



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 17, 2018 – 01:18 AM EDT

PDB ID : 2C6N
Title : Structure of human somatic angiotensin-I converting enzyme N domain with lisinopril
Authors : Corradi, H.R.; Schwager, S.L.U.; Nichinda, A.; Sturrock, E.D.; Acharya, K.R.
Deposited on : 2005-11-10
Resolution : 3.00 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 : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : rb-20031172
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031172

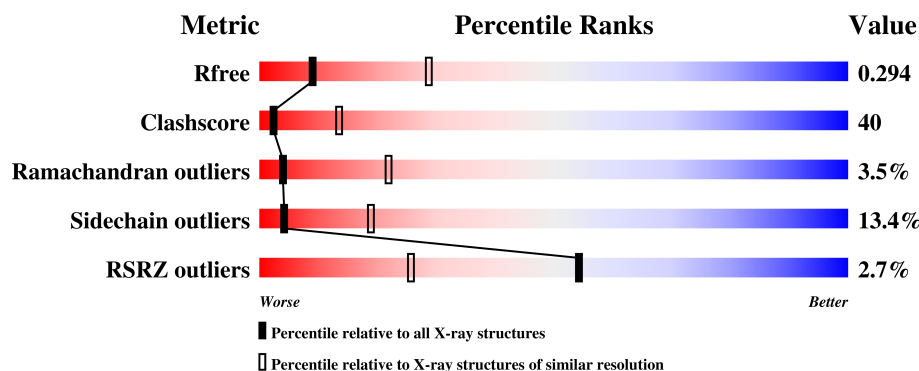
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	1851 (3.00-3.00)
Clashscore	122126	2167 (3.00-3.00)
Ramachandran outliers	120053	2101 (3.00-3.00)
Sidechain outliers	120020	2104 (3.00-3.00)
RSRZ outliers	108989	1751 (3.00-3.00)

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. 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	612	<div> <div>3%</div> <div>49%</div> <div>41%</div> <div>9%</div> <div>.</div> </div>
1	B	612	<div> <div>2%</div> <div>51%</div> <div>38%</div> <div>9%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	NAG	B	693	X	-	X	X
2	NAG	B	695	-	-	-	X
2	NAG	B	696	X	-	-	-

2 Entry composition [i](#)

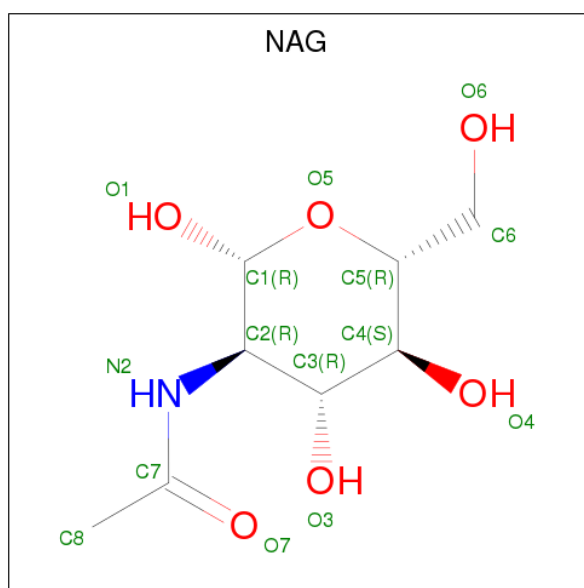
There are 8 unique types of molecules in this entry. The entry contains 9621 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 ANGIOTENSIN-CONVERTING ENZYME, SOMATIC ISOFORM.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	612	Total	C	N	O	S	7	0	0
			4747	3057	811	861	18			
1	B	609	Total	C	N	O	S	9	0	0
			4665	3005	797	845	18			

- Molecule 2 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

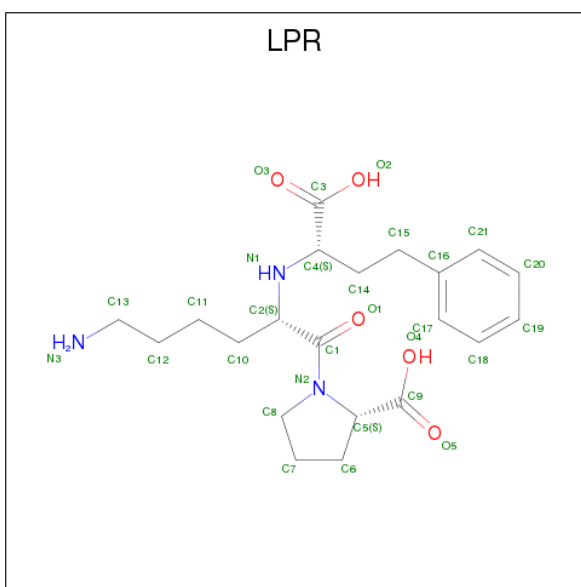
- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Zn	0	0
			1	1		
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

