



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 17, 2016 – 10:51 AM EDT

PDB ID : 5DLT
Title : Crystal structure of Autotaxin (ENPP2) with 7-alpha-hydroxycholesterol
Authors : Hausmann, J.; Joosten, R.P.; Perrakis, A.
Deposited on : 2015-09-07
Resolution : 1.60 Å(reported)

This is a Full wwPDB X-ray Structure Validation 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-20027257
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-20027257

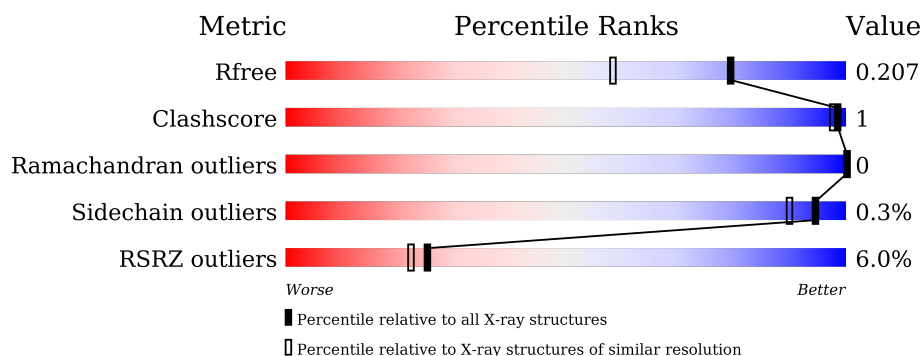
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.60 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	2475 (1.60-1.60)
Clashscore	102246	2732 (1.60-1.60)
Ramachandran outliers	100387	2654 (1.60-1.60)
Sidechain outliers	100360	2653 (1.60-1.60)
RSRZ outliers	91569	2479 (1.60-1.60)

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	827	<div> <div>6%</div> <div>93%</div> <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
10	GOL	A	931	-	-	-	X
10	GOL	A	933	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	GOL	A	935	-	-	-	X

2 Entry composition [i](#)

There are 11 unique types of molecules in this entry. The entry contains 7189 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.

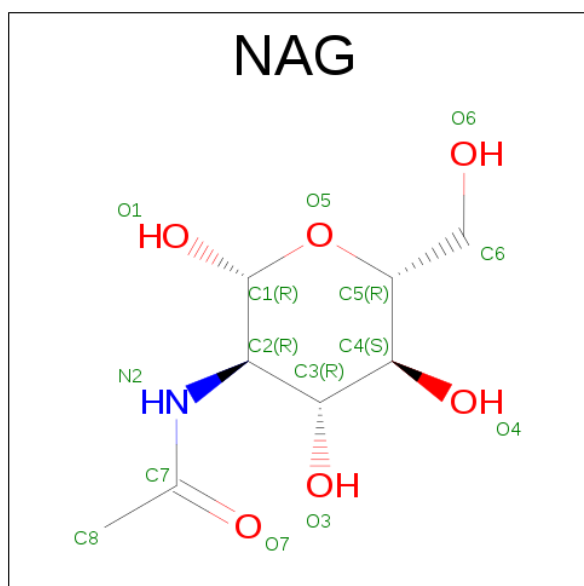
- Molecule 1 is a protein called Ectonucleotide pyrophosphatase/phosphodiesterase family member 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	796	Total	C	N	O	P	S	0	11	1
			6503	4130	1123	1199	1	50			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	410	ALA	ASN	engineered mutation	UNP Q64610
A	581	PHE	LEU	cloning artifact	UNP Q64610
A	591	THR	ARG	cloning artifact	UNP Q64610
A	806	ALA	ASN	engineered mutation	UNP Q64610

