



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 06:07 am GMT

PDB ID : 3WAW
Title : Crystal Structure of Autotaxin in Complex with 2BoA
Authors : Nishimasu, H.; Ishitani, R.; Nureki, O.
Deposited on : 2013-05-09
Resolution : 1.95 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 : trunk28620
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) : recalc28949

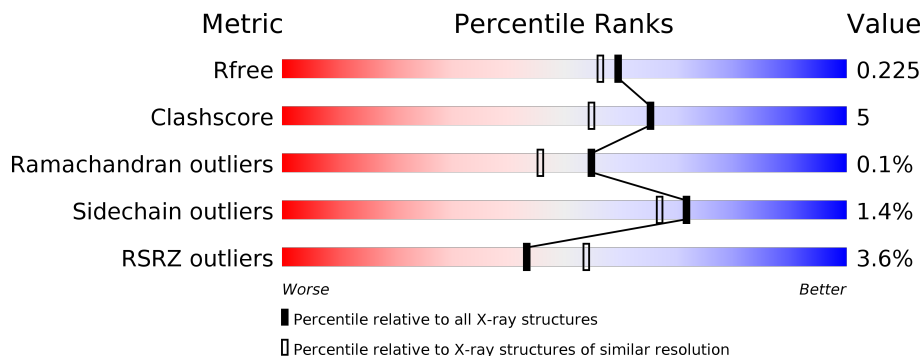
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.95 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	2004 (1.96-1.96)
Clashscore	112137	2136 (1.96-1.96)
Ramachandran outliers	110173	2117 (1.96-1.96)
Sidechain outliers	110143	2117 (1.96-1.96)
RSRZ outliers	101464	2018 (1.96-1.96)

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	831	<div> <div>3%</div> <div>84%</div> <div>9%</div> <div>6%</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	EDO	A	921	-	-	-	X
10	EDO	A	924	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	EDO	A	926	-	-	-	X
10	EDO	A	927	-	-	-	X
10	EDO	A	928	-	-	-	X
10	EDO	A	929	-	-	-	X
10	EDO	A	931	-	-	-	X
11	DWW	A	937	-	-	X	-
3	MAN	A	907	-	-	-	X
9	SCN	A	919	-	-	-	X
9	SCN	A	920	-	-	-	X

2 Entry composition

There are 12 unique types of molecules in this entry. The entry contains 6867 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	779	Total	C	N	O	S	0	0	0
			6249	3972	1069	1160	48			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	?	-	LYS	SEE REMARK 999	UNP Q9R1E6
A	?	-	VAL	SEE REMARK 999	UNP Q9R1E6
A	?	-	GLU	SEE REMARK 999	UNP Q9R1E6
A	?	-	PRO	SEE REMARK 999	UNP Q9R1E6
A	859	SER	-	EXPRESSION TAG	UNP Q9R1E6
A	860	ARG	-	EXPRESSION TAG	UNP Q9R1E6
A	861	GLU	-	EXPRESSION TAG	UNP Q9R1E6
A	862	ASN	-	EXPRESSION TAG	UNP Q9R1E6
A	863	LEU	-	EXPRESSION TAG	UNP Q9R1E6
A	864	TYR	-	EXPRESSION TAG	UNP Q9R1E6
A	865	PHE	-	EXPRESSION TAG	UNP Q9R1E6
A	866	GLN	-	EXPRESSION TAG	UNP Q9R1E6

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

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

- Molecule 3 is a polymer of unknown type called SUGAR (7-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	7	Total	C	N	O	0	0
			83	46	2	35		

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

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

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

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

- Molecule 7 is POTASSIUM ION (three-letter code: K) (formula: K).

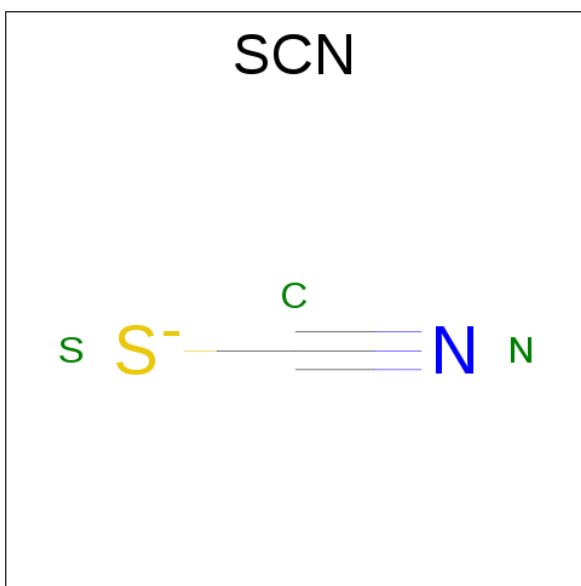
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1	Total	K	0	0
			1	1		