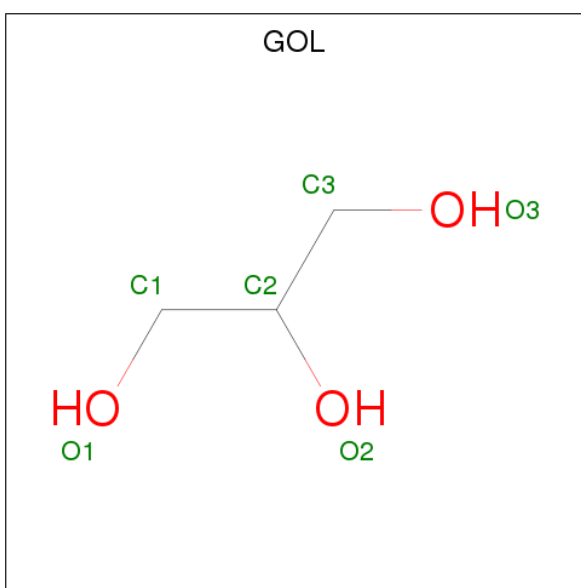
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		
4	A	1	Total	Cl	0	0
			1	1		

- Molecule 5 is [N2-[(S)-1-CARBOXY-3-PHENYLPROPYL]-L-LYSYL-L-PROLINE (three-letter code: LPR) (formula: C₂₁H₃₁N₃O₅).



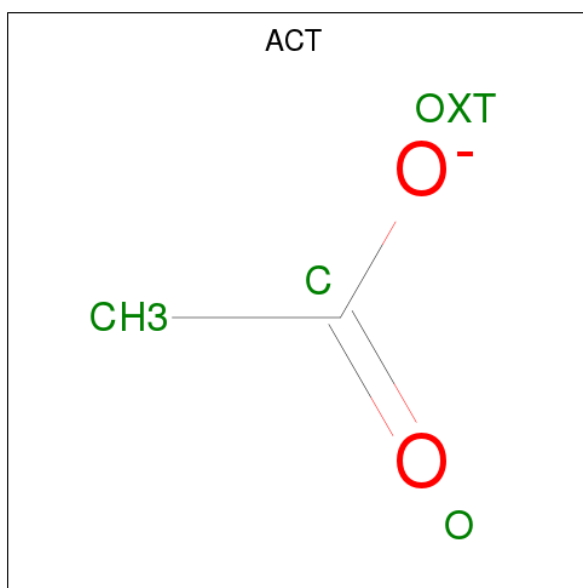
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			29	21	3	5		
5	B	1	Total	C	N	O	0	0
			29	21	3	5		

- Molecule 6 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			6	3	3		
6	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	B	1	Total	C	O	0	0
			4	2	2		

