



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 27, 2016 – 09:34 PM EDT

PDB ID : 5DYT
Title : Crystal structure of human butyrylcholinesterase in complex with N-((1-benzylpiperidin-3-yl)methyl)-N-methylnaphthalene-2-sulfonamide
Authors : Coquelle, N.; Brus, B.; Colletier, J.P.
Deposited on : 2015-09-25
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

<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-20027939
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-20027939

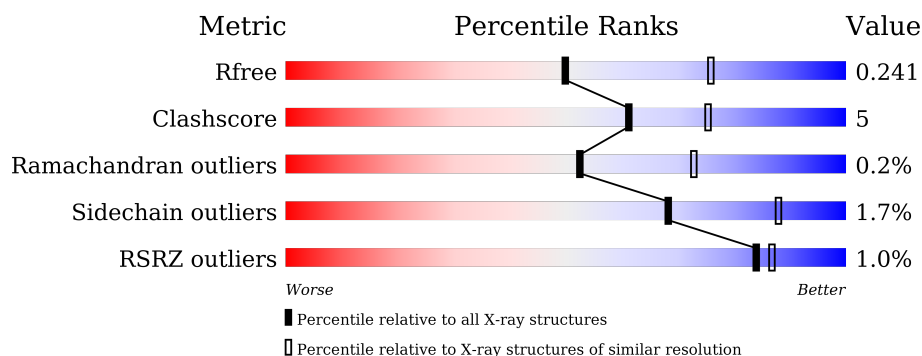
1 Overall quality at a glance ⓘ

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}	91344	4549 (2.58-2.50)
Clashscore	102246	5292 (2.58-2.50)
Ramachandran outliers	100387	5194 (2.58-2.50)
Sidechain outliers	100360	5196 (2.58-2.50)
RSRZ outliers	91569	4561 (2.58-2.50)

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	530	<div> <div></div> <div>86%</div> <div>13%</div> <div>.</div> </div>
1	B	530	<div> <div></div> <div>83%</div> <div>16%</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	A	606	X	-	-	-
2	NAG	A	607	X	-	-	-
2	NAG	A	608	X	-	-	-
2	NAG	A	610	X	-	-	-
2	NAG	A	614	X	-	-	-
2	NAG	B	611	X	-	-	-
3	FUC	A	609	X	-	-	X
3	FUC	A	615	X	-	-	X
3	FUC	B	610	X	-	-	-
4	5HB	B	612	-	-	-	X
5	GOL	A	617	-	-	-	X
5	GOL	A	618	-	-	-	X
5	GOL	A	619	-	-	-	X
5	GOL	B	614	-	-	-	X
6	EDO	B	615	-	-	-	X
6	EDO	B	616	-	-	-	X
7	UNX	A	621	-	-	-	X
7	UNX	A	623	-	-	X	-
7	UNX	B	618	-	-	-	X
8	FUL	B	606	-	-	-	X
9	PEG	B	621	-	-	-	X

2 Entry composition [i](#)

There are 10 unique types of molecules in this entry. The entry contains 9063 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 Cholinesterase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	527	Total	C	N	O	S	0	3	0
			4210	2717	710	768	15			
1	B	525	Total	C	N	O	S	0	0	0
			4160	2688	697	760	15			

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



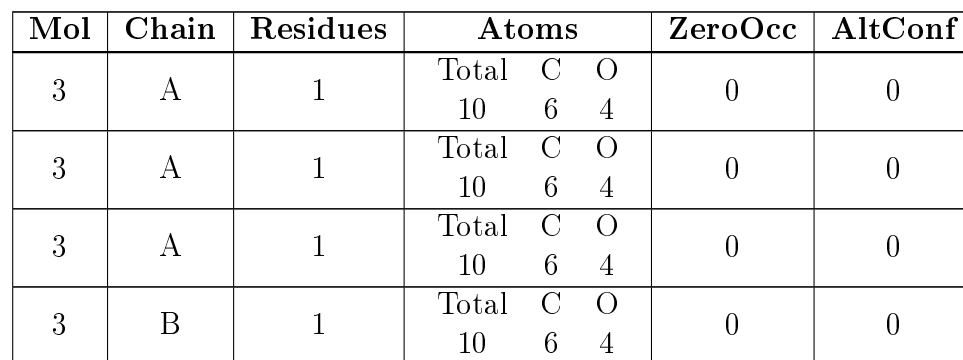
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	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		
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	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		
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		