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



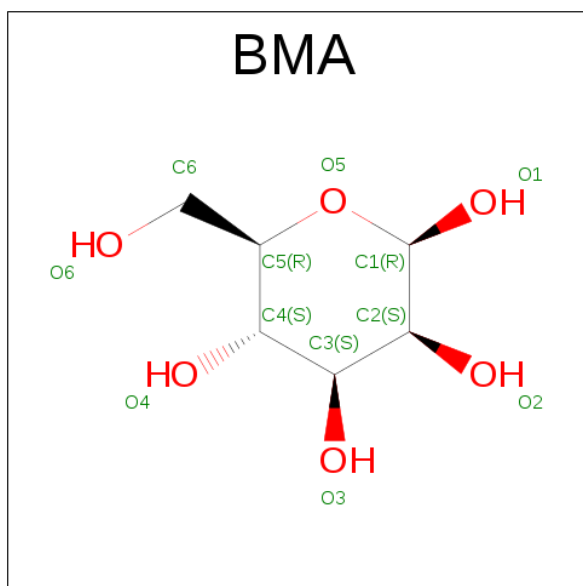
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

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

- Molecule 3 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).

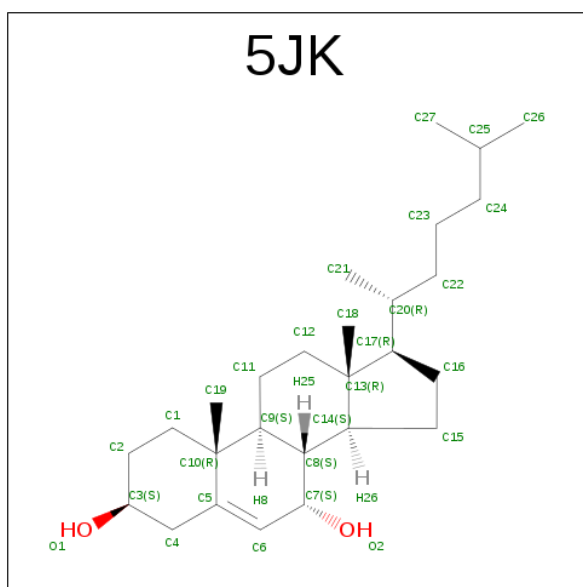


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

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

- Molecule 5 is 7alpha-hydroxycholesterol (three-letter code: 5JK) (formula: $C_{27}H_{46}O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			29	27	2		

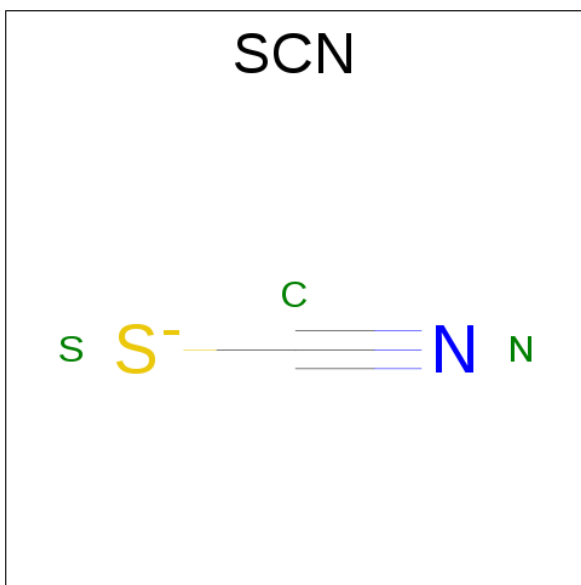
- Molecule 6 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Ca	0	0
			1	1		

- Molecule 7 is IODIDE ION (three-letter code: IOD) (formula: I).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	10	Total	I	0	0
			10	10		

- Molecule 8 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).

