



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:52 AM UTC

PDB ID : 6RRN / pdb_00006rrn
Title : GOLGI ALPHA-MANNOSIDASE II in complex with pentyl 2,5-dideoxy-2,5-imino-D-talo-hexonamide
Authors : Armstrong, Z.; Lahav, D.; Johnson, R.; Kuo, C.L.; Beenakker, T.J.M.; de Boer, C.; Wong, C.S.; van Rijssel, E.R.; Debets, M.; Geurink, P.P.; Ovaa, H.; van der Stelt, M.; Codee, J.D.C.; Aerts, J.M.F.G.; Wu, L.; Overkleeft, H.S.; Davies, G.J.
Deposited on : 2019-05-20
Resolution : 1.59 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	: 4-5-2 with Phenix2.0
Mogul	: 2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	: 2.0
EDS	: 3.0
Buster-report	: wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	: 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	: 9.0.010 (Gargrove)
Density-Fitness	: 1.0.12
Ideal geometry (proteins)	: Engh & Huber (2001)

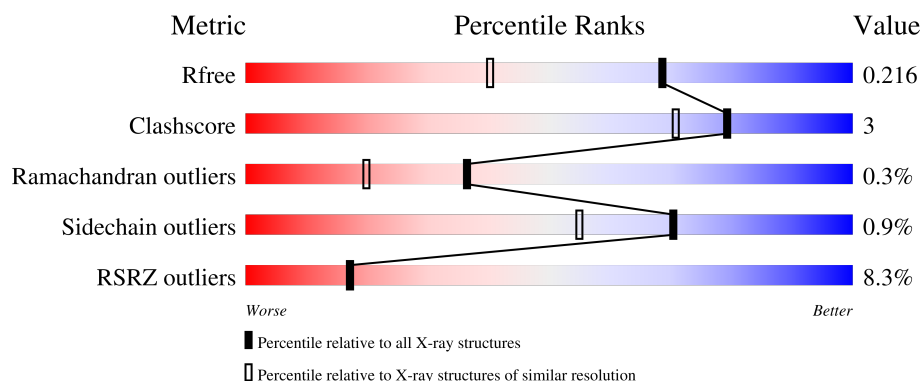
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.59 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}	180053	4673 (1.60-1.60)
Clashscore	190562	4931 (1.60-1.60)
Ramachandran outliers	187476	4831 (1.60-1.60)
Sidechain outliers	187428	4830 (1.60-1.60)
RSRZ outliers	180081	4672 (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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	1033	

Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

2 Entry composition [i](#)

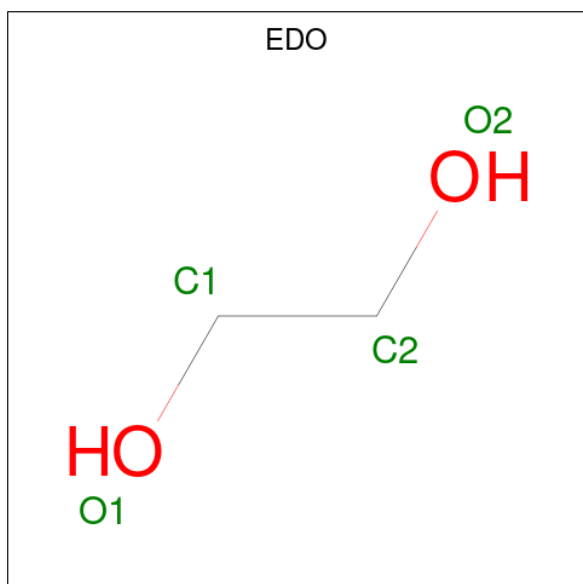
There are 6 unique types of molecules in this entry. The entry contains 8818 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Alpha-mannosidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	989	8115	5163	1420	1491	41	0	20	0

