



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 19, 2016 – 07:50 PM GMT

PDB ID : 4UFA
Title : Crystal structure of the Angiotensin-1 converting enzyme N-domain in complex with Ac-SD
Authors : Masuyer, G.; Douglas, R.G.; Sturrock, E.D.; Acharya, K.R.
Deposited on : 2015-03-16
Resolution : 1.80 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
<http://wwpdb.org/validation/2016/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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026982
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20026982

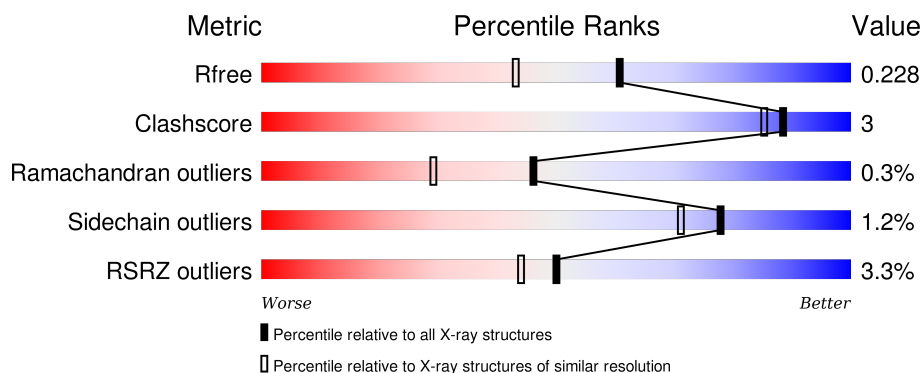
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

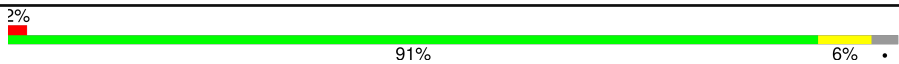
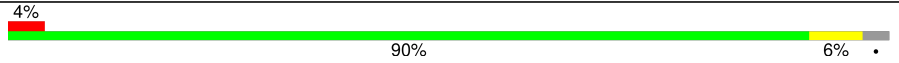
The reported resolution of this entry is 1.80 Å.

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}	91344	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	629	
1	B	629	

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
10	ASP	A	1302	-	-	X	X
10	ASP	B	1302	-	-	X	X
12	NAG	B	1104	-	-	-	X
4	NAG	B	1102	-	-	-	X
7	PEG	A	1201	-	-	-	X
7	PEG	B	1201	-	-	-	X
7	PEG	B	1202	-	-	-	X
8	P6G	A	1202	-	-	-	X
8	P6G	B	1203	-	-	-	X
8	P6G	B	1204	-	-	-	X
9	SAC	A	1301	-	-	X	X
9	SAC	B	1301	-	-	X	X

2 Entry composition

There are 13 unique types of molecules in this entry. The entry contains 10977 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	607	Total	C	N	O	S	0	2	0
			4967	3190	854	904	19			
1	B	607	Total	C	N	O	S	0	0	0
			4941	3175	847	900	19			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	629	LEU	-	EXPRESSION TAG	UNP P12821
A	9	GLN	ASN	ENGINEERED MUTATION	UNP P12821
A	25	GLN	ASN	ENGINEERED MUTATION	UNP P12821
A	82	GLN	ASN	ENGINEERED MUTATION	UNP P12821
A	117	GLN	ASN	ENGINEERED MUTATION	UNP P12821
A	131	GLN	ASN	ENGINEERED MUTATION	UNP P12821
A	289	GLN	ASN	ENGINEERED MUTATION	UNP P12821
A	545	ARG	GLN	ENGINEERED MUTATION	UNP P12821
A	576	LEU	PRO	ENGINEERED MUTATION	UNP P12821
B	629	LEU	-	EXPRESSION TAG	UNP P12821
B	9	GLN	ASN	ENGINEERED MUTATION	UNP P12821
B	25	GLN	ASN	ENGINEERED MUTATION	UNP P12821
B	82	GLN	ASN	ENGINEERED MUTATION	UNP P12821
B	117	GLN	ASN	ENGINEERED MUTATION	UNP P12821
B	131	GLN	ASN	ENGINEERED MUTATION	UNP P12821
B	289	GLN	ASN	ENGINEERED MUTATION	UNP P12821
B	545	ARG	GLN	ENGINEERED MUTATION	UNP P12821
B	576	LEU	PRO	ENGINEERED MUTATION	UNP P12821