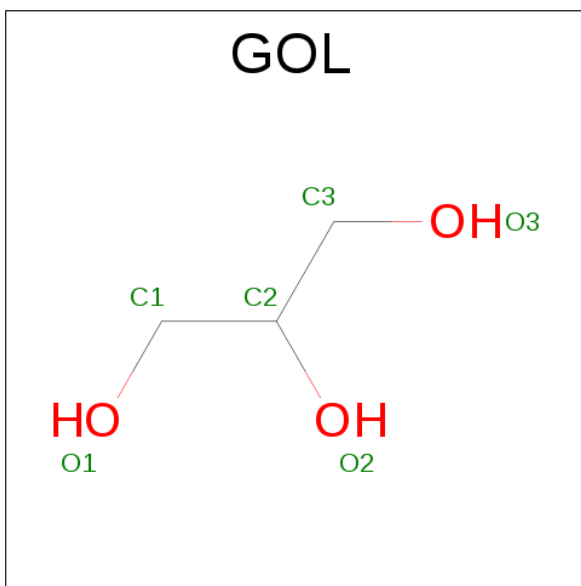


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	A	1	Total	C	N	S	0	0
			3	1	1	1		
8	A	1	Total	C	N	S	0	0
			3	1	1	1		
8	A	1	Total	C	N	S	0	0
			3	1	1	1		
8	A	1	Total	C	N	S	0	0
			3	1	1	1		
8	A	1	Total	C	N	S	0	0
			3	1	1	1		
8	A	1	Total	C	N	S	0	0
			3	1	1	1		
8	A	1	Total	C	N	S	0	0
			3	1	1	1		
8	A	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 9 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	2	Total	Na	0	0
			2	2		

- Molecule 10 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

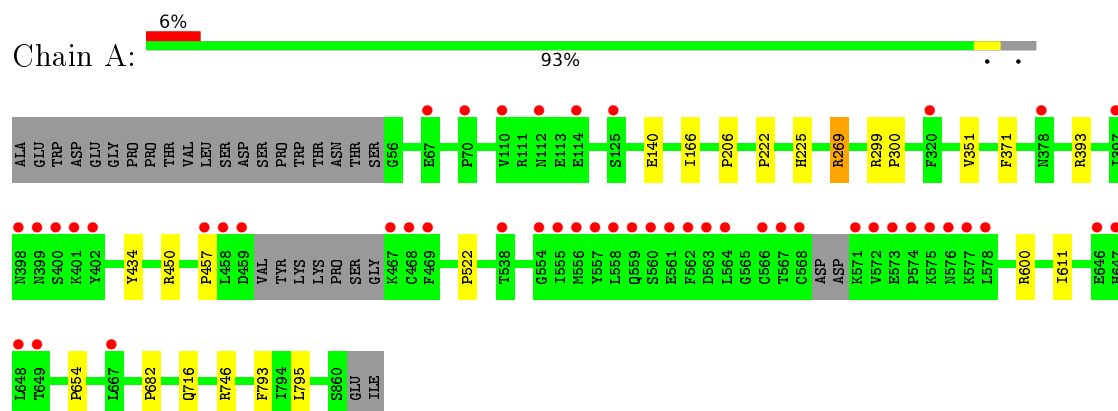
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	526	Total	O	0	2
			528	528		

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 ($RSRZ > 2$). 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: Ectonucleotide pyrophosphatase/phosphodiesterase family member 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	53.67Å 63.48Å 70.72Å 98.72° 105.80° 99.97°	Depositor
Resolution (Å)	44.02 – 1.60 44.02 – 1.60	Depositor EDS
% Data completeness (in resolution range)	92.1 (44.02-1.60) 85.9 (44.02-1.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 1.60Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.171 , 0.196 0.182 , 0.207	Depositor DCC
R_{free} test set	5262 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	19.8	Xtriage
Anisotropy	0.291	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 41.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7189	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.60% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, ZN, BMA, NAG, TPO, NA, CA, SCN, 5JK, IOD

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	0.48	0/6700	0.73	5/9077 (0.1%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	746	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	A	299	ARG	NE-CZ-NH1	5.98	123.29	120.30
1	A	393	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	450	ARG	NE-CZ-NH1	5.34	122.97	120.30
1	A	746	ARG	NE-CZ-NH2	-5.13	117.73	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	6503	0	6295	12	0
2	A	28	0	24	0	0
3	A	11	0	10	0	0
4	A	2	0	0	0	0
5	A	29	0	0	0	0
6	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	A	10	0	0	1	0
8	A	33	0	0	0	0
9	A	2	0	0	0	0
10	A	42	0	55	1	0
11	A	528	0	0	0	0
All	All	7189	0	6384	12	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 1.