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



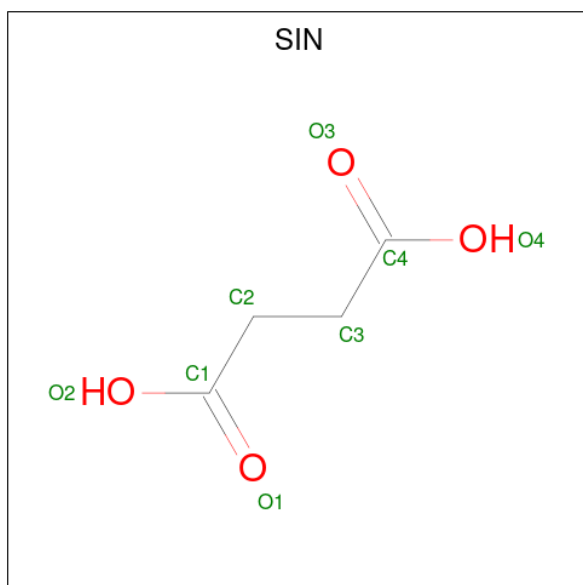
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		

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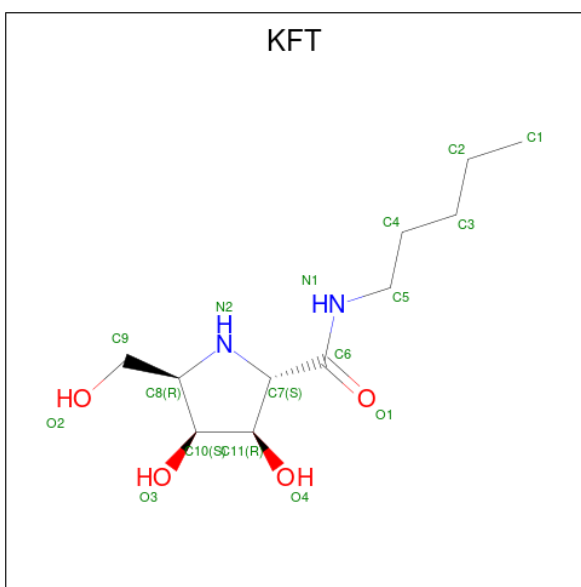
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		
2	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is SUCCINIC ACID (CCD ID: SIN) (formula: C₄H₆O₄).



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

- Molecule 4 is (2 {S},3 {R},4 {S},5 {R})-5-(hydroxymethyl)-3,4-bis(oxidanyl)- {N}-pentylpyrrolidine-2-carboxamide (CCD ID: KFT) (formula: C₁₁H₂₂N₂O₄) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			17	11	2	4		

- Molecule 5 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

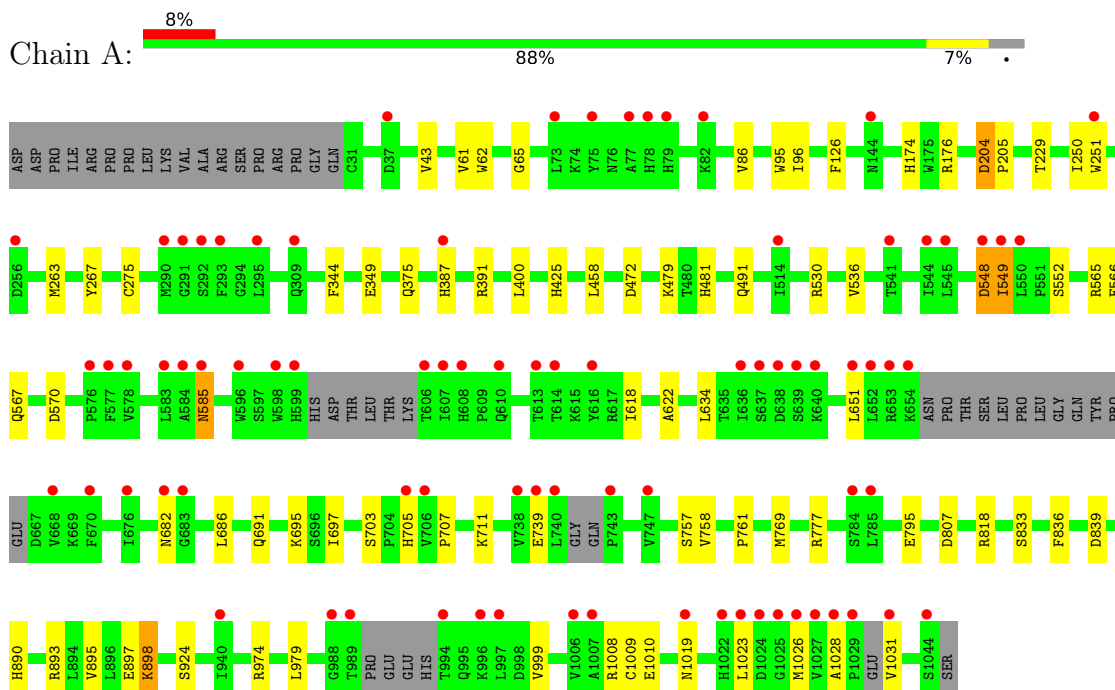
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	649	Total	O	0	0
			649	649		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Alpha-mannosidase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.71Å 90.39Å 130.27Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	74.37 – 1.59 74.26 – 1.59	Depositor EDS
% Data completeness (in resolution range)	100.0 (74.37-1.59) 100.0 (74.26-1.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 1.59Å)	Xtriage
Refinement program	REFMAC 5.8.0238, REFMAC	Depositor
R, R_{free}	0.180 , 0.210 0.189 , 0.216	Depositor DCC
R_{free} test set	7088 reflections (4.88%)	wwPDB-VP
Wilson B-factor (Å ²)	19.1	Xtriage
Anisotropy	0.426	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for k,h,-l	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	8818	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.45% 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, SIN, EDO, KFT

