



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 9, 2017 – 10:51 am GMT

PDB ID : 5DYW
Title : Crystal structure of human butyrylcholinesterase in complex with N-((1-benzylpiperidin-3-yl)methyl)-N-(2-methoxyethyl)naphthalene-2-sulfonamide
Authors : Coquelle, N.; Brus, B.; Colletier, J.P.
Deposited on : 2015-09-25
Resolution : 2.50 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : recal28906
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recal28906

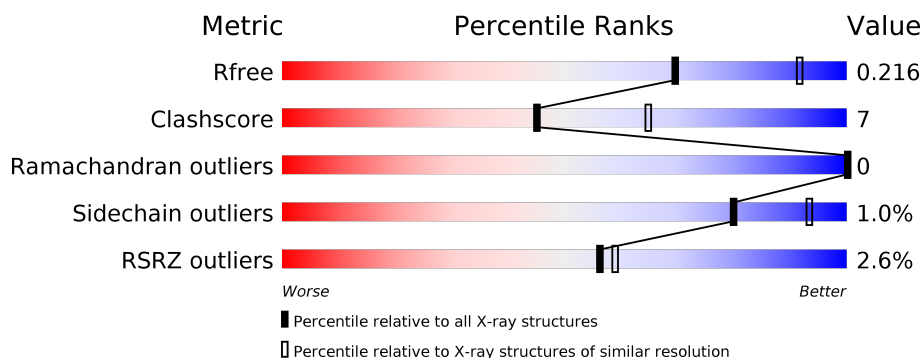
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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}	100719	3846 (2.50-2.50)
Clashscore	112137	4554 (2.50-2.50)
Ramachandran outliers	110173	4463 (2.50-2.50)
Sidechain outliers	110143	4465 (2.50-2.50)
RSRZ outliers	101464	3876 (2.50-2.50)

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> <div></div> <div>84%</div> <div>15%</div> <div>.</div> </div> </div>
1	B	530	<div> <div>4%</div> <div> <div></div> <div>80%</div> <div>18%</div> <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
3	GOL	A	603	-	-	-	X
3	GOL	A	604	-	-	-	X
3	GOL	A	605	-	-	-	X
3	GOL	B	606	-	-	-	X
4	EDO	A	606	-	-	-	X
4	EDO	A	607	-	-	-	X
4	EDO	A	609	-	-	-	X
4	EDO	A	610	-	-	X	-
4	EDO	A	611	-	-	-	X
5	CL	A	613	-	-	-	X
5	CL	B	610	-	-	-	X
7	NAG	A	621	X	-	-	-
7	NAG	A	622	X	-	-	-
7	NAG	A	625	X	-	-	-
7	NAG	A	628	X	-	-	-
7	NAG	B	614	X	-	-	-
7	NAG	B	618	X	-	-	-
8	FUC	A	624	-	-	-	X
9	FUL	A	630	-	-	-	X

2 Entry composition [i](#)

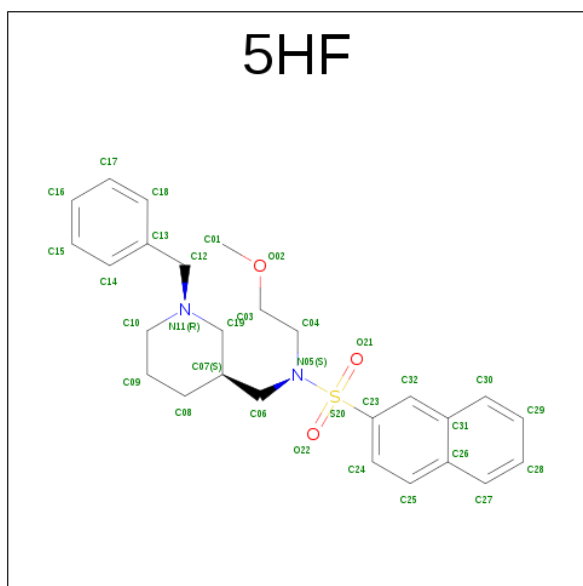
There are 10 unique types of molecules in this entry. The entry contains 9234 atoms, of which 0 are hydrogens and 0 are deuteriums.