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Zn	0	0
			1	1		

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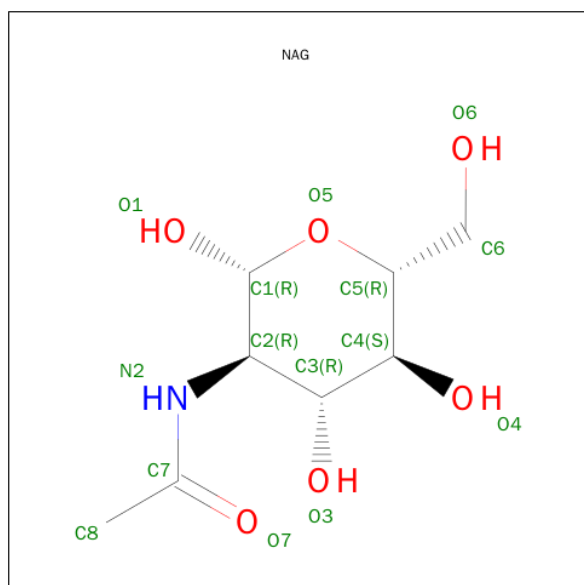
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Zn	0	0
			1	1		

- Molecule 3 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

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

- Molecule 4 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

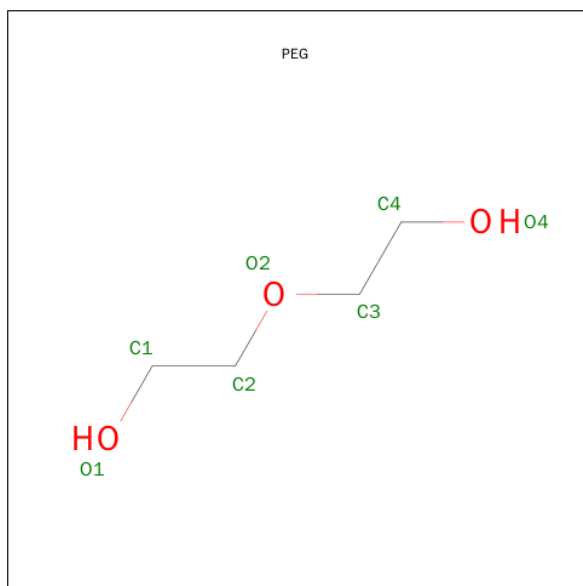
- Molecule 5 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 6 is a polymer of unknown type called SUGAR (4-MER).

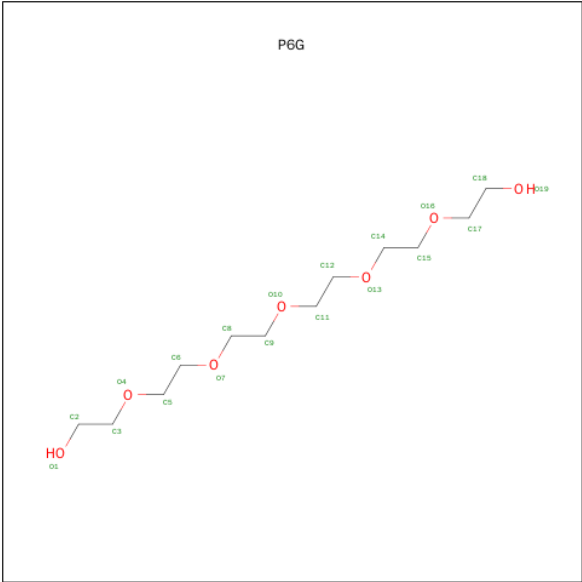
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	4	Total	C	N	O	0	0
			49	28	2	19		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



