



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 8, 2026 – 01:27 PM UTC

PDB ID : 6YMT / pdb_00006ymt
Title : RNASE 3/1 version1
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Deposited on : 2020-04-09
Resolution : 1.58 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 types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

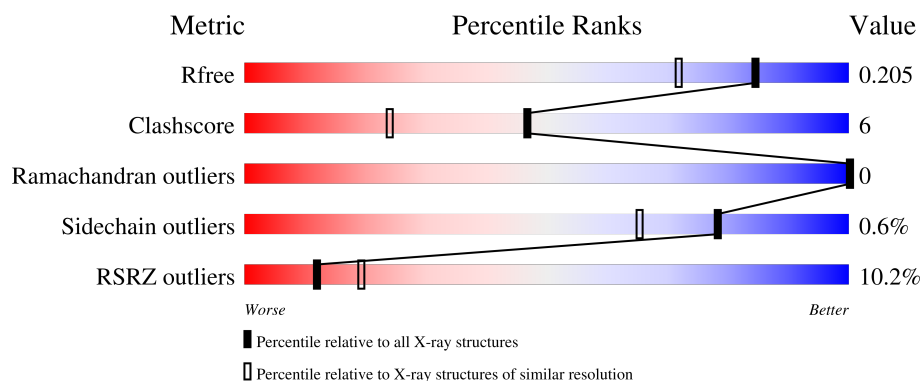
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.58 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}	180053	1094 (1.58-1.58)
Clashscore	190562	1105 (1.58-1.58)
Ramachandran outliers	187476	1082 (1.58-1.58)
Sidechain outliers	187428	1081 (1.58-1.58)
RSRZ outliers	180081	1094 (1.58-1.58)

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 of 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	128	5% 89% 10% .
1	B	128	11% 85% 15% .
1	C	128	9% 88% 11% .
1	D	128	16% 93% 5% ..
1	E	128	10% 87% 12% .

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Mol	Chain	Length	Quality of chain
1	F	128	
1	G	128	
1	H	128	
1	I	128	
1	J	128	
1	K	128	
1	L	128	

2 Entry composition

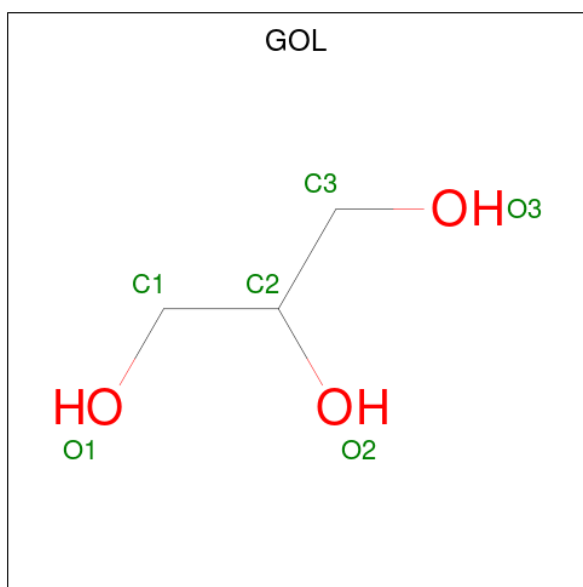
There are 3 unique types of molecules in this entry. The entry contains 14833 atoms, of which 8 are hydrogens and 0 are deuteriums.

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 RNase 3/1 version 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	G	125	Total	C	N	O	S	0	6	0
			1080	669	213	185	13			
1	J	126	Total	C	N	O	S	0	4	0
			1061	658	206	185	12			
1	C	126	Total	C	N	O	S	0	10	0
			1119	693	222	192	12			
1	D	126	Total	C	N	O	S	0	1	0
			1037	643	202	181	11			
1	E	126	Total	C	N	O	S	0	3	0
			1053	652	205	184	12			
1	F	125	Total	C	N	O	S	0	3	0
			1053	656	205	182	10			
1	A	128	Total	C	N	O	S	0	5	0
			1082	671	210	190	11			
1	H	125	Total	C	N	O	S	0	5	0
			1073	668	208	186	11			
1	I	128	Total	C	N	O	S	0	7	0
			1103	681	218	193	11			
1	B	128	Total	C	N	O	S	0	6	0
			1097	680	213	193	11			
1	L	125	Total	C	N	O	S	0	2	0
			1043	648	204	180	11			
1	K	126	Total	C	N	O	S	0	3	0
			1055	657	205	182	11			