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	3	3	0
			4212	2718	710	769	15			
1	B	525	Total	C	N	O	S	7	0	0
			4170	2694	701	760	15			

- Molecule 2 is N-[[[(3S)-1-benzylpiperidin-3-yl]methyl]-N-(2-methoxyethyl)naphthalene-2-sulfonamide (three-letter code: 5HF) (formula: C₂₆H₃₂N₂O₃S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			32	26	2	3	1		
2	B	1	Total	C	N	O	S	0	0
			32	26	2	3	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



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

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).

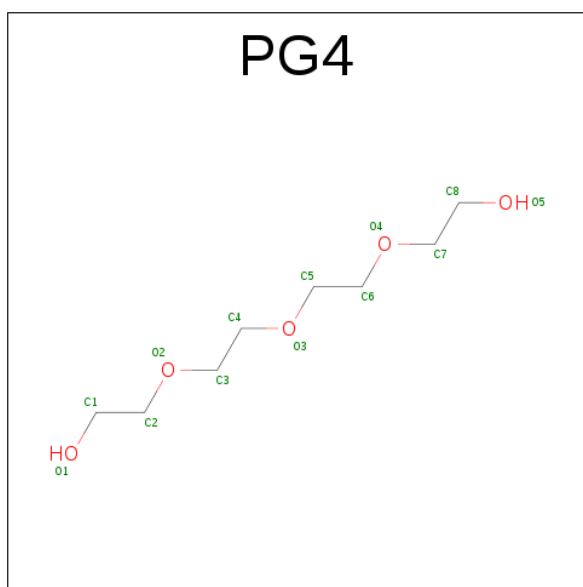


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	A	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		
4	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

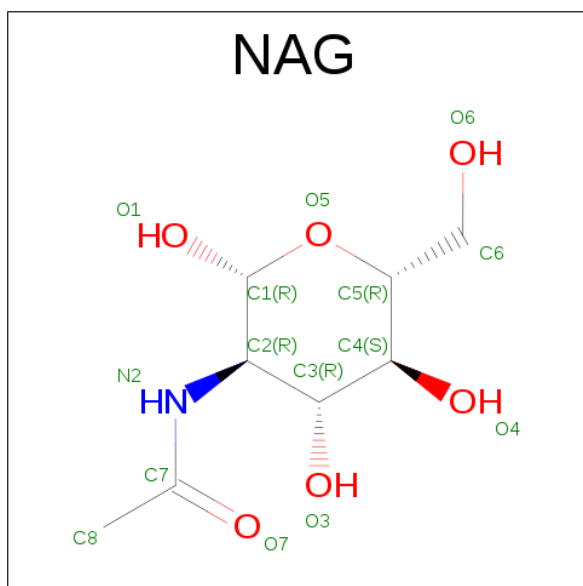
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Cl	0	0
			2	2		
5	A	2	Total	Cl	0	0
			2	2		

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: C₈H₁₈O₅).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			13	8	5		

- Molecule 7 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



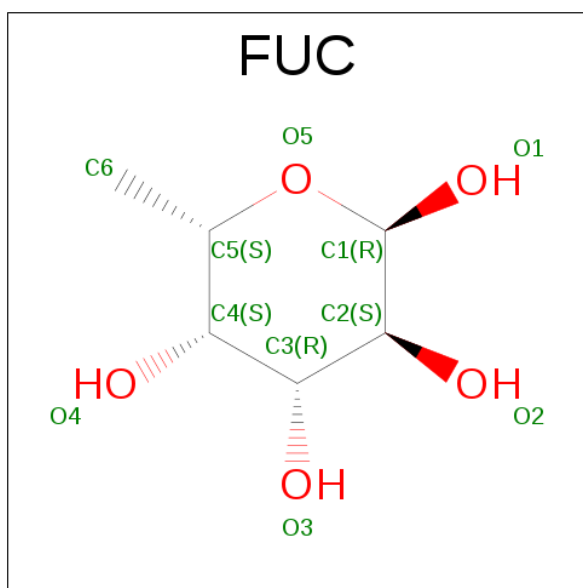
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		