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



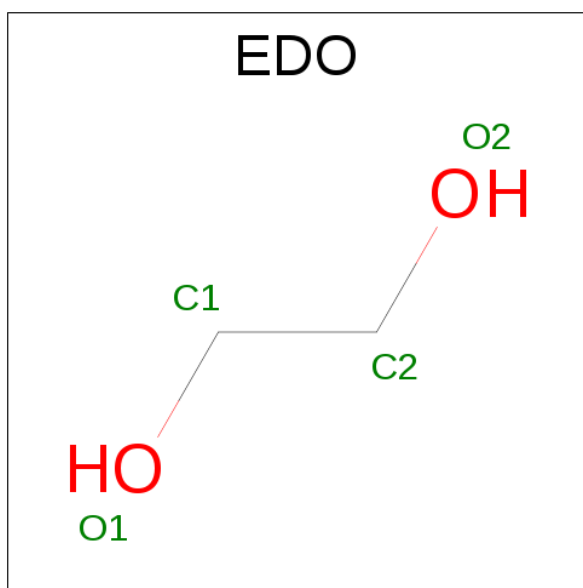
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 9 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



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

- Molecule 10 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



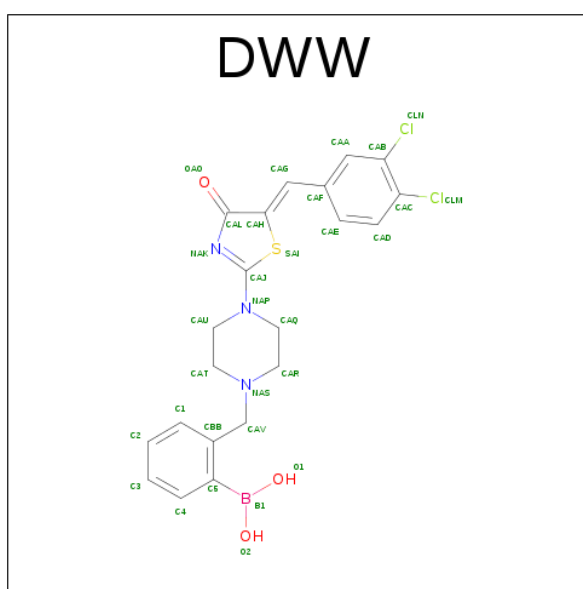
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10	A	1	Total	C	O	0	0
			4	2	2		
10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

Continued on next page...

Continued from previous page...

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

- Molecule 11 is [2-({4-[(5Z)-5-(3,4-DICHLOROBENZYLIDENE)-4-OXO-4,5-DIHYDRO-1,3-THIAZOL-2-YL]PIPERAZIN-1-YL}METHYL)PHENYL]BORONIC ACID (three-letter code: DWW) (formula: C₂₁H₂₀BCl₂N₃O₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
11	A	1	Total	C	Cl	N	O	S	0	0
			23	16	2	3	1	1		

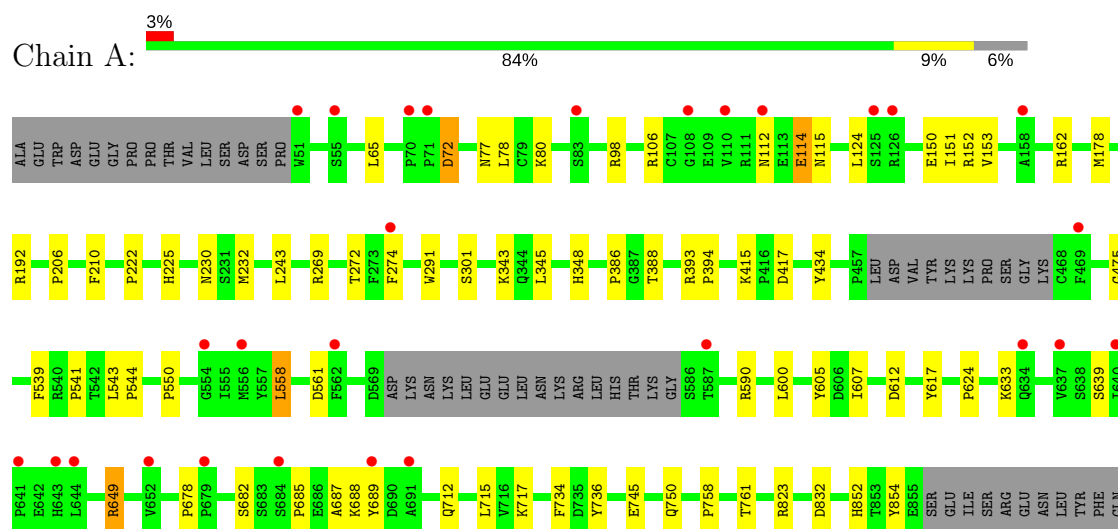
- Molecule 12 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
12	A	373	Total	O	0	0
			373	373		