- Molecule 2 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			14	3	8	3		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	G	179	Total	O	0	0
			179	179		
3	J	157	Total	O	0	0
			157	157		
3	C	146	Total	O	0	0
			146	146		
3	D	154	Total	O	0	0
			154	154		
3	E	167	Total	O	0	0
			167	167		
3	F	151	Total	O	0	0
			151	151		
3	A	182	Total	O	0	0
			182	182		
3	H	163	Total	O	0	0
			163	163		
3	I	173	Total	O	0	0
			173	173		
3	B	171	Total	O	0	0
			171	171		
3	L	143	Total	O	0	0
			143	143		

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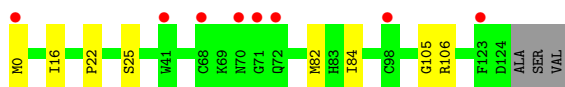
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	K	177	Total	O	0	0
			177	177		

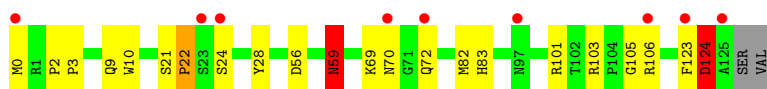
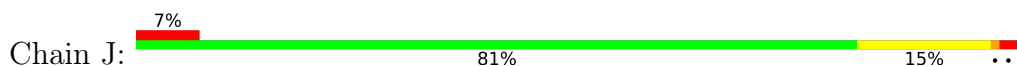
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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.