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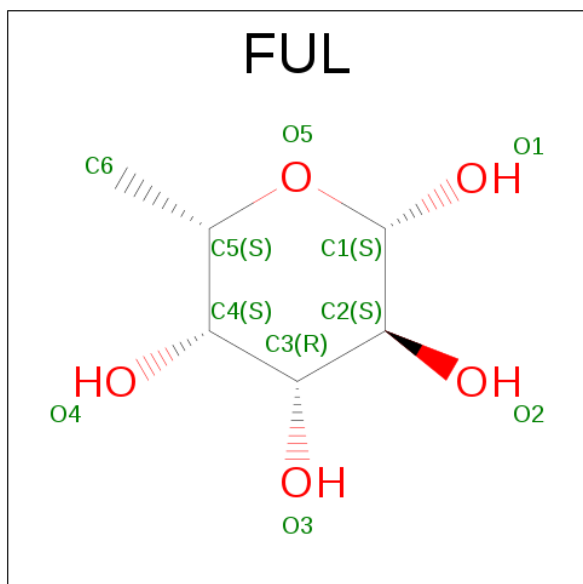
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1	Total	C	N	O	0	0
			14	8	1	5		
7	A	1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

- Molecule 8 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: $C_6H_{12}O_5$).



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

- Molecule 9 is BETA-L-FUCOSE (three-letter code: FUL) (formula: $C_6H_{12}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			10	6	4		

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

- Molecule 10 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	166	Total	O	0	0
			166	166		
10	B	119	Total	O	0	0
			119	119		

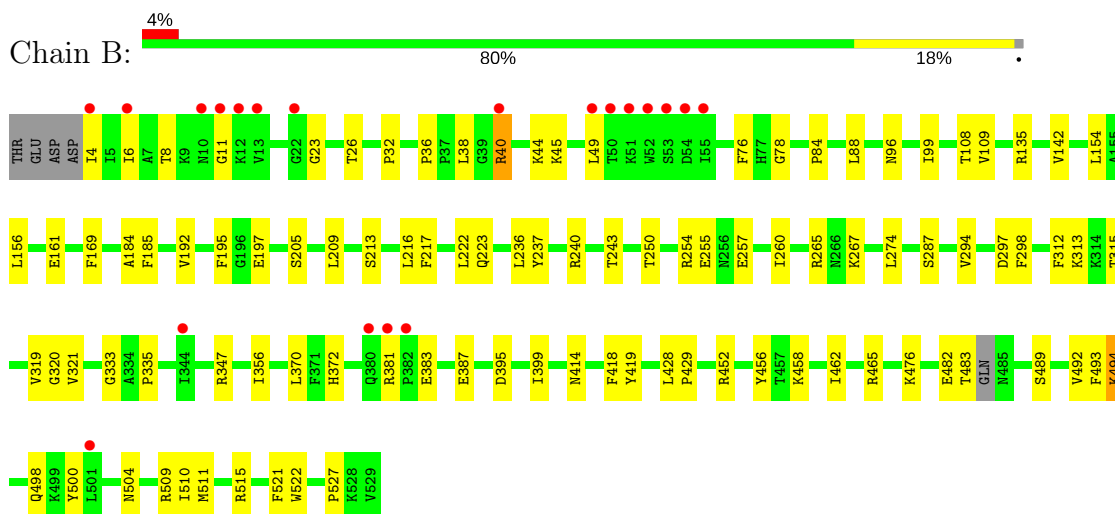
3 Residue-property plots

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: 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	72.21Å 78.86Å 226.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.02 – 2.50 48.20 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (46.02-2.50) 100.0 (48.20-2.50)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.84 (at 2.51Å)	Xtriage
Refinement program	PHENIX (1.10_2155: ???)	Depositor
R, R_{free}	0.190 , 0.216 0.188 , 0.216	Depositor DCC
R_{free} test set	2284 reflections (5.00%)	DCC
Wilson B-factor (Å ²)	44.1	Xtriage
Anisotropy	0.099	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 44.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9234	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.97% 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, 0.333 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: 5HF, GOL, NAG, CL, EDO, PG4, FUC, FUL

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	0.39	0/4341	0.55	0/5894
1	B	0.38	0/4288	0.56	1/5821 (0.0%)
All	All	0.38	0/8629	0.55	1/11715 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	509	ARG	NE-CZ-NH2	-5.47	117.56	120.30

There are no chirality outliers.

There are no planarity outliers.

