



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 1, 2020 – 04:08 PM EDT

PDB ID : 6V6H
Title : Crystal structure of histidine ammonia-lyase from Trypanosoma cruzi
Authors : Miranda, R.R.; Silva, M.; Barison, M.J.; Silber, A.M.; Iulek, J.
Deposited on : 2019-12-05
Resolution : 2.55 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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/XrayValidationReportHelp>

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
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.10.1
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.10.1

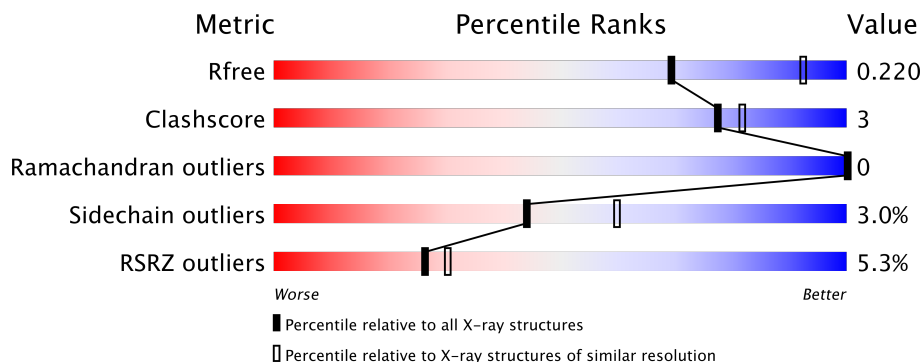
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 Å.

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)	Similar resolution (#Entries, resolution range(Å))
R_{free}	111664	1053 (2.56-2.52)
Clashscore	122126	1098 (2.56-2.52)
Ramachandran outliers	120053	1088 (2.56-2.52)
Sidechain outliers	120020	1088 (2.56-2.52)
RSRZ outliers	108989	1043 (2.56-2.52)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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 $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	538	<div> <div>4%</div> <div> <div></div> <div>86%</div> <div>7%</div> <div>5%</div> </div> </div>
1	B	538	<div> <div>5%</div> <div> <div></div> <div>87%</div> <div>6%</div> <div>6%</div> </div> </div>
1	C	538	<div> <div>5%</div> <div> <div></div> <div>86%</div> <div>8%</div> <div>5%</div> </div> </div>
1	D	538	<div> <div>6%</div> <div> <div></div> <div>85%</div> <div>7%</div> <div>6%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 15683 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called Histidine ammonia-lyase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	510	Total	C	N	O	S	0	1	1
			3782	2398	673	693	18			
1	B	505	Total	C	N	O	S	0	0	1
			3728	2367	663	680	18			
1	C	509	Total	C	N	O	S	0	2	0
			3779	2394	676	691	18			
1	D	505	Total	C	N	O	S	8	2	0
			3742	2385	661	680	16			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-5	HIS	-	expression tag	UNP Q4E133
A	-4	HIS	-	expression tag	UNP Q4E133
A	-3	HIS	-	expression tag	UNP Q4E133
A	-2	HIS	-	expression tag	UNP Q4E133
A	-1	HIS	-	expression tag	UNP Q4E133
A	0	HIS	-	expression tag	UNP Q4E133
A	124	LEU	VAL	conflict	UNP Q4E133
A	143	MDO	ALA	chromophore	UNP Q4E133
A	143	MDO	SER	chromophore	UNP Q4E133
A	143	MDO	GLY	chromophore	UNP Q4E133
B	-5	HIS	-	expression tag	UNP Q4E133
B	-4	HIS	-	expression tag	UNP Q4E133
B	-3	HIS	-	expression tag	UNP Q4E133
B	-2	HIS	-	expression tag	UNP Q4E133
B	-1	HIS	-	expression tag	UNP Q4E133
B	0	HIS	-	expression tag	UNP Q4E133
B	124	LEU	VAL	conflict	UNP Q4E133
B	143	MDO	ALA	chromophore	UNP Q4E133
B	143	MDO	SER	chromophore	UNP Q4E133
B	143	MDO	GLY	chromophore	UNP Q4E133
C	-5	HIS	-	expression tag	UNP Q4E133