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 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: Ectonucleotide pyrophosphatase/phosphodiesterase family member 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	61.65Å 94.26Å 75.36Å 90.00° 94.73° 90.00°	Depositor
Resolution (Å)	47.13 – 1.95 47.13 – 1.95	Depositor EDS
% Data completeness (in resolution range)	98.0 (47.13-1.95) 98.0 (47.13-1.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.24 (at 1.95Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.2_869)	Depositor
R, R_{free}	0.192 , 0.231 0.188 , 0.225	Depositor DCC
R_{free} test set	3079 reflections (5.05%)	DCC
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.152	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6867	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, BMA, NAG, NA, K, EDO, SCN, SO4, DWW, CA, MAN

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	0.34	0/6431	0.52	0/8741

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	6249	0	5947	46	0
2	A	56	0	50	0	0
3	A	83	0	70	0	0
4	A	2	0	0	0	0
5	A	1	0	0	0	0
6	A	1	0	0	0	0
7	A	1	0	0	0	0
8	A	5	0	0	0	0
9	A	9	0	0	0	0
10	A	64	0	96	6	0
11	A	23	0	14	15	0
12	A	373	0	0	1	0
All	All	6867	0	6177	60	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 5.

The worst 5 of 60 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)
11:A:937:DWW:NAS	11:A:937:DWW:CAU	2.08	1.16
11:A:937:DWW:NAP	11:A:937:DWW:CAT	2.07	1.15
11:A:937:DWW:NAP	11:A:937:DWW:CAR	2.13	1.11
11:A:937:DWW:NAS	11:A:937:DWW:CAQ	2.13	1.10
11:A:937:DWW:H14	11:A:937:DWW:CAR	1.47	0.99

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	773/831 (93%)	746 (96%)	26 (3%)	1 (0%)	55 46

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	386	PRO

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	696/756 (92%)	686 (99%)	10 (1%)	71 67

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	232	MET
1	A	269	ARG
1	A	558	LEU
1	A	153	VAL
1	A	345	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	ASN

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	$\# Z > 2$
2	NAG	A	901	1,2	14,14,15	0.50	0	15,19,21	1.14	1 (6%)
2	NAG	A	902	2	14,14,15	0.54	0	15,19,21	0.81	0
3	NAG	A	903	1,3	14,14,15	0.55	0	15,19,21	1.25	2 (13%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAG	A	904	3	14,14,15	0.64	0	15,19,21	0.72	0
3	BMA	A	905	3	11,11,12	0.65	0	13,15,17	0.86	0
3	MAN	A	906	3	11,11,12	0.65	0	13,15,17	0.79	0
3	MAN	A	907	3	11,11,12	0.53	0	13,15,17	0.88	1 (7%)
3	MAN	A	908	3	11,11,12	0.58	0	13,15,17	0.70	0
3	MAN	A	909	3	11,11,12	0.72	0	13,15,17	0.88	1 (7%)
2	NAG	A	910	1,2	14,14,15	0.47	0	15,19,21	1.13	2 (13%)
2	NAG	A	911	2	14,14,15	0.40	0	15,19,21	1.65	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	NAG	A	901	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	902	2	-	0/6/23/26	0/1/1/1
3	NAG	A	903	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	904	3	-	0/6/23/26	0/1/1/1
3	BMA	A	905	3	-	0/2/19/22	0/1/1/1
3	MAN	A	906	3	-	0/2/19/22	0/1/1/1
3	MAN	A	907	3	-	0/2/19/22	0/1/1/1
3	MAN	A	908	3	-	0/2/19/22	0/1/1/1
3	MAN	A	909	3	-	0/2/19/22	0/1/1/1
2	NAG	A	910	1,2	-	0/6/23/26	0/1/1/1
2	NAG	A	911	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	903	NAG	O5-C1-C2	-2.96	107.36	111.47
3	A	903	NAG	O4-C4-C3	-2.34	105.27	110.36
2	A	910	NAG	O5-C1-C2	-2.06	108.61	111.47
3	A	907	MAN	O5-C1-C2	-2.02	107.63	110.79
3	A	909	MAN	C1-C2-C3	2.18	112.42	109.65