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	4212	0	4106	56	0
1	B	4170	0	4057	70	0
2	A	32	0	0	0	0
2	B	32	0	0	0	0
3	A	24	0	32	2	0
3	B	30	0	40	4	0
4	A	24	0	36	8	0
4	B	12	0	18	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	13	0	18	0	0
7	A	182	0	160	5	0
7	B	154	0	137	2	0
8	A	20	0	20	1	0
9	A	10	0	10	0	0
9	B	30	0	30	0	0
10	A	166	0	0	0	0
10	B	119	0	0	5	0
All	All	9234	0	8664	130	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 7.

The worst 5 of 130 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:386:ARG:NH2	4:A:610:EDO:O2	1.94	1.01
1:B:44:LYS:NZ	1:B:161:GLU:OE1	2.08	0.86
1:B:217:PHE:O	1:B:313:LYS:NZ	2.12	0.82
1:A:268:ASP:HB3	1:A:271:GLU:HG3	1.65	0.77
1:A:100:PRO:HG2	1:A:104:PRO:HG3	1.70	0.73

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	528/530 (100%)	505 (96%)	23 (4%)	0	100	100
1	B	521/530 (98%)	488 (94%)	33 (6%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1049/1060 (99%)	993 (95%)	56 (5%)	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	453/455 (100%)	447 (99%)	6 (1%)	73	90
1	B	446/455 (98%)	443 (99%)	3 (1%)	87	96
All	All	899/910 (99%)	890 (99%)	9 (1%)	80	93

5 of 9 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	483	THR
1	B	494	LYS
1	B	40	ARG
1	A	379	ASP
1	A	506	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	35	GLN
1	B	289	ASN
1	B	311	GLN
1	B	498	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 55 ligands modelled in this entry, 4 are monoatomic - leaving 51 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	5HF	A	601	-	35,35,35	2.10	10 (28%)	46,48,48	3.32	11 (23%)
3	GOL	A	602	-	5,5,5	0.29	0	5,5,5	0.51	0
3	GOL	A	603	-	5,5,5	0.27	0	5,5,5	0.47	0
3	GOL	A	604	-	5,5,5	0.41	0	5,5,5	0.20	0
3	GOL	A	605	-	5,5,5	0.35	0	5,5,5	0.23	0
4	EDO	A	606	-	3,3,3	0.50	0	2,2,2	0.36	0
4	EDO	A	607	-	3,3,3	0.57	0	2,2,2	0.39	0
4	EDO	A	608	-	3,3,3	0.58	0	2,2,2	0.45	0
4	EDO	A	609	-	3,3,3	0.51	0	2,2,2	0.20	0
4	EDO	A	610	-	3,3,3	0.28	0	2,2,2	0.62	0
4	EDO	A	611	-	3,3,3	0.45	0	2,2,2	0.47	0
6	PG4	A	614	-	12,12,12	0.56	0	11,11,11	0.24	0
7	NAG	A	615	1,7	14,14,15	0.58	1 (7%)	15,19,21	0.53	0
7	NAG	A	616	7	14,14,15	0.22	0	15,19,21	0.75	1 (6%)
7	NAG	A	617	1,8,7	14,14,15	0.38	0	15,19,21	0.45	0
7	NAG	A	618	7	14,14,15	0.60	0	15,19,21	0.87	1 (6%)
8	FUC	A	619	7	9,10,11	1.75	2 (22%)	13,14,16	0.93	0
7	NAG	A	620	1,7	14,14,15	0.37	0	15,19,21	0.46	0
7	NAG	A	621	7	14,14,15	0.64	0	15,19,21	0.74	0
7	NAG	A	622	1,8,7	14,14,15	0.27	0	15,19,21	1.08	2 (13%)
7	NAG	A	623	7	14,14,15	0.64	0	15,19,21	0.92	1 (6%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	FUC	A	624	7	9,10,11	1.80	2 (22%)	13,14,16	1.77	4 (30%)
7	NAG	A	625	1	14,14,15	0.62	1 (7%)	15,19,21	1.18	1 (6%)
7	NAG	A	626	1,7	14,14,15	0.43	0	15,19,21	0.80	1 (6%)
7	NAG	A	627	7	14,14,15	0.41	0	15,19,21	0.56	0
7	NAG	A	628	1,9,7	14,14,15	1.59	3 (21%)	15,19,21	1.03	1 (6%)
7	NAG	A	629	7	14,14,15	0.37	0	15,19,21	0.55	0
9	FUL	A	630	7	9,10,11	1.82	2 (22%)	13,14,16	1.22	3 (23%)
2	5HF	B	601	-	35,35,35	1.51	7 (20%)	46,48,48	3.24	16 (34%)
3	GOL	B	602	-	5,5,5	0.37	0	5,5,5	0.41	0
3	GOL	B	603	-	5,5,5	0.31	0	5,5,5	0.29	0
3	GOL	B	604	-	5,5,5	0.31	0	5,5,5	0.35	0
3	GOL	B	605	-	5,5,5	0.35	0	5,5,5	0.41	0
3	GOL	B	606	-	5,5,5	0.37	0	5,5,5	0.11	0
4	EDO	B	607	-	3,3,3	0.52	0	2,2,2	0.32	0
4	EDO	B	608	-	3,3,3	0.45	0	2,2,2	0.41	0
4	EDO	B	609	-	3,3,3	0.55	0	2,2,2	0.16	0
7	NAG	B	612	1	14,14,15	0.56	0	15,19,21	0.94	1 (6%)
7	NAG	B	613	1	14,14,15	0.76	1 (7%)	15,19,21	0.72	1 (6%)
7	NAG	B	614	1	14,14,15	0.62	0	15,19,21	1.05	1 (6%)
7	NAG	B	615	1,9,7	14,14,15	0.30	0	15,19,21	0.51	0
7	NAG	B	616	7	14,14,15	0.15	0	15,19,21	0.70	1 (6%)
9	FUL	B	617	7	9,10,11	1.99	2 (22%)	13,14,16	1.51	4 (30%)
7	NAG	B	618	1,9,7	14,14,15	0.15	0	15,19,21	0.51	0
7	NAG	B	619	7	14,14,15	0.24	0	15,19,21	0.42	0
9	FUL	B	620	7	9,10,11	1.92	2 (22%)	13,14,16	1.00	1 (7%)
7	NAG	B	621	1	14,14,15	0.50	0	15,19,21	0.58	0
7	NAG	B	622	1,9,7	14,14,15	0.20	0	15,19,21	0.50	0
7	NAG	B	623	7	14,14,15	0.39	0	15,19,21	1.38	2 (13%)
9	FUL	B	624	7	9,10,11	1.93	2 (22%)	13,14,16	1.44	3 (23%)
7	NAG	B	625	1	14,14,15	0.54	0	15,19,21	0.91	1 (6%)