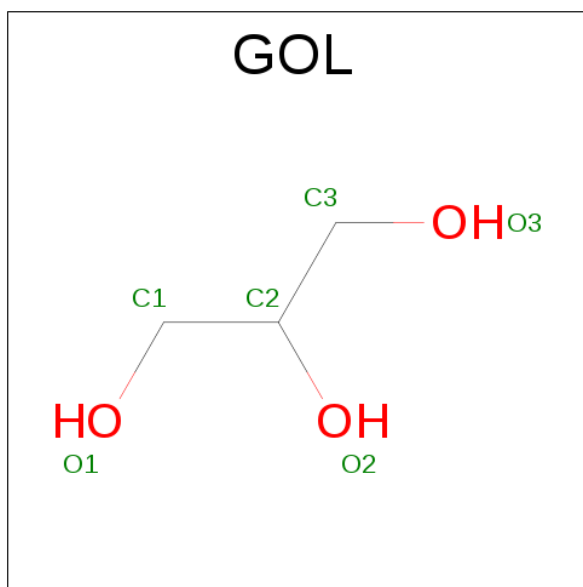
- Molecule 3 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: C₆H₁₂O₅).



- # 5HB
-
- The chemical structure of 5HB (5-Hydroxybenzimidazole) is shown with the following atom labels and stereochemistry:
- Atom Labels:** C12, C13, C14, C15, C16, C17, C18, C19, C07(R), C08, C09, C10, N11(R), C06, N05(R), O21, O22, S20, C23, C24, C25, C26, C27, C28, C29, C30, C31.
 - Stereochemistry:**
 - N11(R) is a chiral center with a wedge bond to C12 and a dashed bond to C07(R).
 - N05(R) is a chiral center with a wedge bond to C04 and a dashed bond to C06.

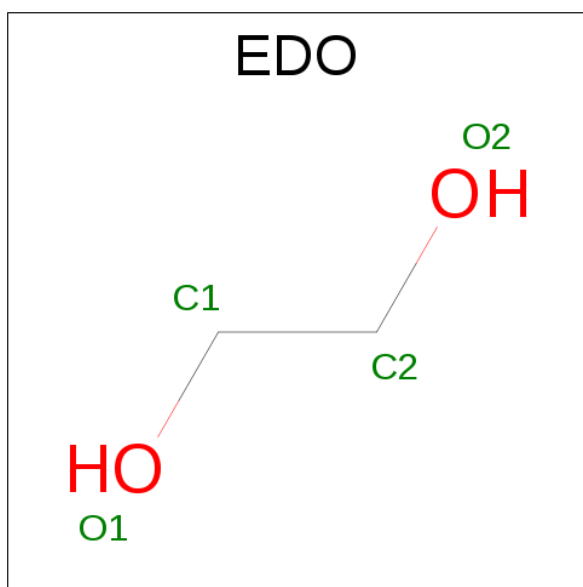
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	S	0	0
			29	24	2	2	1		
4	B	1	Total	C	N	O	S	0	0
			29	24	2	2	1		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

- Molecule 6 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).

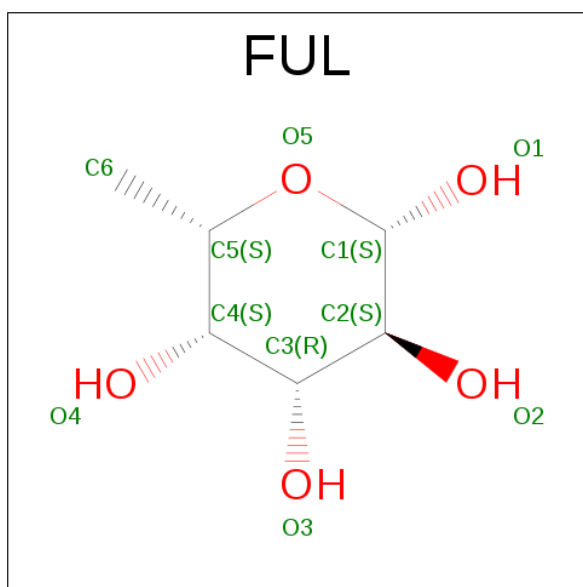


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		
6	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 7 is UNKNOWN ATOM OR ION (three-letter code: UNX) (formula: X).