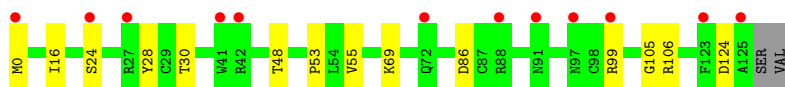
- Molecule 1: RNase 3/1 version 1



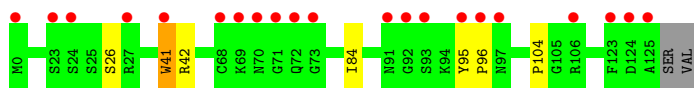
- Molecule 1: RNase 3/1 version 1



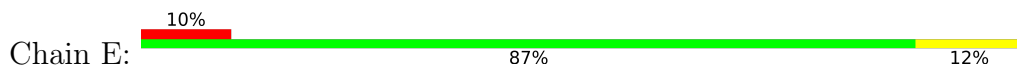
- Molecule 1: RNase 3/1 version 1



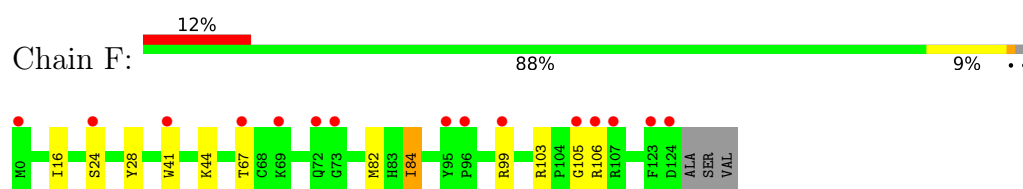
- Molecule 1: RNase 3/1 version 1



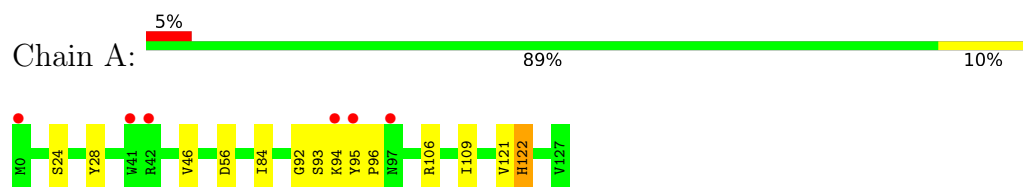
- Molecule 1: RNase 3/1 version 1



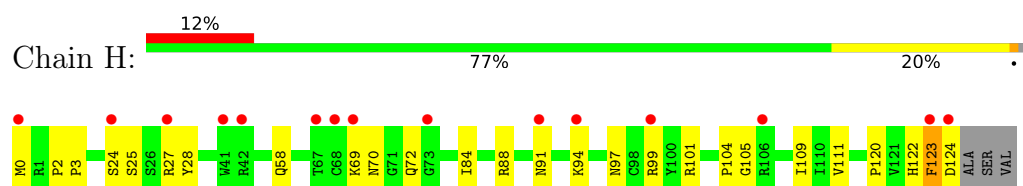
- Molecule 1: RNase 3/1 version 1



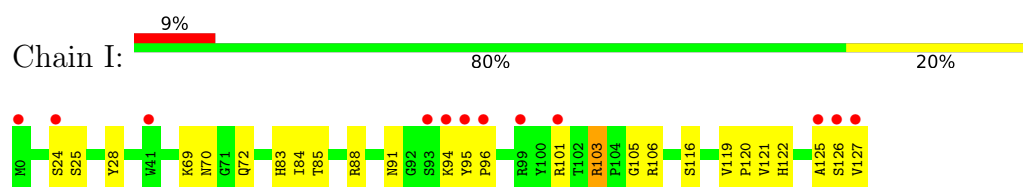
- Molecule 1: RNase 3/1 version 1



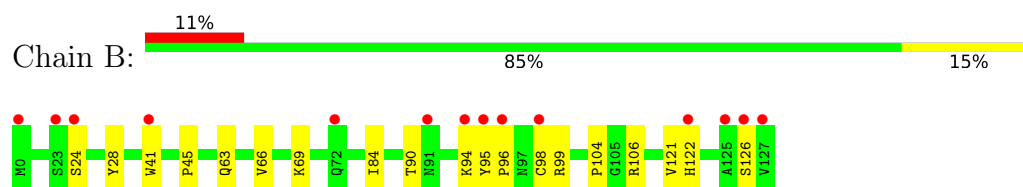
- Molecule 1: RNase 3/1 version 1



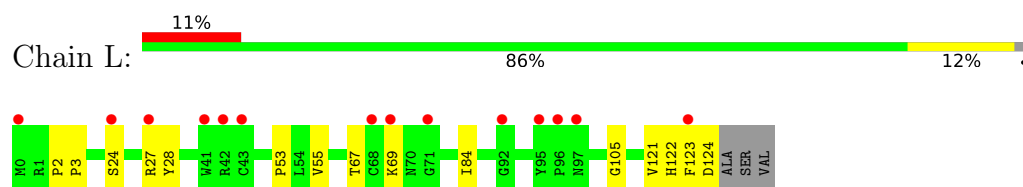
- Molecule 1: RNase 3/1 version 1



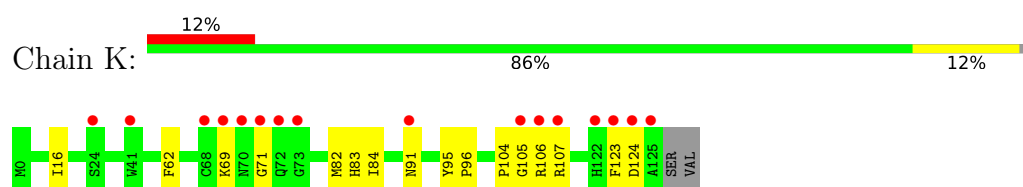
- Molecule 1: RNase 3/1 version 1



- Molecule 1: RNase 3/1 version 1



- Molecule 1: RNase 3/1 version 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	106.84Å 115.68Å 284.74Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.19 – 1.58 71.19 – 1.58	Depositor EDS
% Data completeness (in resolution range)	99.9 (71.19-1.58) 95.4 (71.19-1.58)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 1.56Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660, PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.178 , 0.203 0.180 , 0.205	Depositor DCC
R_{free} test set	11869 reflections (4.80%)	wwPDB-VP
Wilson B-factor (Å ²)	19.6	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.7	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	0.96	EDS
Total number of atoms	14833	wwPDB-VP
Average B, all atoms (Å ²)	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.46% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.55	1/1112 (0.1%)	0.64	0/1506
1	B	0.69	4/1127 (0.4%)	0.68	2/1524 (0.1%)
1	C	0.37	1/1149 (0.1%)	0.54	0/1554