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	1.09	5/8365 (0.1%)	1.19	13/11344 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	481	HIS	CE1-NE2	5.99	1.38	1.32
1	A	707	PRO	C-O	-5.58	1.16	1.23
1	A	757	SER	C-O	5.49	1.30	1.24
1	A	86	VAL	N-CA	5.12	1.50	1.46
1	A	890	HIS	CE1-NE2	5.08	1.37	1.32

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	818	ARG	NE-CZ-NH1	-7.30	114.20	121.50
1	A	818	ARG	NE-CZ-NH2	6.82	125.34	119.20
1	A	425	HIS	CA-CB-CG	-6.30	107.50	113.80
1	A	250	ILE	CA-C-O	-6.03	114.11	120.57
1	A	836	PHE	CA-CB-CG	5.99	119.79	113.80
1	A	126	PHE	CA-CB-CG	5.77	119.57	113.80
1	A	682	ASN	N-CA-C	-5.64	106.30	112.72
1	A	1023	LEU	CA-C-N	5.45	128.50	120.82
1	A	1023	LEU	C-N-CA	5.45	128.50	120.82
1	A	61	VAL	O-C-N	5.09	126.81	121.87
1	A	839	ASP	CA-CB-CG	5.06	117.66	112.60
1	A	703	SER	CB-CA-C	5.02	116.60	108.91
1	A	536	VAL	N-CA-C	-5.02	107.50	111.81

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	8115	0	7915	43	0
2	A	28	0	40	1	0
3	A	8	0	4	0	0
4	A	17	0	0	1	0
5	A	1	0	0	0	0
6	A	649	0	0	9	0
All	All	8818	0	7959	43	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 3.

