7	1
1:A:1:GLY:H3	1:A:23:ASN:HB3	0.44	1.72	1	5
1:A:71:SER:CA	1:A:85:PHE:CD2	0.44	3.01	9	2
1:A:15:GLY:O	1:A:19:ARG:CZ	0.44	2.65	14	1
1:A:22:ASN:H	1:A:25:GLN:C	0.44	2.16	14	4
1:A:54:TYR:CD1	1:A:54:TYR:C	0.44	2.91	15	1
1:A:75:ASP:OD1	1:A:90:ALA:CB	0.44	2.66	10	2
1:A:87:GLN:CD	1:A:87:GLN:C	0.44	2.76	4	7
1:A:23:ASN:OD1	1:A:26:CYS:C	0.44	2.56	9	4
1:A:22:ASN:CG	1:A:23:ASN:HD21	0.44	2.15	14	1
1:A:16:GLY:C	1:A:17:PRO:O	0.44	2.56	4	7
1:A:19:ARG:O	1:A:21:SER:HB2	0.44	2.12	11	2
1:A:79:THR:CA	1:A:87:GLN:OE1	0.44	2.66	17	2
1:A:12:ASN:O	1:A:12:ASN:OD1	0.44	2.35	13	1
1:A:56:TRP:HE1	1:A:58:GLU:C	0.44	2.16	10	1
1:A:22:ASN:O	1:A:26:CYS:O	0.44	2.36	16	1
1:A:5:THR:HB	1:A:93:ALA:H	0.43	1.72	10	10
1:A:69:SER:OG	1:A:70:ASN:OD1	0.43	2.36	7	5
1:A:53:THR:H	1:A:92:HIS:N	0.43	2.11	13	2
1:A:22:ASN:H	1:A:25:GLN:CA	0.43	2.26	14	2
1:A:22:ASN:C	1:A:25:GLN:H	0.43	2.17	7	3
1:A:71:SER:CA	1:A:85:PHE:CD1	0.43	3.01	5	2
1:A:23:ASN:CB	1:A:26:CYS:O	0.43	2.66	18	1
1:A:60:LYS:HB3	1:A:86:CYS:SG	0.43	2.53	2	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:TRP:HB2	1:A:27:ASP:CA	0.43	2.42	18	9
1:A:4:PRO:HA	1:A:43:ARG:CB	0.43	2.43	6	4
1:A:53:THR:HG1	1:A:77:ALA:N	0.43	2.11	10	1
1:A:21:SER:C	1:A:22:ASN:HD22	0.43	2.16	17	1
1:A:30:ARG:HH11	1:A:42:SER:N	0.43	2.11	4	2
1:A:9:ASN:O	1:A:10:GLU:C	0.43	2.56	11	4
1:A:66:ASN:O	1:A:67:ARG:HB2	0.43	2.14	14	5
1:A:20:CYS:HA	1:A:25:GLN:O	0.43	2.13	17	5
1:A:54:TYR:CD2	1:A:75:ASP:CG	0.43	2.91	15	1
1:A:93:ALA:O	1:A:94:ALA:C	0.43	2.57	6	1
1:A:41:THR:O	1:A:41:THR:CG2	0.43	2.67	16	1
1:A:23:ASN:HB3	1:A:30:ARG:CB	0.43	2.43	16	1
1:A:21:SER:OG	1:A:21:SER:O	0.43	2.36	18	2
1:A:3:GLY:O	1:A:6:TYR:N	0.43	2.46	5	3
1:A:22:ASN:C	1:A:23:ASN:ND2	0.43	2.72	5	1
1:A:5:THR:OG1	1:A:5:THR:O	0.43	2.37	19	6
1:A:30:ARG:HG3	1:A:41:THR:N	0.43	2.29	18	2
1:A:32:CYS:H	1:A:36:GLY:C	0.43	2.17	16	2
1:A:21:SER:O	1:A:21:SER:OG	0.43	2.37	9	4
1:A:70:ASN:O	1:A:80:CYS:CB	0.43	2.67	15	3
1:A:56:TRP:CH2	1:A:66:ASN:OD1	0.42	2.72	3	2
1:A:23:ASN:O	1:A:30:ARG:CG	0.42	2.66	3	1
1:A:30:ARG:NH2	1:A:42:SER:OG	0.42	2.52	19	1
1:A:21:SER:C	1:A:22:ASN:ND2	0.42	2.72	17	1
1:A:5:THR:O	1:A:5:THR:OG1	0.42	2.37	11	4
1:A:23:ASN:ND2	1:A:37:PHE:HB2	0.42	2.29	14	4
1:A:54:TYR:C	1:A:54:TYR:CD1	0.42	2.93	11	2
1:A:66:ASN:OD1	1:A:73:GLN:NE2	0.42	2.51	14	1
1:A:65:PRO:O	1:A:66:ASN:C	0.42	2.57	2	4
1:A:11:ALA:N	1:A:17:PRO:HB3	0.42	2.30	4	1