All (12) 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:793[B]:PHE:CD1	1:A:795:LEU:HG	2.36	0.60
1:A:522:PRO:HB2	10:A:932:GOL:H32	1.88	0.56
1:A:600:ARG:HD2	1:A:611:ILE:HD11	1.88	0.55
1:A:654:PRO:HG3	7:A:913:IOD:I	2.79	0.53
1:A:371:PHE:CE1	1:A:457:PRO:HA	2.47	0.50
1:A:269[A]:ARG:HB3	1:A:300:PRO:HA	1.94	0.48
1:A:793[B]:PHE:CE1	1:A:795:LEU:HG	2.48	0.48
1:A:682:PRO:HB3	1:A:716[A]:GLN:HB3	1.96	0.47
1:A:166:ILE:HD12	1:A:351:VAL:HG11	1.96	0.46
1:A:222:PRO:HA	1:A:225:HIS:CE1	2.52	0.44
1:A:682:PRO:HB3	1:A:716[B]:GLN:HB3	2.00	0.43
1:A:206:PRO:HD3	1:A:434:TYR:CE1	2.55	0.42

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	800/827 (97%)	774 (97%)	26 (3%)	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	730/748 (98%)	727 (100%)	3 (0%)	93	88

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	140	GLU
1	A	269[A]	ARG
1	A	269[B]	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	TPO	A	209	1,4	7,10,11	0.58	0	10,14,16	1.68	3 (30%)

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	TPO	A	209	1,4	-	0/8/11/13	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	209	TPO	OG1-P-O1P	-3.26	99.70	107.48
1	A	209	TPO	O-C-CA	-2.14	119.85	125.69
1	A	209	TPO	C-CA-N	2.38	115.20	109.95

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 37 ligands modelled in this entry, 15 are monoatomic - leaving 22 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	901	1,2	14,14,15	0.57	0	15,19,21	0.87	0
2	NAG	A	902	3,2	14,14,15	0.58	0	15,19,21	1.58	2 (13%)
3	BMA	A	903	2	11,11,12	0.48	0	15,15,17	1.49	2 (13%)
5	5JK	A	906	-	32,32,32	0.68	1 (3%)	46,50,50	1.18	4 (8%)
8	SCN	A	918	-	2,2,2	0.67	0	1,1,1	0.38	0
8	SCN	A	919	-	2,2,2	0.66	0	1,1,1	0.48	0
8	SCN	A	920	-	2,2,2	0.59	0	1,1,1	0.52	0
8	SCN	A	921	-	2,2,2	0.64	0	1,1,1	0.25	0
8	SCN	A	922	-	2,2,2	0.61	0	1,1,1	0.46	0
8	SCN	A	923	-	2,2,2	0.51	0	1,1,1	0.57	0
8	SCN	A	924	-	2,2,2	0.68	0	1,1,1	0.42	0
8	SCN	A	925	-	2,2,2	0.78	0	1,1,1	0.55	0
8	SCN	A	926	-	2,2,2	0.62	0	1,1,1	0.47	0
8	SCN	A	927	-	2,2,2	0.67	0	1,1,1	0.55	0
10	GOL	A	930	-	5,5,5	0.33	0	5,5,5	0.27	0
10	GOL	A	931	9	5,5,5	0.25	0	5,5,5	0.28	0
10	GOL	A	932	-	5,5,5	0.28	0	5,5,5	0.44	0
10	GOL	A	933	-	5,5,5	0.22	0	5,5,5	0.50	0
10	GOL	A	934	-	5,5,5	0.20	0	5,5,5	0.20	0
10	GOL	A	935	-	5,5,5	0.35	0	5,5,5	0.45	0
10	GOL	A	936	-	5,5,5	0.69	0	5,5,5	0.69	0
8	SCN	A	937	-	2,2,2	0.66	0	1,1,1	0.42	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	901	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	902	3,2	-	0/6/23/26	0/1/1/1
3	BMA	A	903	2	-	0/2/19/22	0/1/1/1
5	5JK	A	906	-	-	0/10/71/71	0/4/4/4
8	SCN	A	918	-	-	0/0/0/0	0/0/0/0
8	SCN	A	919	-	-	0/0/0/0	0/0/0/0
8	SCN	A	920	-	-	0/0/0/0	0/0/0/0
8	SCN	A	921	-	-	0/0/0/0	0/0/0/0
8	SCN	A	922	-	-	0/0/0/0	0/0/0/0
8	SCN	A	923	-	-	0/0/0/0	0/0/0/0
8	SCN	A	924	-	-	0/0/0/0	0/0/0/0
8	SCN	A	925	-	-	0/0/0/0	0/0/0/0
8	SCN	A	926	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
8	SCN	A	927	-	-	0/0/0/0	0/0/0/0
10	GOL	A	930	-	-	0/4/4/4	0/0/0/0
10	GOL	A	931	9	-	0/4/4/4	0/0/0/0
10	GOL	A	932	-	-	0/4/4/4	0/0/0/0
10	GOL	A	933	-	-	0/4/4/4	0/0/0/0
10	GOL	A	934	-	-	0/4/4/4	0/0/0/0
10	GOL	A	935	-	-	0/4/4/4	0/0/0/0
10	GOL	A	936	-	-	0/4/4/4	0/0/0/0
8	SCN	A	937	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	906	5JK	C6-C5	2.36	1.36	1.32