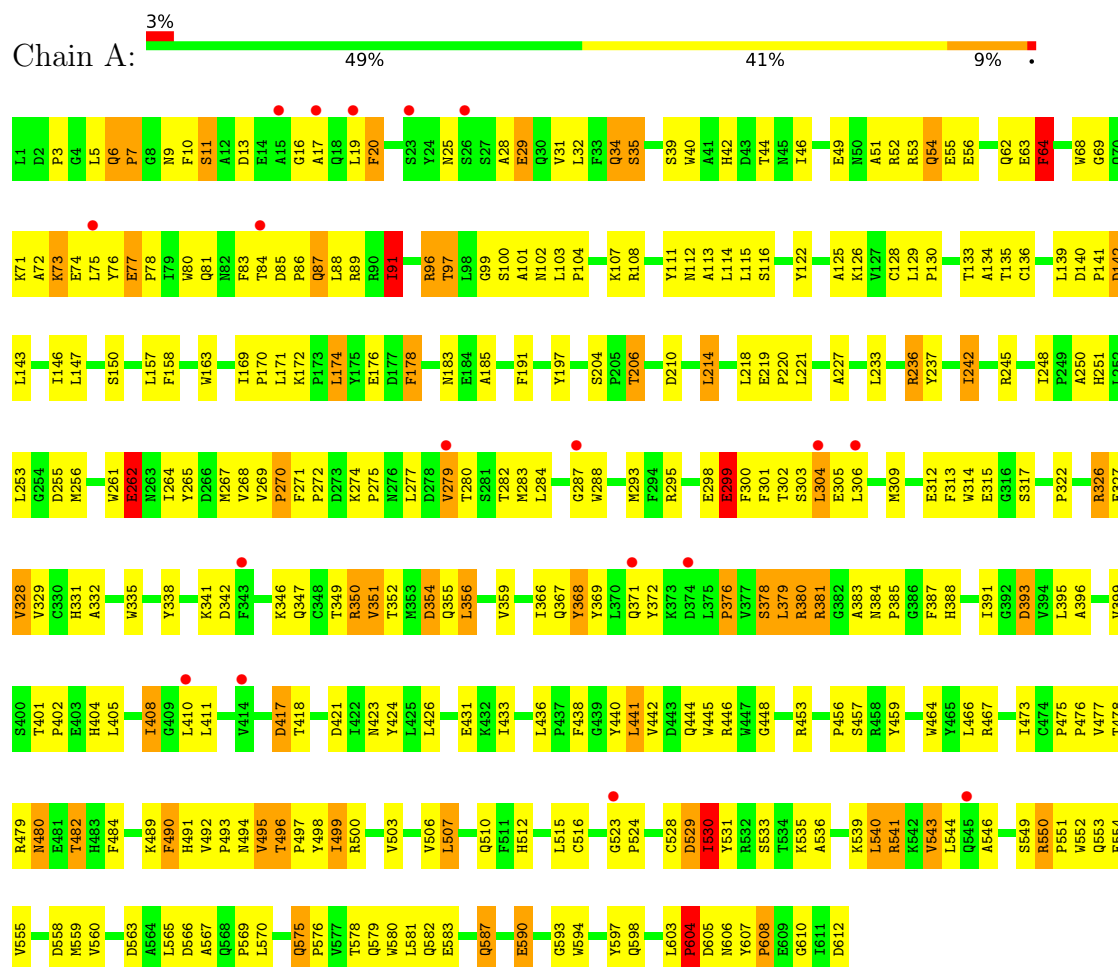
- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	8	Total	O	0	0
			8	8		
8	B	11	Total	O	0	0
			11	11		

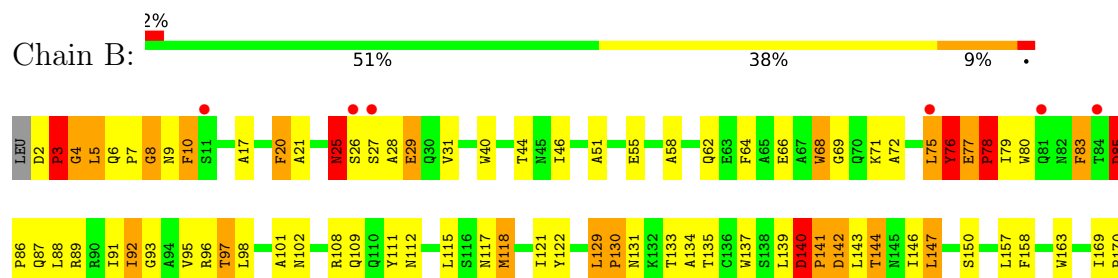
3 Residue-property plots

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: ANGIOTENSIN-CONVERTING ENZYME, SOMATIC ISOFORM



• Molecule 1: ANGIOTENSIN-CONVERTING ENZYME, SOMATIC ISOFORM





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	101.30Å 210.90Å 171.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.76 – 3.00 89.76 – 3.00	Depositor EDS
% Data completeness (in resolution range)	95.1 (28.76-3.00) 95.0 (89.76-3.00)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.04 (at 3.01Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.294 , 0.308 0.287 , 0.294	Depositor DCC
R_{free} test set	1088 reflections (3.09%)	wwPDB-VP
Wilson B-factor (Å ²)	42.6	Xtriage
Anisotropy	0.576	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 66.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	9621	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.13% 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: GOL, ZN, NAG, CL, LPR, ACT