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.6 Ligand geometry [i](#)

Of 26 ligands modelled in this entry, 5 are monoatomic - leaving 21 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	$\# Z > 2$
8	SO4	A	917	4	4,4,4	0.27	0	6,6,6	0.33	0
9	SCN	A	918	-	1,2,2	0.89	0	0,1,1	0.00	-
9	SCN	A	919	-	1,2,2	0.94	0	0,1,1	0.00	-
9	SCN	A	920	-	1,2,2	0.99	0	0,1,1	0.00	-
10	EDO	A	921	-	3,3,3	0.46	0	2,2,2	0.48	0
10	EDO	A	922	-	3,3,3	0.60	0	2,2,2	0.12	0
10	EDO	A	923	-	3,3,3	0.38	0	2,2,2	0.52	0
10	EDO	A	924	-	3,3,3	0.47	0	2,2,2	0.42	0
10	EDO	A	925	-	3,3,3	0.50	0	2,2,2	0.32	0
10	EDO	A	926	-	3,3,3	0.43	0	2,2,2	0.60	0
10	EDO	A	927	-	3,3,3	0.49	0	2,2,2	0.40	0
10	EDO	A	928	-	3,3,3	0.48	0	2,2,2	0.33	0
10	EDO	A	929	-	3,3,3	0.49	0	2,2,2	0.35	0
10	EDO	A	930	-	3,3,3	0.42	0	2,2,2	0.45	0
10	EDO	A	931	-	3,3,3	0.53	0	2,2,2	0.30	0
10	EDO	A	932	-	3,3,3	0.49	0	2,2,2	0.43	0
10	EDO	A	933	-	3,3,3	0.49	0	2,2,2	0.36	0
10	EDO	A	934	-	3,3,3	0.50	0	2,2,2	0.29	0
10	EDO	A	935	-	3,3,3	0.44	0	2,2,2	0.43	0
10	EDO	A	936	-	3,3,3	0.42	0	2,2,2	0.52	0
11	DWW	A	937	-	25,25,34	6.69	13 (52%)	35,35,48	3.11	13 (37%)

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
8	SO4	A	917	4	-	0/0/0/0	0/0/0/0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
9	SCN	A	918	-	-	0/0/0/0	0/0/0/0
9	SCN	A	919	-	-	0/0/0/0	0/0/0/0
9	SCN	A	920	-	-	0/0/0/0	0/0/0/0
10	EDO	A	921	-	-	0/1/1/1	0/0/0/0
10	EDO	A	922	-	-	0/1/1/1	0/0/0/0
10	EDO	A	923	-	-	0/1/1/1	0/0/0/0
10	EDO	A	924	-	-	0/1/1/1	0/0/0/0
10	EDO	A	925	-	-	0/1/1/1	0/0/0/0
10	EDO	A	926	-	-	0/1/1/1	0/0/0/0
10	EDO	A	927	-	-	0/1/1/1	0/0/0/0
10	EDO	A	928	-	-	0/1/1/1	0/0/0/0
10	EDO	A	929	-	-	0/1/1/1	0/0/0/0
10	EDO	A	930	-	-	0/1/1/1	0/0/0/0
10	EDO	A	931	-	-	0/1/1/1	0/0/0/0
10	EDO	A	932	-	-	0/1/1/1	0/0/0/0
10	EDO	A	933	-	-	0/1/1/1	0/0/0/0
10	EDO	A	934	-	-	0/1/1/1	0/0/0/0
10	EDO	A	935	-	-	0/1/1/1	0/0/0/0
10	EDO	A	936	-	-	0/1/1/1	0/0/0/0
11	DWW	A	937	-	-	0/8/32/38	0/3/3/4

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
11	A	937	DWW	CAU-CAT	-17.33	0.83	1.51
11	A	937	DWW	CAQ-CAR	-17.02	0.84	1.51
11	A	937	DWW	CAL-CAH	-7.31	1.40	1.50
11	A	937	DWW	CAJ-SAI	-2.35	1.69	1.75
11	A	937	DWW	CBB-CAV	-2.24	1.36	1.49