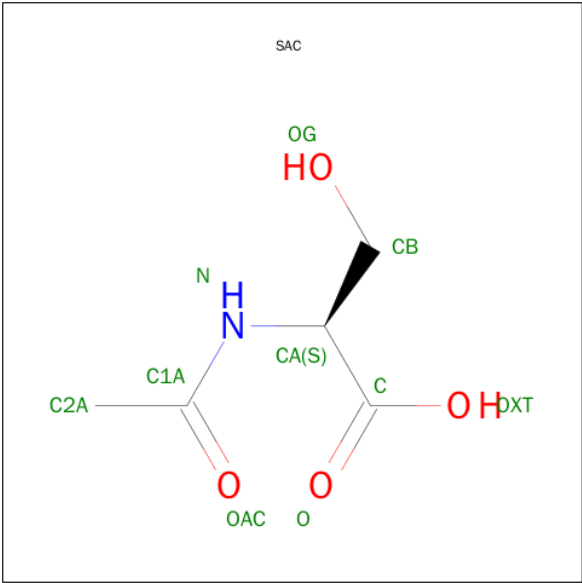
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			7	4	3		
7	A	1	Total	C	O	0	0
			7	4	3		
7	B	1	Total	C	O	0	0
			7	4	3		
7	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 8 is HEXAETHYLENE GLYCOL (three-letter code: P6G) (formula: $C_{12}H_{26}O_7$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	C	O	0	0
			19	12	7		
8	B	1	Total	C	O	0	0
			19	12	7		
8	B	1	Total	C	O	0	0
			19	12	7		

- Molecule 9 is N-ACETYL-SERINE (three-letter code: SAC) (formula: C₅H₉NO₄).



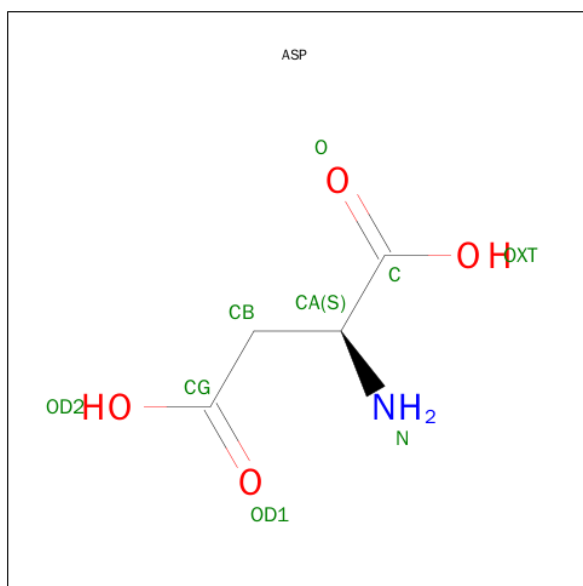
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	A	1	Total	C	N	O	0	0
			9	5	1	3		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
9	B	1	Total	C	N	O	0	0
			9	5	1	3		

- Molecule 10 is ASPARTIC ACID (three-letter code: ASP) (formula: $C_4H_7NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
10	A	1	Total	C	N	O	0	0
			9	4	1	4		
10	B	1	Total	C	N	O	0	0
			9	4	1	4		

- Molecule 11 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	2	Total	C	N	O	0	0
			24	14	1	9		

- Molecule 12 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	B	3	Total	C	N	O	0	0
			39	22	2	15		

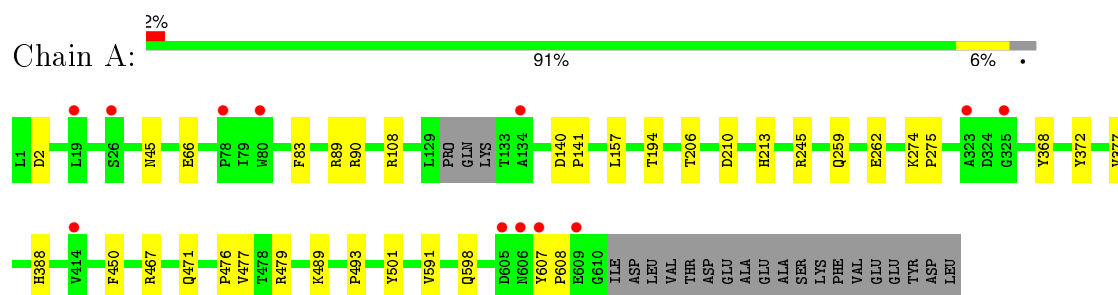
- Molecule 13 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	A	443	Total 443	O 443	0	0
13	B	333	Total 333	O 333	0	0