All (43) 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:251:TRP:HZ3	6:A:1825:HOH:O	1.53	0.89
1:A:974[A]:ARG:NH1	6:A:1203:HOH:O	2.30	0.64
1:A:548:ASP:O	1:A:549:ILE:HG22	1.97	0.64
1:A:530:ARG:HD3	1:A:777:ARG:NH2	2.18	0.58
1:A:565:ARG:HD2	1:A:567[B]:GLN:HE22	1.69	0.56
1:A:974[B]:ARG:NH2	6:A:1211:HOH:O	2.39	0.56
1:A:548:ASP:O	1:A:549:ILE:CG2	2.56	0.54
1:A:530:ARG:HB2	6:A:1248:HOH:O	2.08	0.53
1:A:686:LEU:HG	1:A:769:MET:HE3	1.92	0.51
1:A:1008:ARG:CZ	1:A:1010:GLU:OE2	2.59	0.51
1:A:686:LEU:HD22	1:A:697:ILE:HG12	1.93	0.50
1:A:739:GLU:O	1:A:761:PRO:HG2	2.11	0.50
1:A:1010:GLU:HG2	6:A:1394:HOH:O	2.11	0.50
1:A:548:ASP:C	1:A:549:ILE:HG22	2.36	0.50
1:A:174:HIS:CE1	1:A:176:ARG:HD3	2.49	0.47
1:A:344:PHE:H	1:A:349[A]:GLU:CD	2.24	0.46
1:A:62:TRP:CD2	1:A:65:GLY:HA3	2.50	0.46
1:A:895:VAL:HG12	1:A:897:GLU:HG3	1.98	0.45
1:A:893:ARG:NH1	1:A:924:SER:OG	2.48	0.45
1:A:585:ASN:O	1:A:585:ASN:ND2	2.47	0.43
1:A:979:LEU:HD21	1:A:999:VAL:HG11	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:1010:GLU:OE2	1:A:1019:ASN:ND2	2.51	0.43
1:A:705:HIS:ND1	6:A:1207:HOH:O	2.34	0.43
1:A:548:ASP:OD1	1:A:548:ASP:N	2.37	0.43
1:A:711:LYS:HD2	1:A:795:GLU:OE1	2.19	0.43
1:A:43:VAL:O	1:A:400:LEU:HA	2.19	0.42
1:A:458:LEU:HD13	6:A:1658:HOH:O	2.18	0.42
1:A:387[B]:HIS:O	1:A:391:ARG:HG2	2.20	0.42
1:A:229:THR:HG21	1:A:263:MET:HE2	2.00	0.42
1:A:1028:ALA:HB3	6:A:1700:HOH:O	2.20	0.42
1:A:570:ASP:HA	1:A:618:ILE:O	2.20	0.42
1:A:691:GLN:O	1:A:758:VAL:HG21	2.20	0.41
1:A:96:ILE:HA	1:A:479:LYS:HG3	2.03	0.41
1:A:491:GLN:NE2	6:A:1235:HOH:O	2.52	0.41
1:A:472:ASP:OD1	4:A:1106:KFT:O2	2.39	0.41
1:A:267:TYR:CZ	2:A:1109:EDO:H21	2.56	0.41
1:A:204:ASP:H	1:A:205:PRO:HD3	1.85	0.41
1:A:552:SER:HA	1:A:634:LEU:O	2.21	0.41
1:A:807:ASP:OD2	1:A:833[B]:SER:HB2	2.19	0.41
1:A:898:LYS:HA	1:A:898:LYS:HD2	1.89	0.41
1:A:566:GLU:HA	1:A:622:ALA:O	2.21	0.40
1:A:1009:CYS:HB3	1:A:1026:MET:HA	2.03	0.40
1:A:711:LYS:HD3	1:A:795:GLU:OE2	2.21	0.40

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	997/1033 (96%)	969 (97%)	25 (2%)	3 (0%)	36 20

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	95	TRP
1	A	549	ILE
1	A	204	ASP

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	898/918 (98%)	890 (99%)	8 (1%)	70 55

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	275	CYS
1	A	375	GLN
1	A	548	ASP
1	A	585	ASN
1	A	651	LEU
1	A	695	LYS
1	A	898	LYS
1	A	1031	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	253	ASN
1	A	380	GLN
1	A	491	GLN
1	A	643	HIS
1	A	923	GLN
1	A	937	ASN
1	A	1005	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 1 is monoatomic - leaving 9 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	EDO	A	1108	-	3,3,3	0.23	0	2,2,2	0.41	0
4	KFT	A	1106	5	17,17,17	0.67	0	18,22,22	1.10	1 (5%)
2	EDO	A	1101	-	3,3,3	0.70	0	2,2,2	0.25	0
2	EDO	A	1103	-	3,3,3	0.36	0	2,2,2	0.23	0
2	EDO	A	1105	-	3,3,3	0.14	0	2,2,2	0.16	0
2	EDO	A	1107	-	3,3,3	0.67	0	2,2,2	0.21	0
3	SIN	A	1104	-	7,7,7	1.24	0	8,8,8	0.84	0
2	EDO	A	1102	-	3,3,3	0.34	0	2,2,2	0.43	0
2	EDO	A	1109	-	3,3,3	0.71	0	2,2,2	0.59	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	EDO	A	1108	-	-	1/1/1/1	-
4	KFT	A	1106	5	-	2/12/28/28	0/1/1/1
2	EDO	A	1101	-	-	0/1/1/1	-
2	EDO	A	1103	-	-	0/1/1/1	-
2	EDO	A	1105	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	EDO	A	1107	-	-	0/1/1/1	-
3	SIN	A	1104	-	-	0/5/5/5	-
2	EDO	A	1102	-	-	0/1/1/1	-
2	EDO	A	1109	-	-	0/1/1/1	-