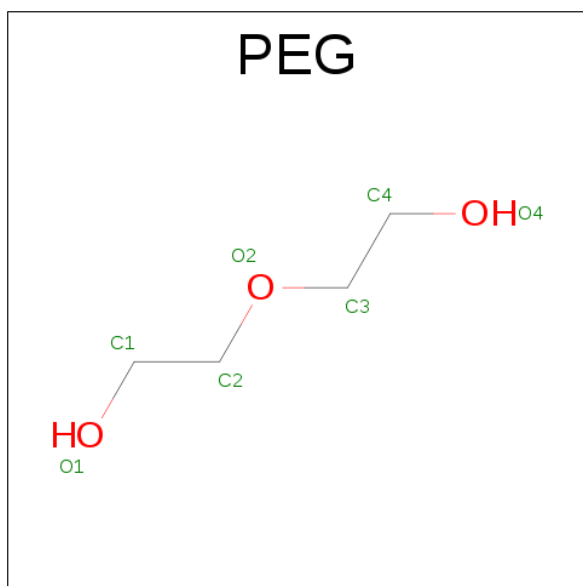
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	B	3	Total	X	0	0
			3	3		
7	A	3	Total	X	0	0
			3	3		

- Molecule 8 is BETA-L-FUCOSE (three-letter code: FUL) (formula: C₆H₁₂O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	B	1	Total	C	O	0	0
			10	6	4		

- Molecule 9 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



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

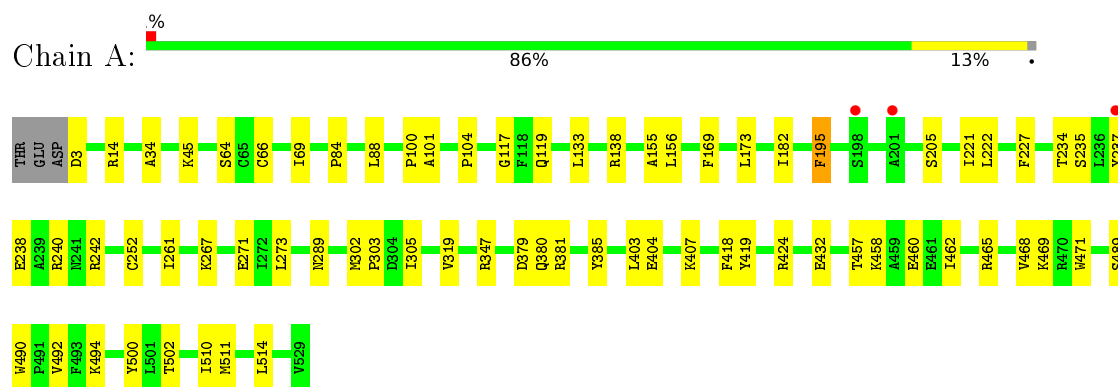
- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	118	Total 118	O 118	0	0
10	B	114	Total 114	O 114	0	0