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	5HF	A	601	-	-	0/24/34/34	0/4/4/4
3	GOL	A	602	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	A	603	-	-	0/4/4/4	0/0/0/0
3	GOL	A	604	-	-	0/4/4/4	0/0/0/0
3	GOL	A	605	-	-	0/4/4/4	0/0/0/0
4	EDO	A	606	-	-	0/1/1/1	0/0/0/0
4	EDO	A	607	-	-	0/1/1/1	0/0/0/0
4	EDO	A	608	-	-	0/1/1/1	0/0/0/0
4	EDO	A	609	-	-	0/1/1/1	0/0/0/0
4	EDO	A	610	-	-	0/1/1/1	0/0/0/0
4	EDO	A	611	-	-	0/1/1/1	0/0/0/0
6	PG4	A	614	-	-	0/10/10/10	0/0/0/0
7	NAG	A	615	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	616	7	-	0/6/23/26	0/1/1/1
7	NAG	A	617	1,8,7	-	0/6/23/26	0/1/1/1
7	NAG	A	618	7	-	0/6/23/26	0/1/1/1
8	FUC	A	619	7	-	0/0/17/20	0/1/1/1
7	NAG	A	620	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	621	7	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	A	622	1,8,7	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	A	623	7	-	0/6/23/26	0/1/1/1
8	FUC	A	624	7	-	0/0/17/20	0/1/1/1
7	NAG	A	625	1	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	A	626	1,7	-	0/6/23/26	0/1/1/1
7	NAG	A	627	7	-	0/6/23/26	0/1/1/1
7	NAG	A	628	1,9,7	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	A	629	7	-	0/6/23/26	0/1/1/1
9	FUL	A	630	7	-	0/0/17/20	0/1/1/1
2	5HF	B	601	-	-	0/24/34/34	0/4/4/4
3	GOL	B	602	-	-	0/4/4/4	0/0/0/0
3	GOL	B	603	-	-	0/4/4/4	0/0/0/0
3	GOL	B	604	-	-	0/4/4/4	0/0/0/0
3	GOL	B	605	-	-	0/4/4/4	0/0/0/0
3	GOL	B	606	-	-	0/4/4/4	0/0/0/0
4	EDO	B	607	-	-	0/1/1/1	0/0/0/0
4	EDO	B	608	-	-	0/1/1/1	0/0/0/0
4	EDO	B	609	-	-	0/1/1/1	0/0/0/0
7	NAG	B	612	1	-	0/6/23/26	0/1/1/1
7	NAG	B	613	1	-	0/6/23/26	0/1/1/1
7	NAG	B	614	1	1/1/5/7	0/6/23/26	0/1/1/1
7	NAG	B	615	1,9,7	-	0/6/23/26	0/1/1/1
7	NAG	B	616	7	-	0/6/23/26	0/1/1/1
9	FUL	B	617	7	-	0/0/17/20	0/1/1/1
7	NAG	B	618	1,9,7	1/1/5/7	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
7	NAG	B	619	7	-	0/6/23/26	0/1/1/1
9	FUL	B	620	7	-	0/0/17/20	0/1/1/1
7	NAG	B	621	1	-	0/6/23/26	0/1/1/1
7	NAG	B	622	1,9,7	-	0/6/23/26	0/1/1/1
7	NAG	B	623	7	-	0/6/23/26	0/1/1/1
9	FUL	B	624	7	-	0/0/17/20	0/1/1/1
7	NAG	B	625	1	-	0/6/23/26	0/1/1/1