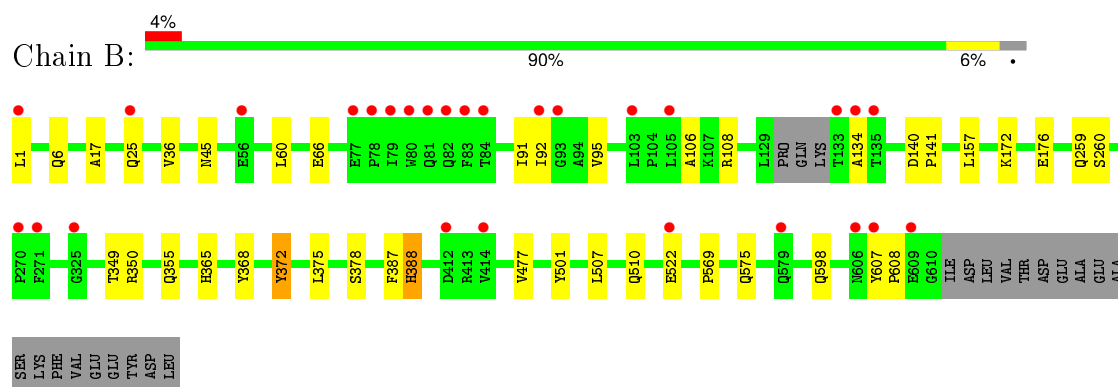
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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 ($\text{RSRZ} > 2$). 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



• Molecule 1: ANGIOTENSIN-CONVERTING ENZYME



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	72.87Å 76.72Å 82.80Å 88.65° 64.31° 75.22°	Depositor
Resolution (Å)	74.24 – 1.80 34.79 – 1.80	Depositor EDS
% Data completeness (in resolution range)	90.4 (74.24-1.80) 88.7 (34.79-1.80)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.62 (at 1.81Å)	Xtriage
Refinement program	REFMAC 5.8.0103	Depositor
R, R_{free}	0.202 , 0.228 0.202 , 0.228	Depositor DCC
R_{free} test set	6455 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	25.0	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 38.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 130326 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	10977	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.97% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: ZN, BMA, NAG, CL, SAC, FUC, P6G, PEG

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	0.53	0/5126	0.65	0/6981
1	B	0.52	0/5096	0.64	0/6942
All	All	0.52	0/10222	0.65	0/13923

There are no bond length outliers.

There are no bond angle outliers.

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	4967	0	4737	20	0
1	B	4941	0	4707	25	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
5	A	28	0	25	0	0
6	A	49	0	43	0	0
7	A	14	0	20	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	14	0	20	0	0
8	A	19	0	26	0	0
8	B	38	0	52	1	0
9	A	9	0	8	4	0
9	B	9	0	8	4	0
10	A	9	0	4	4	0
10	B	9	0	4	4	0
11	B	24	0	22	0	0
12	B	39	0	34	1	0
13	A	443	0	0	3	0
13	B	333	0	0	2	0
All	All	10977	0	9736	50	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 3.

The worst 5 of 50 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:B:365:HIS:HD1	1:B:388:HIS:HD2	1.18	0.89
1:B:259:GLN:NE2	10:B:1302:ASP:HB2	1.87	0.88
1:B:259:GLN:HE21	10:B:1302:ASP:HB2	1.41	0.85
1:A:467:ARG:HH11	1:A:471:GLN:HE22	1.29	0.80
9:A:1301:SAC:HA	10:A:1302:ASP:OXT	1.81	0.78

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	605/629 (96%)	593 (98%)	11 (2%)	1 (0%)	52 35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	B	603/629 (96%)	592 (98%)	8 (1%)	3 (0%)	34 17
All	All	1208/1258 (96%)	1185 (98%)	19 (2%)	4 (0%)	46 29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	45	ASN
1	B	575	GLN
1	A	45	ASN
1	B	134	ALA

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	521/541 (96%)	514 (99%)	7 (1%)	76 68
1	B	517/541 (96%)	512 (99%)	5 (1%)	82 77
All	All	1038/1082 (96%)	1026 (99%)	12 (1%)	78 71

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

Mol	Chain	Res	Type
1	A	388	HIS
1	A	598	GLN
1	B	368	TYR
1	A	377	VAL
1	B	260	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	87	GLN
1	B	109	GLN

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Mol	Chain	Res	Type
1	B	491	HIS
1	B	25	GLN
1	B	582	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