1:A:5:THR:O	1:A:6:TYR:C	0.42	2.57	2	7
1:A:23:ASN:HD22	1:A:23:ASN:N	0.42	2.13	5	1
1:A:73:GLN:CA	1:A:73:GLN:OE1	0.42	2.67	5	1
1:A:32:CYS:N	1:A:38:CYS:N	0.42	2.67	9	2
1:A:23:ASN:O	1:A:25:GLN:N	0.42	2.52	16	2
1:A:1:GLY:HA3	1:A:30:ARG:CA	0.42	2.45	14	1
1:A:10:GLU:OE1	1:A:85:PHE:CE1	0.42	2.72	20	2
1:A:33:SER:N	1:A:38:CYS:SG	0.42	2.92	18	1
1:A:71:SER:C	1:A:85:PHE:CG	0.42	2.93	13	1
1:A:78:ARG:NH1	1:A:89:THR:C	0.42	2.73	4	1
1:A:73:GLN:OE1	1:A:73:GLN:CA	0.42	2.68	14	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:8:TRP:HB2	1:A:27:ASP:H	0.42	1.72	15	3
1:A:35:SER:O	1:A:36:GLY:C	0.42	2.58	7	3
1:A:53:THR:N	1:A:92:HIS:CA	0.42	2.83	4	2
1:A:23:ASN:OD1	1:A:27:ASP:CG	0.42	2.58	5	2
1:A:56:TRP:HB2	1:A:74:CYS:O	0.42	2.15	7	3
1:A:24:LYS:HB2	1:A:30:ARG:NE	0.41	2.30	20	1
1:A:89:THR:HG22	1:A:90:ALA:C	0.41	2.36	14	1
1:A:24:LYS:CB	1:A:30:ARG:NH1	0.41	2.84	16	1
1:A:76:GLY:C	1:A:78:ARG:H	0.41	2.13	7	1
1:A:37:PHE:O	1:A:37:PHE:CD1	0.41	2.74	20	1
1:A:23:ASN:C	1:A:30:ARG:HG2	0.41	2.35	16	1
1:A:43:ARG:O	1:A:43:ARG:HD2	0.41	2.15	13	1
1:A:56:TRP:CE2	1:A:66:ASN:OD1	0.41	2.73	10	1
1:A:23:ASN:N	1:A:37:PHE:O	0.41	2.54	14	1
1:A:51:GLY:C	1:A:91:GLY:HA3	0.41	2.36	18	1
1:A:89:THR:HG23	1:A:90:ALA:N	0.41	2.30	18	2
1:A:65:PRO:O	1:A:67:ARG:HG2	0.41	2.15	2	1
1:A:67:ARG:NH1	1:A:67:ARG:HG3	0.41	2.31	4	1
1:A:78:ARG:HH11	1:A:89:THR:C	0.41	2.19	4	1
1:A:67:ARG:HG3	1:A:67:ARG:NH1	0.41	2.31	9	1
1:A:42:SER:C	1:A:44:LYS:N	0.41	2.74	11	1
1:A:50:LYS:NZ	1:A:77:ALA:O	0.41	2.50	17	1
1:A:30:ARG:CD	1:A:41:THR:C	0.41	2.89	18	1
1:A:31:THR:OG1	1:A:39:GLN:HG3	0.41	2.15	4	4
1:A:51:GLY:O	1:A:91:GLY:C	0.41	2.59	10	2
1:A:32:CYS:HB2	1:A:37:PHE:C	0.41	2.36	16	1
1:A:74:CYS:HB2	1:A:85:PHE:CB	0.41	2.46	19	1
1:A:31:THR:C	1:A:38:CYS:N	0.41	2.70	9	1
1:A:12:ASN:OD1	1:A:12:ASN:O	0.41	2.39	14	1
1:A:46:ASP:OD1	1:A:48:GLY:N	0.41	2.54	14	1
1:A:89:THR:HG22	1:A:90:ALA:O	0.41	2.15	14	1
1:A:22:ASN:N	1:A:25:GLN:CA	0.41	2.82	20	1
1:A:38:CYS:SG	1:A:38:CYS:O	0.41	2.79	7	1
1:A:80:CYS:SG	1:A:85:PHE:HB3	0.41	2.56	3	2
1:A:6:TYR:O	1:A:7:CYS:HB3	0.41	2.15	4	1
1:A:54:TYR:CA	1:A:76:GLY:HA3	0.41	2.45	20	1
1:A:46:ASP:C	1:A:46:ASP:OD1	0.40	2.59	14	1
1:A:43:ARG:HE	1:A:53:THR:HB	0.40	1.76	18	1
1:A:53:THR:HG1	1:A:77:ALA:CA	0.40	2.30	6	1
1:A:43:ARG:NE	1:A:53:THR:CB	0.40	2.83	8	1
1:A:11:ALA:N	1:A:18:ASN:H	0.40	2.14	11	1