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	0.60	4/4901 (0.1%)	0.89	23/6707 (0.3%)
1	B	0.58	3/4819 (0.1%)	0.92	26/6608 (0.4%)
All	All	0.59	7/9720 (0.1%)	0.90	49/13315 (0.4%)

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	1
1	B	1	8
All	All	1	9

The worst 5 of 7 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	381	ARG	CB-CG	8.17	1.74	1.52
1	B	25	ASN	CB-CG	-6.37	1.36	1.51
1	B	541	ARG	CB-CG	6.19	1.69	1.52
1	A	381	ARG	CG-CD	6.03	1.67	1.51
1	A	351	VAL	CB-CG1	-5.53	1.41	1.52

The worst 5 of 49 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	307	SER	C-N-CD	-10.95	96.50	120.60
1	B	305	GLU	N-CA-C	9.82	137.53	111.00
1	B	77	GLU	C-N-CD	-8.88	101.06	120.60
1	A	523	GLY	N-CA-C	-8.38	92.16	113.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	76	TYR	N-CA-C	8.24	133.24	111.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	530	ILE	CB

5 of 9 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	380	ARG	Mainchain
1	B	76	TYR	Sidechain
1	B	83	PHE	Peptide
1	B	85	ASP	Peptide
1	B	86	PRO	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	4747	0	4318	390	0
1	B	4665	0	4155	332	0
2	A	56	0	51	9	0
2	B	56	0	51	17	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	1	0
5	A	29	0	27	2	0
5	B	29	0	27	0	0
6	A	12	0	14	5	0
7	B	4	0	3	1	0
8	A	8	0	0	1	0
8	B	11	0	0	1	0
All	All	9621	0	8646	730	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 40.

The worst 5 of 730 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:381:ARG:CG	1:A:381:ARG:CB	1.74	1.63
1:B:482:THR:CG2	2:B:691:NAG:H82	1.56	1.33
1:A:6:GLN:HG3	1:A:7:PRO:CD	1.78	1.11
2:B:693:NAG:O3	2:B:693:NAG:H83	1.50	1.11
2:A:693:NAG:O7	2:A:693:NAG:H3	1.48	1.10

There are no symmetry-related clashes.

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	610/612 (100%)	506 (83%)	83 (14%)	21 (3%)	4	22
1	B	605/612 (99%)	514 (85%)	70 (12%)	21 (4%)	4	22
All	All	1215/1224 (99%)	1020 (84%)	153 (13%)	42 (4%)	4	22

5 of 42 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	PRO
1	A	85	ASP
1	B	3	PRO
1	B	130	PRO
1	B	308	PRO

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	458/526 (87%)	398 (87%)	60 (13%)	4	20
1	B	437/526 (83%)	377 (86%)	60 (14%)	4	18
All	All	895/1052 (85%)	775 (87%)	120 (13%)	4	19

5 of 120 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	582	GLN
1	B	85	ASP
1	B	477	VAL
1	A	587	GLN
1	B	3	PRO

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 29 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	109	GLN
1	B	183	ASN
1	B	579	GLN
1	B	112	ASN
1	B	188	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 17 ligands modelled in this entry, 4 are monoatomic - leaving 13 for Mogul analysis.

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$
6	GOL	A	2433	-	5,5,5	3.44	3 (60%)	5,5,5	2.02	1 (20%)
6	GOL	A	2434	-	5,5,5	3.59	3 (60%)	5,5,5	1.47	1 (20%)
2	NAG	A	691	1,2	14,14,15	2.60	3 (21%)	17,19,21	1.40	3 (17%)
2	NAG	A	693	1	14,14,15	0.25	0	17,19,21	1.04	1 (5%)
2	NAG	A	695	1	14,14,15	0.25	0	17,19,21	1.04	1 (5%)
2	NAG	A	696	2	14,14,15	2.18	1 (7%)	17,19,21	1.30	3 (17%)
5	LPR	A	705	3	24,30,30	5.11	14 (58%)	29,39,39	2.16	8 (27%)
2	NAG	B	691	1,2	14,14,15	0.25	0	17,19,21	1.04	1 (5%)
2	NAG	B	693	1	14,14,15	0.24	0	17,19,21	1.18	2 (11%)
2	NAG	B	695	1	14,14,15	0.25	0	17,19,21	1.04	1 (5%)
2	NAG	B	696	2	14,14,15	2.27	1 (7%)	17,19,21	1.07	1 (5%)
5	LPR	B	705	3	24,30,30	5.39	13 (54%)	29,39,39	1.85	6 (20%)
7	ACT	B	710	-	1,3,3	3.78	1 (100%)	0,3,3	0.00	-