11 carbohydrates 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	$\# Z > 2$
5	NAG	A	1102	1,5	14,14,15	0.55	0	15,19,21	1.23	1 (6%)
5	NAG	A	1103	5	14,14,15	0.65	0	15,19,21	1.17	1 (6%)
6	NAG	A	1104	1,6	14,14,15	0.43	0	15,19,21	0.94	1 (6%)
6	NAG	A	1105	6	14,14,15	0.44	0	15,19,21	1.17	2 (13%)
6	BMA	A	1106	6	11,11,12	0.69	0	15,15,17	1.23	2 (13%)
6	FUC	A	1107	6	10,10,11	0.77	0	13,14,16	0.70	0
11	NAG	B	1100	1,11	14,14,15	0.57	0	15,19,21	1.38	3 (20%)
11	FUC	B	1101	11	10,10,11	0.83	0	13,14,16	1.90	3 (23%)
12	NAG	B	1104	1,12	14,14,15	0.63	0	15,19,21	1.40	2 (13%)
12	NAG	B	1105	12	14,14,15	0.58	0	15,19,21	1.83	4 (26%)
12	BMA	B	1106	12	11,11,12	0.74	0	15,15,17	1.20	2 (13%)

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
5	NAG	A	1102	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1103	5	-	0/6/23/26	0/1/1/1
6	NAG	A	1104	1,6	-	0/6/23/26	0/1/1/1
6	NAG	A	1105	6	-	0/6/23/26	0/1/1/1
6	BMA	A	1106	6	-	0/2/19/22	0/1/1/1
6	FUC	A	1107	6	-	0/0/17/20	0/1/1/1
11	NAG	B	1100	1,11	-	0/6/23/26	0/1/1/1
11	FUC	B	1101	11	-	0/0/17/20	0/1/1/1
12	NAG	B	1104	1,12	-	0/6/23/26	0/1/1/1
12	NAG	B	1105	12	-	0/6/23/26	0/1/1/1
12	BMA	B	1106	12	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
12	B	1106	BMA	C1-O5-C5	2.11	115.24	112.14
6	A	1105	NAG	C4-C3-C2	2.17	114.71	111.34
11	B	1100	NAG	O5-C5-C6	2.19	112.02	107.34
12	B	1105	NAG	O5-C5-C4	2.32	113.97	110.13
11	B	1100	NAG	C4-C3-C2	2.34	114.98	111.34

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
12	B	1106	BMA	1	0

5.6 Ligand geometry ⓘ

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
4	NAG	A	1100	1	14,14,15	0.60	0	15,19,21	1.33	3 (20%)
7	PEG	A	1200	-	6,6,6	0.42	0	5,5,5	0.34	0
7	PEG	A	1201	-	6,6,6	0.44	0	5,5,5	0.38	0
8	P6G	A	1202	-	18,18,18	0.51	0	17,17,17	0.27	0
9	SAC	A	1301	10	7,8,9	1.23	1 (14%)	7,9,11	0.92	1 (14%)
10	ASP	A	1302	9	2,8,8	0.07	0	1,10,10	1.00	0
4	NAG	B	1102	1	14,14,15	0.61	0	15,19,21	0.90	0
7	PEG	B	1201	-	6,6,6	0.51	0	5,5,5	0.28	0
7	PEG	B	1202	-	6,6,6	0.42	0	5,5,5	0.40	0
8	P6G	B	1203	-	18,18,18	0.60	0	17,17,17	0.26	0
8	P6G	B	1204	-	18,18,18	0.51	0	17,17,17	0.27	0
9	SAC	B	1301	10	7,8,9	1.28	1 (14%)	7,9,11	0.83	1 (14%)
10	ASP	B	1302	9	2,8,8	0.02	0	1,10,10	0.84	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
4	NAG	A	1100	1	-	0/6/23/26	0/1/1/1
7	PEG	A	1200	-	-	0/4/4/4	0/0/0/0
7	PEG	A	1201	-	-	0/4/4/4	0/0/0/0
8	P6G	A	1202	-	-	0/16/16/16	0/0/0/0
9	SAC	A	1301	10	-	0/6/8/10	0/0/0/0
10	ASP	A	1302	9	-	0/2/8/8	0/0/0/0
4	NAG	B	1102	1	-	0/6/23/26	0/1/1/1
7	PEG	B	1201	-	-	0/4/4/4	0/0/0/0
7	PEG	B	1202	-	-	0/4/4/4	0/0/0/0
8	P6G	B	1203	-	-	0/16/16/16	0/0/0/0
8	P6G	B	1204	-	-	0/16/16/16	0/0/0/0
9	SAC	B	1301	10	-	0/6/8/10	0/0/0/0
10	ASP	B	1302	9	-	0/2/8/8	0/0/0/0