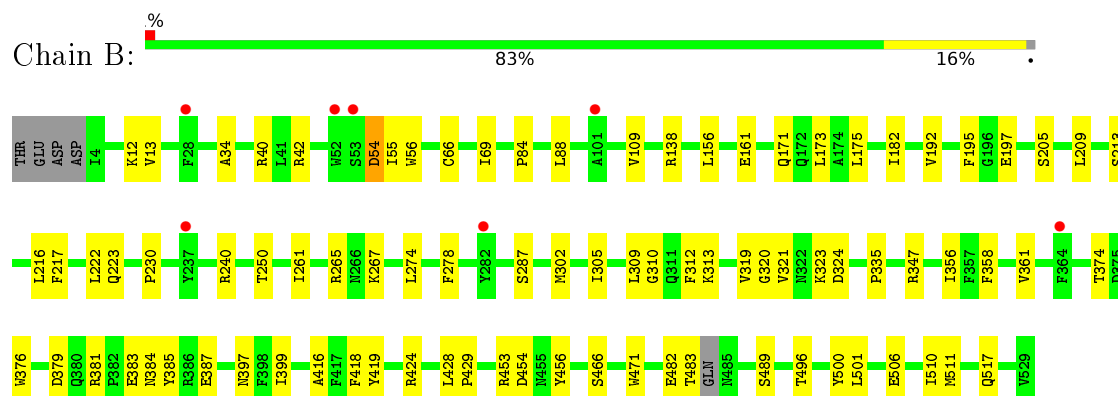
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Cholinesterase



• Molecule 1: Cholinesterase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	76.47Å 80.23Å 231.28Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.12 – 2.55 46.91 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.6 (46.12-2.55) 99.7 (46.91-2.55)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.21 (at 2.54Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.179 , 0.232 0.190 , 0.241	Depositor DCC
R_{free} test set	1415 reflections (3.09%)	DCC
Wilson B-factor (Å ²)	56.5	Xtriage
Anisotropy	0.323	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 48.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.024 for k,h,-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	9063	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.38% 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, CSO, 5HB, NAG, UNX, EDO, FUC, FUL, 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	0.44	0/4331	0.60	0/5879
1	B	0.43	0/4270	0.58	0/5796
All	All	0.43	0/8601	0.59	0/11675

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

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	155	ALA	Peptide

5.2 Too-close contacts [i](#)

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	4210	0	4103	42	1
1	B	4160	0	4034	50	1
2	A	168	0	148	1	0
2	B	126	0	114	1	0
3	A	30	0	30	0	0
3	B	10	0	10	0	0
4	A	29	0	0	0	0
4	B	29	0	0	0	0
5	A	18	0	24	0	0
5	B	12	0	16	1	0
6	A	4	0	6	0	0
6	B	12	0	18	0	0
7	A	3	0	0	2	0
7	B	3	0	0	1	0
8	B	10	0	10	1	0
9	B	7	0	10	2	0
10	A	118	0	0	5	0
10	B	114	0	0	2	0
All	All	9063	0	8523	95	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 5.

The worst 5 of 95 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:217:PHE:O	1:B:313:LYS:NZ	2.06	0.89
1:B:12:LYS:HB2	1:B:55:ILE:HD12	1.62	0.82
1:B:109:VAL:HB	1:B:192:VAL:HG12	1.58	0.82
1:B:192:VAL:HG23	1:B:217:PHE:HA	1.62	0.81
7:A:621:UNX:UNK	7:A:623:UNX:UNK	1.26	0.77

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)
1:A:237:TYR:OH	1:B:453:ARG:O[1_545]	2.12	0.08

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	527/530 (99%)	504 (96%)	23 (4%)	0	100	100
1	B	520/530 (98%)	495 (95%)	23 (4%)	2 (0%)	39	60
All	All	1047/1060 (99%)	999 (95%)	46 (4%)	2 (0%)	52	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	54	ASP
1	B	506	GLU

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	451/454 (99%)	446 (99%)	5 (1%)	80	93
1	B	442/454 (97%)	432 (98%)	10 (2%)	58	82
All	All	893/908 (98%)	878 (98%)	15 (2%)	68	88

5 of 15 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	138	ARG
1	B	195	PHE
1	B	471	TRP
1	B	40	ARG

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Mol	Chain	Res	Type
1	B	466	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	311	GLN
1	B	10	ASN
1	B	397	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 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	CSO	A	66	1	3,6,7	0.82	0	2,6,8	1.22	0
1	CSO	B	66	1	3,6,7	2.15	1 (33%)	2,6,8	1.56	1 (50%)

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	CSO	A	66	1	-	0/1/5/7	0/0/0/0
1	CSO	B	66	1	-	0/1/5/7	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	66	CSO	CB-SG	-3.65	1.77	1.82