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
C	-4	HIS	-	expression tag	UNP Q4E133
C	-3	HIS	-	expression tag	UNP Q4E133
C	-2	HIS	-	expression tag	UNP Q4E133
C	-1	HIS	-	expression tag	UNP Q4E133
C	0	HIS	-	expression tag	UNP Q4E133
C	124	LEU	VAL	conflict	UNP Q4E133
C	143	MDO	ALA	chromophore	UNP Q4E133
C	143	MDO	SER	chromophore	UNP Q4E133
C	143	MDO	GLY	chromophore	UNP Q4E133
D	-5	HIS	-	expression tag	UNP Q4E133
D	-4	HIS	-	expression tag	UNP Q4E133
D	-3	HIS	-	expression tag	UNP Q4E133
D	-2	HIS	-	expression tag	UNP Q4E133
D	-1	HIS	-	expression tag	UNP Q4E133
D	0	HIS	-	expression tag	UNP Q4E133
D	124	LEU	VAL	conflict	UNP Q4E133
D	143	MDO	ALA	chromophore	UNP Q4E133
D	143	MDO	SER	chromophore	UNP Q4E133
D	143	MDO	GLY	chromophore	UNP Q4E133

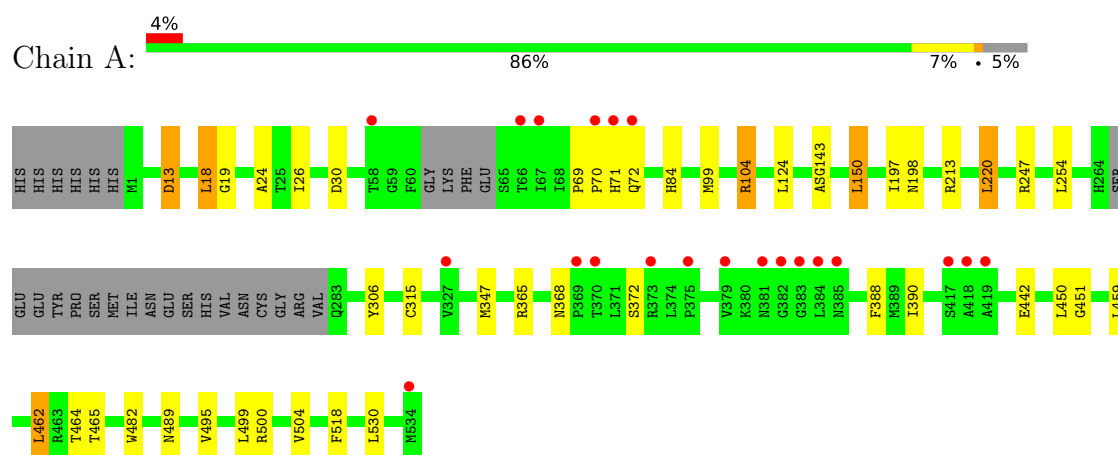
- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	180	Total O 180 180	0	0
2	B	148	Total O 148 148	0	0
2	C	178	Total O 178 178	0	0
2	D	146	Total O 146 146	0	0