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	A	1301	SAC	CA-N	3.12	1.50	1.46

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
9	B	1301	SAC	CA-N	3.21	1.50	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
9	A	1301	SAC	O-C-CA	-2.31	119.38	125.69
9	B	1301	SAC	O-C-CA	-2.05	120.08	125.69
4	A	1100	NAG	O5-C5-C6	2.07	111.76	107.34
4	A	1100	NAG	C4-C3-C2	2.33	114.95	111.34
4	A	1100	NAG	C1-O5-C5	3.67	117.54	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1301	SAC	4	0
10	A	1302	ASP	4	0
8	B	1204	P6G	1	0
9	B	1301	SAC	4	0
10	B	1302	ASP	4	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	607/629 (96%)	-0.10	12 (1%) 68 64	13, 23, 43, 69	0
1	B	607/629 (96%)	0.19	28 (4%) 36 30	14, 28, 51, 73	0
All	All	1214/1258 (96%)	0.05	40 (3%) 50 44	13, 25, 48, 73	0

The worst 5 of 40 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	325	GLY	5.9
1	A	325	GLY	5.4
1	A	323	ALA	5.0
1	B	134	ALA	4.8
1	B	81	GLN	4.4

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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
12	NAG	B	1104	14/15	0.86	0.25	4.65	58,63,68,68	0
5	NAG	A	1102	14/15	0.83	0.21	1.80	38,45,51,57	0
11	NAG	B	1100	14/15	0.84	0.14	1.40	39,45,52,53	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	NAG	A	1104	14/15	0.94	0.14	1.14	36,39,44,45	0
5	NAG	A	1103	14/15	0.76	0.33	-	57,66,73,74	0
6	FUC	A	1107	10/11	0.86	0.24	-	44,46,48,50	0
6	BMA	A	1106	11/12	0.78	0.22	-	63,65,67,68	0
11	FUC	B	1101	10/11	0.65	0.38	-	61,66,70,72	0
12	BMA	B	1106	11/12	0.70	0.29	-	82,85,85,87	0
6	NAG	A	1105	14/15	0.89	0.19	-	45,51,58,58	0
12	NAG	B	1105	14/15	0.87	0.25	-	71,73,75,79	0

6.4 Ligands ⓘ

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
7	PEG	A	1201	7/7	0.68	0.23	8.13	53,56,61,62	0
9	SAC	B	1301	9/10	0.80	0.23	7.93	41,45,49,50	0
8	P6G	A	1202	19/19	0.71	0.25	7.75	50,65,72,73	0
10	ASP	B	1302	9/9	0.79	0.23	6.21	25,31,38,41	0
7	PEG	B	1201	7/7	0.87	0.21	4.75	39,41,43,46	0
10	ASP	A	1302	9/9	0.79	0.24	4.61	23,35,41,42	0
8	P6G	B	1203	19/19	0.78	0.17	4.50	41,43,52,53	0
8	P6G	B	1204	19/19	0.77	0.26	4.15	60,64,74,76	0
9	SAC	A	1301	9/10	0.85	0.18	3.42	47,49,50,51	0
4	NAG	B	1102	14/15	0.80	0.29	3.30	43,47,48,51	0
7	PEG	B	1202	7/7	0.92	0.15	2.80	35,36,41,41	0
4	NAG	A	1100	14/15	0.83	0.16	1.31	30,35,40,44	0
3	CL	A	1002	1/1	1.00	0.09	-0.26	17,17,17,17	0
3	CL	B	1002	1/1	0.99	0.11	-0.43	21,21,21,21	0
2	ZN	A	1001	1/1	1.00	0.08	-	17,17,17,17	0
7	PEG	A	1200	7/7	0.88	0.17	-	43,45,48,50	0
2	ZN	B	1001	1/1	1.00	0.07	-	17,17,17,17	0

6.5 Other polymers ⓘ

There are no such residues in this entry.