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Clash(Å)	Distance(Å)	Models	
				Worst	Total
1:A:72:LYS:HA	1:A:85:PHE:CE2	0.40	2.52	11	1
1:A:30:ARG:HE	1:A:41:THR:CA	0.40	2.29	16	1
1:A:8:TRP:HB2	1:A:27:ASP:HB3	0.40	1.92	1	1
1:A:16:GLY:N	1:A:19:ARG:HD3	0.40	2.31	2	1
1:A:55:CYS:H	1:A:75:ASP:C	0.40	2.19	18	1
1:A:91:GLY:O	1:A:92:HIS:CG	0.40	2.75	14	1
1:A:38:CYS:O	1:A:38:CYS:SG	0.40	2.79	4	1
1:A:32:CYS:O	1:A:39:GLN:CG	0.40	2.69	19	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	84/95 (88%)	24±2 (29±2%)	25±2 (29±3%)	35±2 (42±2%)	0	0
All	All	1680/1900 (88%)	488 (29%)	491 (29%)	701 (42%)	0	0

All 47 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	18	ASN	20
1	A	20	CYS	20
1	A	90	ALA	20
1	A	6	TYR	20
1	A	54	TYR	20
1	A	52	PRO	20
1	A	5	THR	20
1	A	17	PRO	20
1	A	30	ARG	20
1	A	58	GLU	20
1	A	37	PHE	20
1	A	38	CYS	20
1	A	87	GLN	20
1	A	92	HIS	20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	48	GLY	20
1	A	71	SER	20
1	A	4	PRO	20
1	A	45	PRO	20
1	A	29	ALA	20
1	A	88	GLY	20
1	A	80	CYS	20
1	A	12	ASN	20
1	A	73	GLN	20
1	A	57	ASP	20
1	A	49	PRO	20
1	A	91	GLY	19
1	A	66	ASN	16
1	A	19	ARG	16
1	A	67	ARG	15
1	A	27	ASP	14
1	A	69	SER	13
1	A	14	PRO	13
1	A	43	ARG	13
1	A	9	ASN	13
1	A	68	CYS	11
1	A	72	LYS	9
1	A	25	GLN	8
1	A	76	GLY	8
1	A	77	ALA	7
1	A	8	TRP	6
1	A	47	PRO	6
1	A	11	ALA	5
1	A	44	LYS	3
1	A	65	PRO	2
1	A	23	ASN	2
1	A	15	GLY	1
1	A	85	PHE	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	67/72 (93%)	45±2 (68±3%)	22±2 (32±3%)	1	12
All	All	1340/1440 (93%)	906 (68%)	434 (32%)	1	12