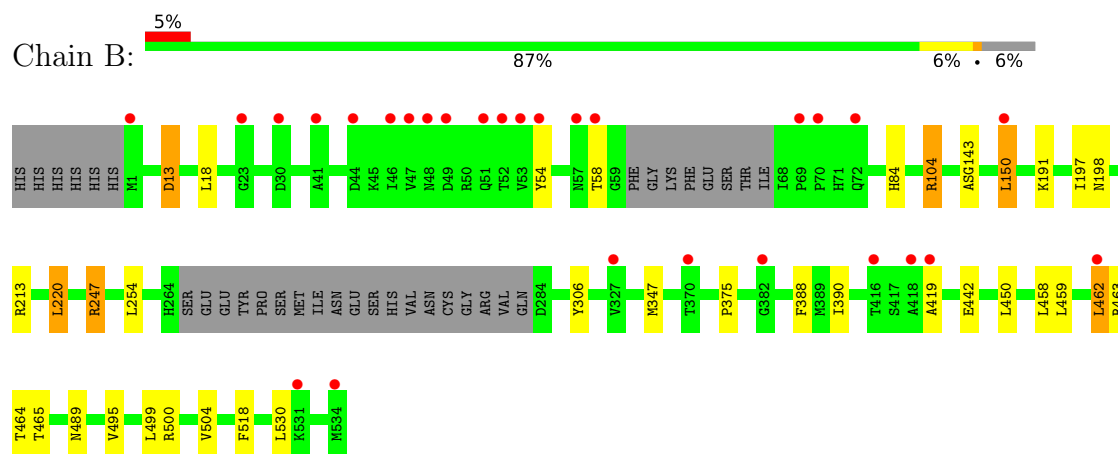
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-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. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

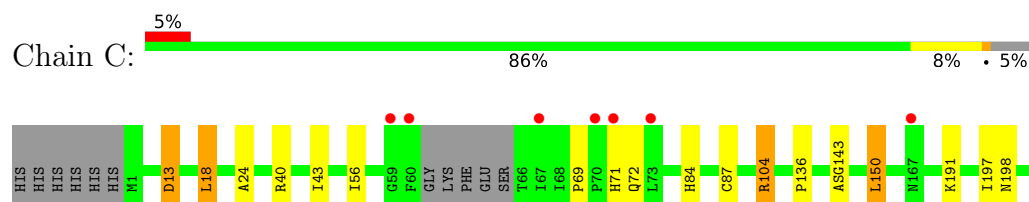
• Molecule 1: Histidine ammonia-lyase

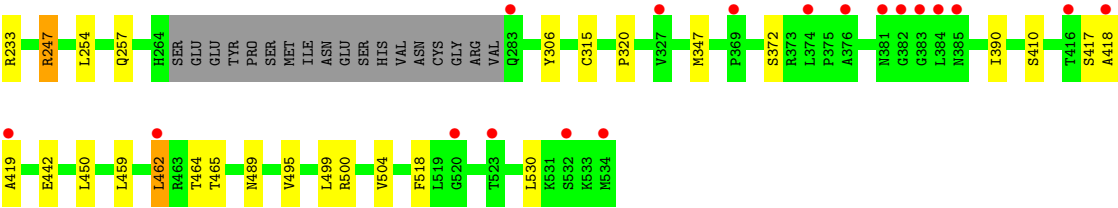


• Molecule 1: Histidine ammonia-lyase

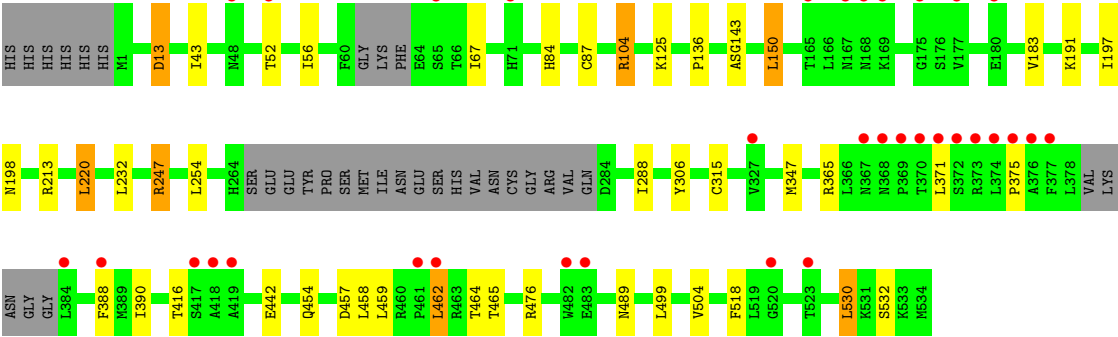
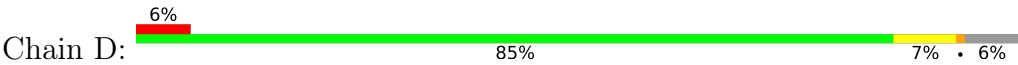