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1106	KFT	C11-C7-C6	4.21	119.07	110.69

There are no chirality outliers.

All (4) torsion outliers are listed below:

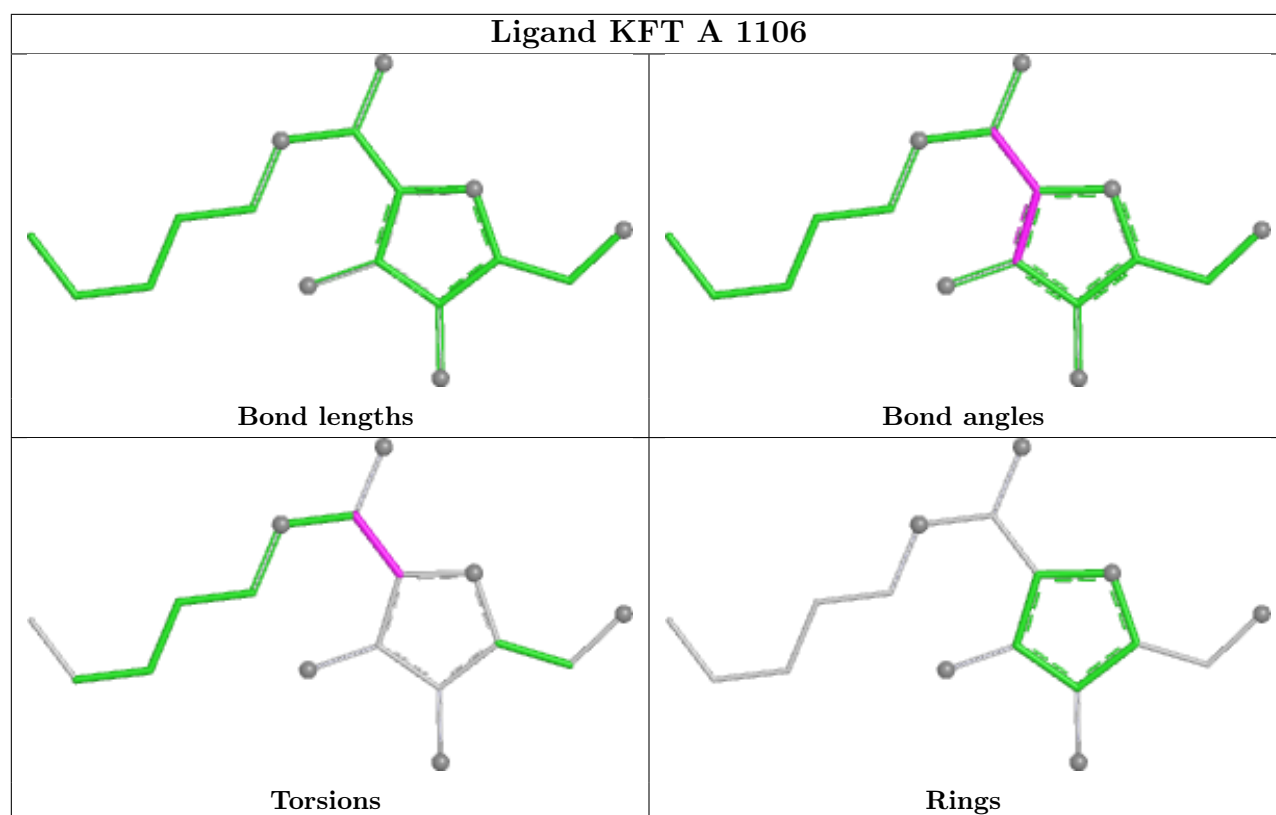
Mol	Chain	Res	Type	Atoms
4	A	1106	KFT	O1-C6-C7-C11
4	A	1106	KFT	N1-C6-C7-C11
2	A	1105	EDO	O1-C1-C2-O2
2	A	1108	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1106	KFT	1	0
2	A	1109	EDO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