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	66	CSO	O-C-CA	-2.20	119.83	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	66	CSO	1	0
1	B	66	CSO	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 44 ligands modelled in this entry, 6 are unknown - leaving 38 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	$\# Z > 2$
2	NAG	A	601	1	14,14,15	0.63	0	15,19,21	0.39	0
2	NAG	A	602	1,3,2	14,14,15	0.25	0	15,19,21	0.42	0
2	NAG	A	603	2	14,14,15	0.73	1 (7%)	15,19,21	0.82	1 (6%)
3	FUC	A	604	2	10,10,11	1.80	4 (40%)	13,14,16	0.67	0
2	NAG	A	605	1,2	14,14,15	0.52	0	15,19,21	0.79	0
2	NAG	A	606	2	14,14,15	0.70	0	15,19,21	0.47	0
2	NAG	A	607	1,3,2	14,14,15	0.25	0	15,19,21	0.87	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAG	A	608	2	14,14,15	0.72	1 (7%)	15,19,21	0.83	1 (6%)
3	FUC	A	609	2	10,10,11	1.78	4 (40%)	13,14,16	1.81	3 (23%)
2	NAG	A	610	1	14,14,15	0.51	0	15,19,21	1.03	1 (6%)
2	NAG	A	611	1,2	14,14,15	0.25	0	15,19,21	0.61	1 (6%)
2	NAG	A	612	2	14,14,15	0.84	1 (7%)	15,19,21	0.81	1 (6%)
2	NAG	A	613	1,3,2	14,14,15	0.50	0	15,19,21	0.38	0
2	NAG	A	614	2	14,14,15	0.29	0	15,19,21	0.26	0
3	FUC	A	615	2	10,10,11	1.72	2 (20%)	13,14,16	1.11	0
4	5HB	A	616	-	32,32,32	2.56	3 (9%)	43,45,45	1.51	4 (9%)
5	GOL	A	617	-	5,5,5	0.30	0	5,5,5	0.48	0
5	GOL	A	618	-	5,5,5	0.51	0	5,5,5	0.48	0
5	GOL	A	619	-	5,5,5	0.44	0	5,5,5	0.23	0
6	EDO	A	620	-	3,3,3	0.63	0	2,2,2	0.42	0
2	NAG	B	601	1	14,14,15	0.91	1 (7%)	15,19,21	1.04	1 (6%)
2	NAG	B	602	1	14,14,15	0.44	0	15,19,21	0.37	0
2	NAG	B	603	1	14,14,15	0.39	0	15,19,21	1.32	2 (13%)
2	NAG	B	604	1,2	14,14,15	0.45	0	15,19,21	0.54	0
2	NAG	B	605	2	14,14,15	0.24	0	15,19,21	0.40	0
8	FUL	B	606	-	10,10,11	1.63	2 (20%)	13,14,16	1.99	3 (23%)
2	NAG	B	607	1	14,14,15	0.42	0	15,19,21	0.74	1 (6%)
2	NAG	B	608	1	14,14,15	0.48	0	15,19,21	0.58	0
2	NAG	B	609	1,3	14,14,15	0.40	0	15,19,21	0.59	0
3	FUC	B	610	2	10,10,11	1.65	2 (20%)	13,14,16	1.18	2 (15%)
2	NAG	B	611	1	14,14,15	0.49	0	15,19,21	1.00	1 (6%)
4	5HB	B	612	-	32,32,32	2.54	4 (12%)	43,45,45	1.63	6 (13%)
5	GOL	B	613	-	5,5,5	0.34	0	5,5,5	0.26	0
5	GOL	B	614	-	5,5,5	0.37	0	5,5,5	0.65	0
6	EDO	B	615	-	3,3,3	0.59	0	2,2,2	0.02	0
6	EDO	B	616	-	3,3,3	1.68	1 (33%)	2,2,2	1.68	0
6	EDO	B	617	-	3,3,3	1.25	0	2,2,2	1.46	0
9	PEG	B	621	-	6,6,6	0.49	0	5,5,5	0.92	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	NAG	A	601	1	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	602	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	A	603	2	-	0/6/23/26	0/1/1/1
3	FUC	A	604	2	-	0/0/17/20	0/1/1/1
2	NAG	A	605	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	606	2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	A	607	1,3,2	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	A	608	2	1/1/5/7	0/6/23/26	0/1/1/1
3	FUC	A	609	2	1/1/4/5	0/0/17/20	0/1/1/1
2	NAG	A	610	1	1/1/5/7	0/6/23/26	0/1/1/1
2	NAG	A	611	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	612	2	-	0/6/23/26	0/1/1/1
2	NAG	A	613	1,3,2	-	0/6/23/26	0/1/1/1
2	NAG	A	614	2	1/1/5/7	0/6/23/26	0/1/1/1
3	FUC	A	615	2	1/1/4/5	0/0/17/20	0/1/1/1
4	5HB	A	616	-	-	0/20/30/30	0/4/4/4
5	GOL	A	617	-	-	0/4/4/4	0/0/0/0
5	GOL	A	618	-	-	0/4/4/4	0/0/0/0
5	GOL	A	619	-	-	0/4/4/4	0/0/0/0
6	EDO	A	620	-	-	0/1/1/1	0/0/0/0
2	NAG	B	601	1	-	0/6/23/26	0/1/1/1
2	NAG	B	602	1	-	0/6/23/26	0/1/1/1
2	NAG	B	603	1	-	0/6/23/26	0/1/1/1
2	NAG	B	604	1,2	-	0/6/23/26	0/1/1/1
2	NAG	B	605	2	-	0/6/23/26	0/1/1/1
8	FUL	B	606	-	-	0/0/17/20	0/1/1/1
2	NAG	B	607	1	-	0/6/23/26	0/1/1/1
2	NAG	B	608	1	-	0/6/23/26	0/1/1/1
2	NAG	B	609	1,3	-	0/6/23/26	0/1/1/1
3	FUC	B	610	2	1/1/4/5	0/0/17/20	0/1/1/1
2	NAG	B	611	1	1/1/5/7	0/6/23/26	0/1/1/1
4	5HB	B	612	-	-	0/20/30/30	0/4/4/4
5	GOL	B	613	-	-	0/4/4/4	0/0/0/0
5	GOL	B	614	-	-	0/4/4/4	0/0/0/0
6	EDO	B	615	-	-	0/1/1/1	0/0/0/0
6	EDO	B	616	-	-	0/1/1/1	0/0/0/0
6	EDO	B	617	-	-	0/1/1/1	0/0/0/0
9	PEG	B	621	-	-	0/4/4/4	0/0/0/0