• Molecule 1: Histidine ammonia-lyase





● Molecule 1: Histidine ammonia-lyase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	87.81Å 144.56Å 173.76Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	32.31 – 2.55 32.31 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.4 (32.31-2.55) 99.4 (32.31-2.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.95 (at 2.54Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.179 , 0.217 0.183 , 0.220	Depositor DCC
R_{free} test set	2004 reflections (2.77%)	wwPDB-VP
Wilson B-factor (Å ²)	30.0	Xtriage
Anisotropy	0.301	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 56.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	15683	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.64% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MDO, CSS

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 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	0.23	0/3826	0.41	0/5204
1	B	0.23	0/3767	0.41	0/5123
1	C	0.23	0/3826	0.41	0/5204
1	D	0.23	0/3792	0.40	0/5158
All	All	0.23	0/15211	0.41	0/20689

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 outliers	#Planarity outliers
1	A	0	2
1	B	0	2
1	C	0	2
1	D	0	2
All	All	0	8

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

5 of 8 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	143	MDO	Mainchain,Peptide
1	B	143	MDO	Mainchain,Peptide
1	C	143	MDO	Mainchain,Peptide
1	D	143	MDO	Mainchain,Peptide

5.2 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 the 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 within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3782	0	3777	25	0
1	B	3728	0	3733	23	0
1	C	3779	0	3777	31	0
1	D	3742	0	3728	31	0
2	A	180	0	0	1	1
2	B	148	0	0	2	0
2	C	178	0	0	2	1
2	D	146	0	0	1	0
All	All	15683	0	15015	96	1

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 3.

The worst 5 of 96 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:365:ARG:NH1	1:B:419:ALA:O	2.21	0.73
1:C:347:MET:HG2	1:D:347:MET:HG2	1.72	0.71
1:C:233[A]:ARG:NH1	1:C:372:SER:O	2.25	0.69
1:A:500:ARG:NH2	2:A:601:HOH:O	2.26	0.67
1:B:104:ARG:NH2	1:B:198:ASN:O	2.29	0.66

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:765:HOH:O	2:C:627:HOH:O[4_566]	2.19	0.01

5.3 Torsion angles [i](#)

5.3.1 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 X-ray entries followed by that with respect to entries of similar resolution.

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	503/538 (94%)	493 (98%)	10 (2%)	0	100	100
1	B	497/538 (92%)	482 (97%)	15 (3%)	0	100	100
1	C	503/538 (94%)	489 (97%)	14 (3%)	0	100	100
1	D	497/538 (92%)	485 (98%)	12 (2%)	0	100	100
All	All	2000/2152 (93%)	1949 (98%)	51 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 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 X-ray entries followed by that with respect to entries of similar resolution.

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	382/445 (86%)	370 (97%)	12 (3%)	43	59
1	B	374/445 (84%)	363 (97%)	11 (3%)	45	61
1	C	381/445 (86%)	370 (97%)	11 (3%)	45	61
1	D	373/445 (84%)	362 (97%)	11 (3%)	45	61
All	All	1510/1780 (85%)	1465 (97%)	45 (3%)	44	60

5 of 45 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	489	ASN
1	C	104	ARG
1	D	462	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	530	LEU
1	C	150	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	229	HIS
1	B	494	ASN
1	C	494	ASN
1	B	198	ASN
1	C	229	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