1	D	0.60	4/1066 (0.4%)	0.68	0/1443
1	E	0.59	1/1082 (0.1%)	0.69	0/1464
1	F	0.70	2/1084 (0.2%)	0.71	0/1470
1	G	0.53	2/1109 (0.2%)	0.59	0/1498
1	H	0.77	4/1102 (0.4%)	0.70	0/1492
1	I	0.78	7/1133 (0.6%)	0.76	1/1534 (0.1%)
1	J	0.79	8/1090 (0.7%)	0.74	2/1475 (0.1%)
1	K	0.40	0/1084	0.72	6/1467 (0.4%)
1	L	0.69	3/1073 (0.3%)	0.70	0/1453
All	All	0.64	37/13211 (0.3%)	0.68	11/17880 (0.1%)

The worst 5 of 37 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	106	ARG	C-N	-9.98	1.21	1.33
1	L	2	PRO	C-O	-9.04	1.14	1.24
1	L	105	GLY	C-O	-7.64	1.16	1.23
1	J	2	PRO	C-O	-7.62	1.16	1.24
1	H	105	GLY	C-O	-7.61	1.16	1.23

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	K	123	PHE	CA-C-N	6.19	133.43	121.18
1	K	123	PHE	C-N-CA	6.19	133.43	121.18
1	K	124	ASP	CA-CB-CG	5.92	118.52	112.60
1	K	124	ASP	CA-C-N	5.53	131.65	121.70
1	K	124	ASP	C-N-CA	5.53	131.65	121.70

There are no chirality outliers.

There are no planarity outliers.

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	1082	0	1040	10	0
1	B	1097	0	1054	12	0
1	C	1119	0	1079	9	0
1	D	1037	0	996	10	0
1	E	1053	0	1009	12	0
1	F	1053	0	1004	9	0
1	G	1080	0	1044	5	0
1	H	1073	0	1040	16	0
1	I	1103	0	1060	27	0
1	J	1061	0	1019	20	0
1	K	1055	0	1022	17	0
1	L	1043	0	1001	15	0
2	A	6	8	8	1	0
3	A	182	0	0	2	0
3	B	171	0	0	1	0
3	C	146	0	0	4	0
3	D	154	0	0	1	0
3	E	167	0	0	4	0
3	F	151	0	0	1	0
3	G	179	0	0	1	0
3	H	163	0	0	2	0
3	I	173	0	0	2	0
3	J	157	0	0	1	0
3	K	177	0	0	5	0
3	L	143	0	0	1	0
All	All	14825	8	12376	143	0

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 6.

The worst 5 of 143 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:J:83:HIS:CD2	1:J:106:ARG:HD3	1.91	1.05
1:J:83:HIS:CD2	1:J:106:ARG:CD	2.50	0.94
1:J:0:MET:HE3	1:F:67:THR:HB	1.58	0.85
1:I:94:LYS:HE3	1:B:41:TRP:HE1	1.43	0.82
1:D:41:TRP:HB2	1:L:27:ARG:HD3	1.59	0.82