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	A	937	DWW	CAF-CAG-CAH	-8.75	119.05	131.03
11	A	937	DWW	SAI-CAJ-NAK	-6.25	107.91	116.28
11	A	937	DWW	CAL-CAH-SAI	-4.84	106.39	109.09
11	A	937	DWW	CAQ-NAP-CAJ	-4.36	111.55	122.08
11	A	937	DWW	OAO-CAL-CAH	-3.66	120.49	122.45

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 21 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
10	A	921	EDO	1	0
10	A	922	EDO	1	0
10	A	924	EDO	1	0
10	A	926	EDO	1	0
10	A	930	EDO	2	0
11	A	937	DWW	15	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	779/831 (93%)	0.12	28 (3%) 43 54	17, 36, 65, 77	0

The worst 5 of 28 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	51	TRP	5.2
1	A	644	LEU	4.8
1	A	640	ILE	4.5
1	A	637	VAL	4.1
1	A	554	GLY	4.0

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
3	MAN	A	907	11/12	0.94	0.14	5.01	40,46,55,62	0
2	NAG	A	910	14/15	0.94	0.09	0.27	30,37,48,49	0
2	NAG	A	901	14/15	0.88	0.21	0.04	68,73,76,81	0
3	NAG	A	903	14/15	0.98	0.10	-0.56	16,24,30,31	0
3	MAN	A	908	11/12	0.92	0.09	-	31,41,45,49	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	MAN	A	909	11/12	0.79	0.13	-	74,76,81,82	0
3	NAG	A	904	14/15	0.96	0.09	-	28,36,45,47	0
2	NAG	A	902	14/15	0.84	0.16	-	74,81,85,86	0
3	BMA	A	905	11/12	0.90	0.09	-	50,57,65,72	0
2	NAG	A	911	14/15	0.85	0.14	-	51,60,64,65	0
3	MAN	A	906	11/12	0.91	0.09	-	46,50,53,54	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
10	EDO	A	924	4/4	0.90	0.20	18.38	35,36,40,41	0
10	EDO	A	929	4/4	0.86	0.16	7.95	34,39,40,46	0
10	EDO	A	928	4/4	0.95	0.15	7.38	29,34,36,37	0
10	EDO	A	926	4/4	0.90	0.23	4.06	32,36,42,46	0
10	EDO	A	921	4/4	0.95	0.15	3.06	31,34,38,41	0
9	SCN	A	920	3/3	0.93	0.14	2.93	33,33,42,49	0
9	SCN	A	919	3/3	0.98	0.16	2.68	32,32,47,66	0
10	EDO	A	931	4/4	0.93	0.12	2.42	31,37,41,43	0
10	EDO	A	927	4/4	0.94	0.12	2.19	33,33,34,38	0
10	EDO	A	930	4/4	0.92	0.16	1.66	45,46,46,54	0
11	DWW	A	937	23/31	0.86	0.16	1.38	38,48,59,72	0
10	EDO	A	933	4/4	0.92	0.12	0.96	38,41,50,52	0
10	EDO	A	925	4/4	0.94	0.13	0.93	39,40,41,44	0
9	SCN	A	918	3/3	0.89	0.12	0.87	47,47,50,50	0
10	EDO	A	922	4/4	0.89	0.13	0.56	35,36,39,42	0
10	EDO	A	923	4/4	0.88	0.14	0.06	38,38,41,53	0
4	ZN	A	913	1/1	1.00	0.12	-0.43	20,20,20,20	0
10	EDO	A	935	4/4	0.97	0.07	-1.13	29,31,33,38	0
7	K	A	916	1/1	0.93	0.06	-1.38	65,65,65,65	0
5	CA	A	914	1/1	0.99	0.07	-1.42	29,29,29,29	0
10	EDO	A	934	4/4	0.99	0.06	-1.58	25,26,26,30	0
8	SO4	A	917	5/5	0.97	0.09	-1.83	27,28,33,36	0
4	ZN	A	912	1/1	0.99	0.11	-1.87	25,25,25,25	0
6	NA	A	915	1/1	0.97	0.05	-2.71	30,30,30,30	0
10	EDO	A	936	4/4	0.95	0.11	-	31,33,34,50	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
10	EDO	A	932	4/4	0.96	0.12	-	37,41,47,54	0

6.5 Other polymers [i](#)

There are no such residues in this entry.