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	906	5JK	O2-C7-C6	-3.16	102.06	109.36
3	A	903	BMA	O5-C1-C2	-2.99	106.11	110.89
5	A	906	5JK	C19-C10-C5	-2.64	103.80	108.30
5	A	906	5JK	C1-C2-C3	-2.48	107.12	110.41
3	A	903	BMA	C1-C2-C3	2.79	112.93	109.55
2	A	902	NAG	C4-C3-C2	3.25	116.39	111.34
5	A	906	5JK	C4-C5-C10	3.39	121.33	116.41
2	A	902	NAG	C2-N2-C7	3.91	128.19	123.11

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
10	A	932	GOL	1	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 ⓘ

6.1 Protein, DNA and RNA chains ⓘ

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	795/827 (96%)	0.24	48 (6%) 25 22	12, 25, 54, 97	0

All (48) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	572	VAL	12.5
1	A	397	ILE	10.7
1	A	398	ASN	7.2
1	A	558	LEU	6.7
1	A	458	LEU	6.5
1	A	571	LYS	6.4
1	A	400	SER	5.5
1	A	563	ASP	5.3
1	A	568	CYS	5.0
1	A	110	VAL	4.7
1	A	401	LYS	4.6
1	A	538	THR	4.4
1	A	559	GLN	4.2
1	A	468	CYS	4.2
1	A	557	TYR	4.2
1	A	573	GLU	4.1
1	A	646	GLU	4.1
1	A	459	ASP	4.1
1	A	567	THR	4.0
1	A	467	LYS	3.8
1	A	378	ASN	3.7
1	A	647	HIS	3.7
1	A	562	PHE	3.6
1	A	469	PHE	3.5
1	A	70	PRO	3.5
1	A	564	LEU	3.4
1	A	67	GLU	3.3