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
6	GOL	A	2433	-	-	0/4/4/4	0/0/0/0
6	GOL	A	2434	-	-	0/4/4/4	0/0/0/0
2	NAG	A	691	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	693	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	695	1	-	0/6/23/26	0/1/1/1
2	NAG	A	696	2	-	0/6/23/26	0/1/1/1
5	LPR	A	705	3	-	0/22/40/40	0/2/2/2
2	NAG	B	691	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	693	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	B	695	1	-	0/6/23/26	0/1/1/1
2	NAG	B	696	2	1/1/5/7	0/6/23/26	0/1/1/1
5	LPR	B	705	3	-	0/22/40/40	0/2/2/2
7	ACT	B	710	-	-	0/0/0/0	0/0/0/0

The worst 5 of 39 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	705	LPR	C4-N1	-22.81	1.17	1.47
5	A	705	LPR	C4-N1	-21.38	1.19	1.47
2	B	696	NAG	C8-C7	-8.44	1.32	1.50
2	A	691	NAG	C8-C7	-8.36	1.32	1.50
2	A	696	NAG	C8-C7	-7.93	1.33	1.50

The worst 5 of 29 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	705	LPR	C14-C4-C3	-7.95	100.31	112.11
5	B	705	LPR	C14-C4-C3	-7.09	101.58	112.11
6	A	2433	GOL	O3-C3-C2	-3.98	90.80	110.11
2	B	693	NAG	C1-C2-N2	-3.31	104.84	110.49
2	A	693	NAG	C1-C2-N2	-3.23	104.96	110.49

All (2) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	B	693	NAG	C1
2	B	696	NAG	C2

There are no torsion outliers.

There are no ring outliers.

11 monomers are involved in 34 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	2433	GOL	3	0
6	A	2434	GOL	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	691	NAG	2	0
2	A	693	NAG	5	0
2	A	695	NAG	2	0
2	A	696	NAG	1	0
5	A	705	LPR	2	0
2	B	691	NAG	6	0
2	B	693	NAG	10	0
2	B	695	NAG	1	0
7	B	710	ACT	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	612/612 (100%)	0.27	18 (2%)	51 23	5, 39, 64, 72	4 (0%)
1	B	609/612 (99%)	0.25	15 (2%)	57 29	4, 41, 67, 81	4 (0%)
All	All	1221/1224 (99%)	0.26	33 (2%)	54 26	4, 40, 66, 81	8 (0%)

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	520	GLY	3.2
1	A	15	ALA	3.1
1	B	417	ASP	3.1
1	B	376	PRO	3.0
1	B	544	LEU	2.9

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 carbohydrates 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(\AA^2)	Q<0.9
2	NAG	B	693	14/15	0.56	0.54	66,69,70,70	0
2	NAG	B	695	14/15	0.66	0.53	77,78,81,83	0
2	NAG	B	696	14/15	0.68	0.38	90,92,93,94	0
2	NAG	A	696	14/15	0.70	0.37	100,101,103,103	0
2	NAG	A	693	14/15	0.73	0.31	69,72,74,75	0
2	NAG	A	691	14/15	0.76	0.31	29,32,35,37	0
2	NAG	A	695	14/15	0.81	0.33	73,74,75,76	0
7	ACT	B	710	4/4	0.83	0.28	29,30,30,32	0
4	CL	A	703	1/1	0.84	0.15	31,31,31,31	0
6	GOL	A	2434	6/6	0.87	0.34	28,29,30,31	0
6	GOL	A	2433	6/6	0.87	0.31	25,27,27,27	0
5	LPR	A	705	29/29	0.87	0.38	43,47,49,49	0
2	NAG	B	691	14/15	0.89	0.25	32,35,37,38	0
5	LPR	B	705	29/29	0.92	0.30	35,40,43,45	0
3	ZN	B	701	1/1	0.97	0.09	31,31,31,31	0
4	CL	B	702	1/1	0.97	0.14	25,25,25,25	0
3	ZN	A	701	1/1	0.98	0.08	33,33,33,33	0

6.5 Other polymers [i](#)

There are no such residues in this entry.