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	616	5HB	C12-C13	-6.67	1.38	1.51

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	612	5HB	C12-C13	-6.45	1.39	1.51
3	A	609	FUC	O5-C1	-3.34	1.38	1.43
3	A	604	FUC	O5-C1	-3.15	1.38	1.43
8	B	606	FUL	O5-C1	-3.12	1.38	1.43

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	612	5HB	O21-S20-O22	-5.21	110.54	119.47
4	A	616	5HB	O21-S20-O22	-4.43	111.89	119.47
3	A	609	FUC	O5-C1-C2	-3.70	104.97	110.89
4	A	616	5HB	C06-N05-S20	-3.23	109.81	117.97
4	B	612	5HB	C04-N05-C06	-2.57	111.07	115.46

5 of 9 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	A	615	FUC	C1
2	A	614	NAG	C1
2	A	610	NAG	C1
2	A	606	NAG	C1
2	A	607	NAG	C1

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	612	NAG	1	0
8	B	606	FUL	1	0
2	B	608	NAG	1	0
5	B	614	GOL	1	0
9	B	621	PEG	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	526/530 (99%)	-0.12	3 (0%) 90 92	28, 50, 82, 133	0
1	B	524/530 (98%)	-0.01	7 (1%) 79 83	32, 53, 93, 149	1 (0%)
All	All	1050/1060 (99%)	-0.06	10 (0%) 84 87	28, 52, 88, 149	1 (0%)

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	237	TYR	3.2
1	B	52	TRP	2.7
1	B	282	TYR	2.6
1	A	237	TYR	2.5
1	B	101	ALA	2.4