8 non-standard protein/DNA/RNA residues are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. 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 $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
1	MDO	B	143	1	12,13,14	3.84	3 (25%)	15,18,20	6.74	7 (46%)
1	CSS	D	393	1	4,6,7	1.20	0	1,6,8	0.72	0
1	CSS	A	393	1	4,6,7	1.22	1 (25%)	1,6,8	0.69	0
1	CSS	C	393	1	4,6,7	1.12	0	1,6,8	1.24	0
1	CSS	B	393	1	4,6,7	1.10	0	1,6,8	0.92	0
1	MDO	C	143	1	12,13,14	3.83	4 (33%)	15,18,20	6.48	7 (46%)
1	MDO	A	143	1	12,13,14	3.85	4 (33%)	15,18,20	6.41	7 (46%)
1	MDO	D	143	1	12,13,14	3.81	3 (25%)	15,18,20	6.61	6 (40%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral

centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MDO	B	143	1	-	2/4/23/24	0/1/1/1
1	CSS	D	393	1	-	1/1/5/7	-
1	CSS	A	393	1	-	1/1/5/7	-
1	CSS	C	393	1	-	1/1/5/7	-
1	CSS	B	393	1	-	1/1/5/7	-
1	MDO	C	143	1	-	2/4/23/24	0/1/1/1
1	MDO	A	143	1	-	2/4/23/24	0/1/1/1
1	MDO	D	143	1	-	2/4/23/24	0/1/1/1

The worst 5 of 15 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	143	MDO	O2-C2	11.93	1.48	1.23
1	B	143	MDO	O2-C2	11.91	1.48	1.23
1	C	143	MDO	O2-C2	11.89	1.48	1.23
1	D	143	MDO	O2-C2	11.71	1.47	1.23
1	D	143	MDO	C1-N2	3.94	1.38	1.32

The worst 5 of 27 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	143	MDO	CA2-C2-N3	18.49	112.11	103.37
1	D	143	MDO	CA2-C2-N3	18.48	112.11	103.37
1	C	143	MDO	CA2-C2-N3	18.11	111.93	103.37
1	A	143	MDO	CA2-C2-N3	18.04	111.90	103.37
1	B	143	MDO	O2-C2-CA2	-12.59	123.89	130.96

There are no chirality outliers.

5 of 12 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	D	393	CSS	N-CA-CB-SG
1	A	393	CSS	N-CA-CB-SG
1	C	393	CSS	N-CA-CB-SG
1	B	393	CSS	N-CA-CB-SG
1	B	143	MDO	N2-C1-CA-CB

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	508/538 (94%)	-0.13	21 (4%) 37 43	16, 27, 71, 119	0
1	B	503/538 (93%)	0.00	28 (5%) 24 28	20, 33, 62, 135	0
1	C	507/538 (94%)	-0.15	25 (4%) 29 34	17, 28, 61, 109	0
1	D	503/538 (93%)	0.06	34 (6%) 17 20	18, 32, 68, 119	0
All	All	2021/2152 (93%)	-0.05	108 (5%) 26 30	16, 30, 65, 135	0

The worst 5 of 108 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	382	GLY	6.6
1	A	418	ALA	5.7
1	C	416	THR	4.9
1	A	381	ASN	4.6
1	D	374	LEU	4.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q < 0.9’ lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
1	CSS	D	393	7/8	0.88	0.18	36,40,59,95	0
1	CSS	B	393	7/8	0.89	0.16	24,26,41,79	0
1	CSS	A	393	7/8	0.91	0.16	27,29,59,62	0
1	MDO	D	143	13/14	0.93	0.19	22,26,32,33	0
1	CSS	C	393	7/8	0.94	0.17	26,28,53,64	0
1	MDO	C	143	13/14	0.95	0.20	22,31,36,37	0
1	MDO	B	143	13/14	0.95	0.17	30,31,37,46	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
1	MDO	A	143	13/14	0.96	0.22	15,24,33,34	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.