The worst 5 of 35 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	A	628	NAG	O5-C1	-3.67	1.37	1.43
2	B	601	5HF	C23-S20	-3.64	1.71	1.76
2	B	601	5HF	C19-C07	-3.25	1.48	1.52
9	B	624	FUL	C2-C3	-3.05	1.48	1.52
2	B	601	5HF	C08-C07	-3.05	1.43	1.52

The worst 5 of 57 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	5HF	O21-S20-O22	-11.33	100.40	119.46
2	A	601	5HF	O21-S20-O22	-9.87	102.86	119.46
2	B	601	5HF	C06-N05-S20	-4.83	106.86	117.75
2	B	601	5HF	C04-N05-C06	-4.01	110.06	116.76
2	B	601	5HF	C04-N05-S20	-3.12	111.34	117.92

5 of 6 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
7	B	614	NAG	C1
7	A	628	NAG	C1
7	A	621	NAG	C1
7	A	622	NAG	C1
7	B	618	NAG	C1

There are no torsion outliers.

There are no ring outliers.

18 monomers are involved in 22 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	603	GOL	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	605	GOL	1	0
4	A	606	EDO	1	0
4	A	609	EDO	2	0
4	A	610	EDO	5	0
7	A	615	NAG	1	0
7	A	617	NAG	1	0
7	A	618	NAG	1	0
7	A	620	NAG	1	0
7	A	621	NAG	2	0
7	A	622	NAG	1	0
7	A	623	NAG	1	0
8	A	624	FUC	1	0
3	B	603	GOL	1	0
3	B	605	GOL	1	0
3	B	606	GOL	2	0
7	B	615	NAG	1	0
7	B	623	NAG	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	527/530 (99%)	0.09	7 (1%) 77 78	28, 41, 58, 76	2 (0%)
1	B	525/530 (99%)	0.22	20 (3%) 41 43	33, 48, 72, 105	4 (0%)
All	All	1052/1060 (99%)	0.15	27 (2%) 56 59	28, 44, 66, 105	6 (0%)

The worst 5 of 27 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	4	ILE	5.2
1	B	53	SER	4.1
1	B	54	ASP	3.9
1	B	344	ILE	3.7
1	A	529	VAL	3.6