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. 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
1	CSO	A	66	7/8	0.99	0.11	-	43,46,56,57	0
1	CSO	B	66	7/8	0.97	0.17	-	36,38,56,57	0

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

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(Å ²)	Q<0.9
7	UNX	B	618	1/1	0.96	0.70	12.98	62,62,62,62	0
3	FUC	A	615	10/11	0.72	0.37	10.26	114,117,119,120	0
5	GOL	B	614	6/6	0.79	0.35	8.34	78,83,87,93	0
5	GOL	A	619	6/6	0.89	0.28	8.28	78,83,87,91	0
8	FUL	B	606	10/11	0.85	0.36	7.72	96,103,105,105	0
3	FUC	A	609	10/11	0.85	0.41	7.45	111,114,115,116	0
6	EDO	B	616	4/4	0.85	0.34	7.31	82,83,84,87	0
5	GOL	A	618	6/6	0.86	0.30	7.25	64,73,77,78	0
7	UNX	A	621	1/1	0.96	0.48	5.86	82,82,82,82	0
9	PEG	B	621	7/7	0.82	0.21	3.41	75,83,87,87	0
5	GOL	A	617	6/6	0.88	0.23	3.00	76,79,81,82	0
6	EDO	B	615	4/4	0.76	0.20	2.40	67,71,75,76	0
4	5HB	B	612	29/29	0.89	0.25	2.13	60,82,89,89	0
2	NAG	B	608	14/15	0.91	0.28	1.96	67,74,82,83	0
4	5HB	A	616	29/29	0.90	0.24	1.78	55,90,95,95	0
2	NAG	A	611	14/15	0.89	0.16	0.71	65,73,78,78	0
5	GOL	B	613	6/6	0.93	0.19	0.65	60,65,74,77	0
6	EDO	A	620	4/4	0.87	0.14	0.14	75,77,78,78	0
2	NAG	A	610	14/15	0.83	0.21	-	74,79,84,84	0
2	NAG	B	609	14/15	0.61	0.33	-	100,108,119,126	0
2	NAG	A	603	14/15	0.64	0.38	-	117,119,123,124	0
2	NAG	A	612	14/15	0.77	0.24	-	73,83,90,93	0
6	EDO	B	617	4/4	0.92	0.11	-	80,81,83,84	0
2	NAG	A	613	14/15	0.82	0.23	-	102,113,116,122	0
2	NAG	A	614	14/15	0.80	0.49	-	127,131,133,133	0
2	NAG	B	605	14/15	0.71	0.37	-	105,114,119,121	0
3	FUC	A	604	10/11	0.90	0.24	-	103,108,111,113	0
2	NAG	A	606	14/15	0.81	0.36	-	100,106,115,115	0
2	NAG	B	603	14/15	0.83	0.35	-	97,100,109,110	0
2	NAG	A	607	14/15	0.78	0.28	-	106,116,118,124	0
2	NAG	A	602	14/15	0.81	0.25	-	95,101,106,112	0
2	NAG	B	611	14/15	0.81	0.28	-	96,111,115,117	0
3	FUC	B	610	10/11	0.79	0.27	-	129,131,133,133	0
2	NAG	A	608	14/15	0.75	0.51	-	126,129,137,139	0
2	NAG	B	601	14/15	0.65	0.30	-	105,114,121,122	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
2	NAG	A	601	14/15	0.74	0.31	-	76,91,96,99	0
2	NAG	B	604	14/15	0.92	0.29	-	86,96,108,111	0
7	UNX	B	620	1/1	0.96	0.61	-	64,64,64,64	0
2	NAG	A	605	14/15	0.92	0.21	-	68,76,83,92	0
7	UNX	B	619	1/1	0.98	1.09	-	73,73,73,73	0
2	NAG	B	607	14/15	0.78	0.17	-	103,108,112,113	0
7	UNX	A	623	1/1	0.97	0.52	-	66,66,66,66	0
2	NAG	B	602	14/15	0.67	0.24	-	96,113,122,123	0
7	UNX	A	622	1/1	0.98	0.72	-	65,65,65,65	0

6.5 Other polymers [i](#)

There are no such residues in this entry.