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 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 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	131/128 (102%)	129 (98%)	2 (2%)	0	100	100
1	B	132/128 (103%)	128 (97%)	4 (3%)	0	100	100
1	C	134/128 (105%)	130 (97%)	4 (3%)	0	100	100
1	D	125/128 (98%)	121 (97%)	4 (3%)	0	100	100
1	E	127/128 (99%)	125 (98%)	2 (2%)	0	100	100
1	F	126/128 (98%)	123 (98%)	3 (2%)	0	100	100
1	G	128/128 (100%)	126 (98%)	2 (2%)	0	100	100
1	H	129/128 (101%)	126 (98%)	3 (2%)	0	100	100
1	I	133/128 (104%)	129 (97%)	4 (3%)	0	100	100
1	J	128/128 (100%)	126 (98%)	2 (2%)	0	100	100
1	K	127/128 (99%)	125 (98%)	2 (2%)	0	100	100
1	L	125/128 (98%)	120 (96%)	5 (4%)	0	100	100
All	All	1545/1536 (101%)	1508 (98%)	37 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 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 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	122/117 (104%)	120 (98%)	2 (2%)	55	28
1	B	123/117 (105%)	123 (100%)	0	100	100
1	C	125/117 (107%)	123 (98%)	2 (2%)	55	28
1	D	116/117 (99%)	116 (100%)	0	100	100
1	E	118/117 (101%)	117 (99%)	1 (1%)	73	57
1	F	117/117 (100%)	116 (99%)	1 (1%)	70	52
1	G	121/117 (103%)	120 (99%)	1 (1%)	73	57
1	H	121/117 (103%)	118 (98%)	3 (2%)	42	12
1	I	124/117 (106%)	124 (100%)	0	100	100
1	J	119/117 (102%)	117 (98%)	2 (2%)	53	25
1	K	118/117 (101%)	118 (100%)	0	100	100
1	L	117/117 (100%)	117 (100%)	0	100	100
All	All	1441/1404 (103%)	1429 (99%)	12 (1%)	78	57

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122[A]	HIS
1	A	122[B]	HIS
1	H	123	PHE
1	H	91[A]	ASN
1	C	106[A]	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
1	K	122	HIS
1	K	59	ASN
1	H	122	HIS
1	F	122	HIS

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Mol	Chain	Res	Type
1	L	74	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
2	GOL	A	201	-	5,5,5	0.25	0	5,5,5	0.35	0

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
2	GOL	A	201	-	-	0/4/4/4	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	201	GOL	1	0

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	128/128 (100%)	0.26	6 (4%)	36	48	8, 22, 52, 59	5 (3%)
1	B	128/128 (100%)	0.30	14 (10%)	10	17	9, 23, 47, 59	6 (4%)
1	C	126/128 (98%)	0.51	12 (9%)	14	21	8, 26, 55, 65	10 (7%)
1	D	126/128 (98%)	0.59	21 (16%)	4	7	16, 25, 65, 76	2 (1%)
1	E	126/128 (98%)	0.47	13 (10%)	12	19	10, 25, 54, 80	3 (2%)
1	F	125/128 (97%)	0.59	15 (12%)	9	14	10, 25, 57, 100	3 (2%)
1	G	125/128 (97%)	0.24	8 (6%)	25	34	11, 22, 46, 88	6 (4%)
1	H	125/128 (97%)	0.57	15 (12%)	9	14	7, 25, 56, 84	5 (4%)
1	I	128/128 (100%)	0.47	12 (9%)	14	22	11, 24, 62, 87	7 (5%)
1	J	126/128 (98%)	0.49	9 (7%)	22	31	10, 25, 54, 80	4 (3%)
1	K	126/128 (98%)	0.63	16 (12%)	8	13	10, 25, 54, 83	3 (2%)
1	L	125/128 (97%)	0.58	14 (11%)	10	16	13, 26, 63, 97	2 (1%)
All	All	1514/1536 (98%)	0.47	155 (10%)	12	19	7, 24, 57, 100	56 (3%)

The worst 5 of 155 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	125	ALA	9.4
1	H	123	PHE	8.7
1	F	41[A]	TRP	8.6
1	I	127	VAL	8.4
1	J	125	ALA	7.3

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [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($\text{\AA}^2$)	Q<0.9
2	GOL	A	201	6/6	0.94	0.10	28,39,47,47	0

6.5 Other polymers [i](#)

There are no such residues in this entry.