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

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	989/1033 (95%)	0.58	82 (8%)	17 17	8, 21, 41, 65	20 (2%)

All (82) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1029	PRO	7.0
1	A	549	ILE	6.9
1	A	1028	ALA	6.2
1	A	1027	VAL	4.8
1	A	1031	VAL	4.3
1	A	293	PHE	4.2
1	A	545	LEU	4.1
1	A	577	PHE	4.1
1	A	387[A]	HIS	4.0
1	A	599	HIS	4.0
1	A	989	THR	3.9
1	A	1006	VAL	3.7
1	A	668	VAL	3.6
1	A	606	THR	3.6
1	A	740	LEU	3.6
1	A	613	THR	3.5
1	A	651	LEU	3.4
1	A	614	THR	3.4
1	A	640	LYS	3.3
1	A	654	LYS	3.2
1	A	544	ILE	3.2
1	A	1044	SER	3.2
1	A	550	LEU	3.1
1	A	1023	LEU	3.1
1	A	78	HIS	3.1
1	A	1022	HIS	3.1
1	A	1025	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	584	ALA	3.1
1	A	292	SER	3.0
1	A	251	TRP	2.9
1	A	607	ILE	2.9
1	A	291	GLY	2.9
1	A	608	HIS	2.8
1	A	73	LEU	2.8
1	A	683	GLY	2.8
1	A	988	GLY	2.7
1	A	785	LEU	2.7
1	A	739	GLU	2.7
1	A	747	VAL	2.7
1	A	596	TRP	2.7
1	A	548	ASP	2.7
1	A	653	ARG	2.7
1	A	1007	ALA	2.6
1	A	585	ASN	2.6
1	A	676	ILE	2.6
1	A	637	SER	2.6
1	A	77	ALA	2.5
1	A	295	LEU	2.5
1	A	610	GLN	2.5
1	A	514	ILE	2.5
1	A	616	TYR	2.5
1	A	670	PHE	2.5
1	A	1026	MET	2.4
1	A	682	ASN	2.4
1	A	578	VAL	2.4
1	A	1019	ASN	2.4
1	A	705	HIS	2.4
1	A	309	GLN	2.4
1	A	576	PRO	2.3
1	A	652	LEU	2.3
1	A	784	SER	2.3
1	A	37	ASP	2.3
1	A	82	LYS	2.3
1	A	583	LEU	2.3
1	A	541	THR	2.2
1	A	598	TRP	2.2
1	A	144	ASN	2.2
1	A	994	THR	2.2
1	A	636	ILE	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	738	VAL	2.2
1	A	290	MET	2.2
1	A	1024	ASP	2.1
1	A	706	VAL	2.1
1	A	638	ASP	2.1
1	A	997	LEU	2.1
1	A	996	LYS	2.1
1	A	940	ILE	2.1
1	A	79	HIS	2.1
1	A	743	PRO	2.0
1	A	639	SER	2.0
1	A	256	ASP	2.0
1	A	75	TYR	2.0

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](#)