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. 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
4	EDO	A	611	4/4	0.81	0.53	17.25	45,48,52,53	0
4	EDO	A	607	4/4	0.77	0.23	9.57	51,52,53,65	0
3	GOL	A	604	6/6	0.87	0.25	7.30	44,47,52,52	0
3	GOL	B	606	6/6	0.88	0.27	6.45	51,52,52,53	0
3	GOL	A	605	6/6	0.84	0.29	5.48	47,50,58,62	0
8	FUC	A	624	10/11	0.87	0.43	5.05	63,69,80,82	0
5	CL	A	613	1/1	0.97	0.31	4.35	47,47,47,47	0
4	EDO	A	606	4/4	0.94	0.32	3.98	48,49,52,54	0
3	GOL	A	603	6/6	0.88	0.28	2.67	40,46,46,46	0
4	EDO	A	609	4/4	0.84	0.25	2.54	54,55,62,67	0
9	FUL	A	630	10/11	0.77	0.23	2.43	71,84,92,93	0
5	CL	B	610	1/1	0.76	0.24	2.21	69,69,69,69	0
4	EDO	A	610	4/4	0.84	0.24	1.65	53,55,56,63	0
4	EDO	B	609	4/4	0.85	0.21	1.34	42,43,44,47	0
7	NAG	A	627	14/15	0.84	0.18	0.69	50,55,59,59	0
3	GOL	B	603	6/6	0.82	0.22	0.67	58,61,63,66	0
2	5HF	A	601	32/32	0.91	0.19	0.65	35,48,52,58	0
2	5HF	B	601	32/32	0.90	0.19	0.47	36,45,52,58	0
5	CL	B	611	1/1	0.91	0.19	0.39	46,46,46,46	0
7	NAG	B	625	14/15	0.74	0.19	0.31	77,86,87,88	0
4	EDO	A	608	4/4	0.93	0.14	0.15	44,47,49,56	0
3	GOL	B	602	6/6	0.92	0.16	0.11	49,51,52,56	0
9	FUL	B	617	10/11	0.85	0.17	-0.07	57,64,69,72	0
7	NAG	B	621	14/15	0.94	0.20	-0.17	54,55,58,60	0
4	EDO	B	607	4/4	0.85	0.15	-0.21	50,53,59,62	0
7	NAG	B	618	14/15	0.88	0.19	-0.31	85,93,100,103	0
3	GOL	B	605	6/6	0.93	0.16	-0.35	43,47,55,61	0
7	NAG	A	625	14/15	0.90	0.13	-1.24	59,60,65,66	0
7	NAG	A	626	14/15	0.94	0.11	-1.86	46,50,53,53	0
3	GOL	A	602	6/6	0.96	0.08	-3.64	41,43,46,55	0
7	NAG	A	620	14/15	0.88	0.28	-	59,62,71,76	0
7	NAG	B	613	14/15	0.50	0.32	-	87,92,96,104	0
7	NAG	B	619	14/15	0.77	0.41	-	108,111,114,116	0
7	NAG	B	615	14/15	0.87	0.21	-	66,72,76,76	0
7	NAG	B	616	14/15	0.81	0.34	-	78,81,90,91	0
7	NAG	A	623	14/15	0.71	0.48	-	97,104,106,109	0
7	NAG	B	614	14/15	0.89	0.29	-	76,78,83,85	0
7	NAG	A	616	14/15	0.76	0.36	-	75,79,81,84	0
7	NAG	A	621	14/15	0.82	0.41	-	82,87,89,90	0
7	NAG	A	618	14/15	0.76	0.32	-	83,96,101,102	0
7	NAG	B	622	14/15	0.85	0.19	-	65,81,93,106	0
7	NAG	A	622	14/15	0.68	0.29	-	84,99,104,107	0
8	FUC	A	619	10/11	0.86	0.38	-	78,80,81,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
7	NAG	B	612	14/15	0.67	0.34	-	84,93,100,102	0
7	NAG	A	617	14/15	0.93	0.22	-	62,74,84,88	0
9	FUL	B	620	10/11	0.72	0.39	-	108,114,120,121	0
6	PG4	A	614	13/13	0.78	0.27	-	66,71,77,77	0
7	NAG	A	628	14/15	0.74	0.22	-	79,97,103,107	0
7	NAG	B	623	14/15	0.75	0.37	-	70,94,106,113	0
9	FUL	B	624	10/11	0.57	0.44	-	113,119,122,122	0
5	CL	A	612	1/1	0.83	0.37	-	75,75,75,75	0
7	NAG	A	615	14/15	0.90	0.26	-	59,61,69,73	0
3	GOL	B	604	6/6	0.82	0.24	-	58,59,60,67	0
4	EDO	B	608	4/4	0.82	0.16	-	62,64,66,68	0
7	NAG	A	629	14/15	0.78	0.28	-	100,109,110,112	0

6.5 Other polymers [i](#)

There are no such residues in this entry.