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Mol	Chain	Res	Type	RSRZ
1	A	320	PHE	3.2
1	A	649	THR	3.2
1	A	574	PRO	3.2
1	A	399	ASN	3.2
1	A	578	LEU	3.1
1	A	575	LYS	3.1
1	A	555	ILE	3.0
1	A	566	CYS	3.0
1	A	402	TYR	3.0
1	A	560	SER	2.9
1	A	577	LYS	2.9
1	A	561	GLU	2.7
1	A	648	LEU	2.6
1	A	554	GLY	2.5
1	A	576	ASN	2.5
1	A	457	PRO	2.4
1	A	125	SER	2.4
1	A	667	LEU	2.3
1	A	112	ASN	2.3
1	A	556	MET	2.1
1	A	114	GLU	2.1

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	TPO	A	209	11/12	0.85	0.13	-	14,19,29,42	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
10	GOL	A	935	6/6	0.90	0.11	2.43	32,36,38,42	0
10	GOL	A	931	6/6	0.81	0.23	2.14	50,54,57,58	0
10	GOL	A	933	6/6	0.83	0.16	2.08	38,44,48,49	0
10	GOL	A	936	6/6	0.86	0.22	1.04	22,30,36,45	0
5	5JK	A	906	29/29	0.89	0.11	0.96	21,24,38,40	0
6	CA	A	907	1/1	1.00	0.10	0.94	16,16,16,16	0
8	SCN	A	918	3/3	0.82	0.15	0.82	56,56,56,66	0
8	SCN	A	919	3/3	0.89	0.12	0.66	41,41,46,55	0
8	SCN	A	921	3/3	0.95	0.11	0.50	33,33,40,42	0
2	NAG	A	901	14/15	0.97	0.10	0.50	15,17,20,21	0
8	SCN	A	925	3/3	0.84	0.13	0.21	32,32,34,46	0
8	SCN	A	927	3/3	0.94	0.11	0.15	47,47,51,55	0
7	IOD	A	910	1/1	0.99	0.09	-0.01	37,37,37,37	1
8	SCN	A	937	3/3	0.96	0.10	-0.43	41,41,43,47	0
9	NA	A	928	1/1	0.92	0.07	-0.76	31,31,31,31	0
8	SCN	A	924	3/3	0.91	0.10	-0.86	44,44,45,56	0
7	IOD	A	916	1/1	1.00	0.07	-0.88	31,31,31,31	1
8	SCN	A	926	3/3	0.97	0.07	-0.91	39,39,44,46	0
8	SCN	A	920	3/3	0.97	0.07	-1.17	31,31,38,41	0
7	IOD	A	908	1/1	1.00	0.07	-1.28	22,22,22,22	0
9	NA	A	929	1/1	0.97	0.07	-1.34	18,18,18,18	0
8	SCN	A	923	3/3	0.93	0.08	-1.43	26,26,33,48	0
4	ZN	A	904	1/1	1.00	0.07	-1.44	18,18,18,18	0
7	IOD	A	917	1/1	0.99	0.06	-1.54	42,42,42,42	1
7	IOD	A	914	1/1	0.99	0.04	-2.03	46,46,46,46	1
7	IOD	A	913	1/1	1.00	0.03	-2.04	54,54,54,54	1
4	ZN	A	905	1/1	1.00	0.05	-2.26	21,21,21,21	0
7	IOD	A	915	1/1	1.00	0.04	-2.55	28,28,28,28	1
7	IOD	A	909	1/1	1.00	0.05	-3.59	37,37,37,37	1
7	IOD	A	912	1/1	0.99	0.05	-4.21	38,38,38,38	1
10	GOL	A	930	6/6	0.71	0.25	-	39,47,48,52	0
7	IOD	A	911	1/1	1.00	0.09	-	36,36,36,36	1
8	SCN	A	922	3/3	0.99	0.09	-	30,30,31,37	0
2	NAG	A	902	14/15	0.90	0.12	-	27,35,43,44	0
3	BMA	A	903	11/12	0.44	0.29	-	56,68,74,76	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
10	GOL	A	932	6/6	0.81	0.17	-	44,48,50,60	0
10	GOL	A	934	6/6	0.91	0.18	-	47,50,51,53	0

6.5 Other polymers [i](#)

There are no such residues in this entry.