All 38 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	18	ASN	20
1	A	54	TYR	20
1	A	5	THR	20
1	A	50	LYS	20
1	A	43	ARG	20
1	A	66	ASN	20
1	A	41	THR	20
1	A	13	ASN	20
1	A	39	GLN	20
1	A	23	ASN	20
1	A	53	THR	19
1	A	46	ASP	18
1	A	30	ARG	17
1	A	19	ARG	17
1	A	42	SER	16
1	A	89	THR	16
1	A	80	CYS	15
1	A	25	GLN	14
1	A	87	GLN	13
1	A	21	SER	11
1	A	85	PHE	10
1	A	55	CYS	9
1	A	38	CYS	9
1	A	60	LYS	8
1	A	68	CYS	5
1	A	12	ASN	5
1	A	2	SER	4
1	A	75	ASP	4
1	A	56	TRP	4
1	A	72	LYS	4
1	A	22	ASN	3
1	A	69	SER	2
1	A	14	PRO	2
1	A	79	THR	2
1	A	71	SER	2
1	A	73	GLN	2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Models (Total)
1	A	57	ASP	2
1	A	49	PRO	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](#)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
1	12-A	4
1	3-A	3
1	18-A	3
1	16-A	3
1	4-A	3
1	1-A	3
1	14-A	3
1	10-A	3
1	7-A	3
1	17-A	2

Continued on next page...

Continued from previous page...

Mol	Chain	Number of breaks
1	13-A	2
1	6-A	2
1	2-A	2
1	20-A	2
1	11-A	1
1	9-A	1
1	19-A	1
1	5-A	1
1	8-A	1
1	15-A	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	A	80:CYS	C	81:SER	N	1.20
3	A	9:ASN	C	10:GLU	N	1.20
4	A	33:SER	C	34:SER	N	1.20
7	A	53:THR	C	54:TYR	N	1.20
7	A	72:LYS	C	73:GLN	N	1.20
10	A	9:ASN	C	10:GLU	N	1.20
12	A	9:ASN	C	10:GLU	N	1.20
12	A	15:GLY	C	16:GLY	N	1.20
13	A	33:SER	C	34:SER	N	1.20
14	A	33:SER	C	34:SER	N	1.20
14	A	80:CYS	C	81:SER	N	1.20
16	A	9:ASN	C	10:GLU	N	1.20
18	A	72:LYS	C	73:GLN	N	1.20
20	A	9:ASN	C	10:GLU	N	1.20
2	A	15:GLY	C	16:GLY	N	1.19
4	A	15:GLY	C	16:GLY	N	1.19
6	A	15:GLY	C	16:GLY	N	1.19
7	A	15:GLY	C	16:GLY	N	1.19
10	A	33:SER	C	34:SER	N	1.19
11	A	15:GLY	C	16:GLY	N	1.19
12	A	33:SER	C	34:SER	N	1.19
15	A	72:LYS	C	73:GLN	N	1.19
16	A	33:SER	C	34:SER	N	1.19
17	A	33:SER	C	34:SER	N	1.19
18	A	26:CYS	C	27:ASP	N	1.19
19	A	72:LYS	C	73:GLN	N	1.19
1	A	15:GLY	C	16:GLY	N	1.18
3	A	15:GLY	C	16:GLY	N	1.18
6	A	72:LYS	C	73:GLN	N	1.18

Continued on next page...

Continued from previous page...

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
18	A	15:GLY	C	16:GLY	N	1.18
3	A	72:LYS	C	73:GLN	N	1.15
14	A	72:LYS	C	73:GLN	N	1.15
4	A	72:LYS	C	73:GLN	N	1.14
10	A	72:LYS	C	73:GLN	N	1.14
16	A	72:LYS	C	73:GLN	N	1.14
17	A	72:LYS	C	73:GLN	N	1.14
20	A	72:LYS	C	73:GLN	N	1.14
1	A	72:LYS	C	73:GLN	N	1.13
5	A	72:LYS	C	73:GLN	N	1.13
8	A	72:LYS	C	73:GLN	N	1.13
9	A	72:LYS	C	73:GLN	N	1.13
12	A	72:LYS	C	73:GLN	N	1.13
13	A	72:LYS	C	73:GLN	N	1.13
2	A	72:LYS	C	73:GLN	N	1.12

7 Chemical shift validation

No chemical shift data were provided