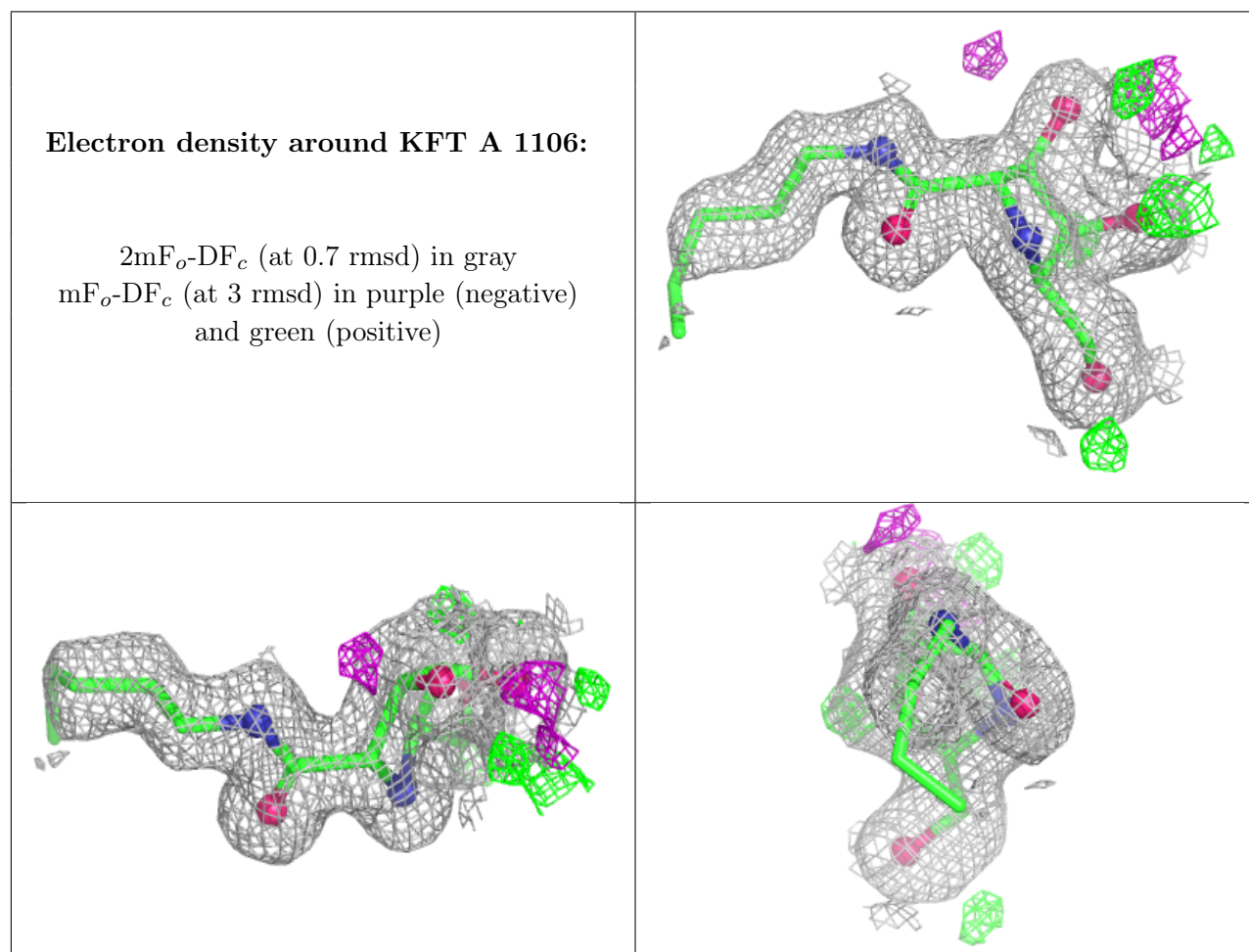
There are no oligosaccharides in this entry.

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. 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	B-factors($\text{\AA}^2$)	Q<0.9
3	SIN	A	1104	8/8	0.85	0.11	28,33,37,39	0
2	EDO	A	1105	4/4	0.86	0.12	36,37,38,40	0
2	EDO	A	1102	4/4	0.92	0.10	22,22,22,23	0
2	EDO	A	1103	4/4	0.92	0.11	25,31,31,33	0
2	EDO	A	1109	4/4	0.93	0.13	20,27,28,31	0
2	EDO	A	1101	4/4	0.94	0.08	16,17,18,18	0
2	EDO	A	1108	4/4	0.94	0.12	21,21,27,27	0
2	EDO	A	1107	4/4	0.96	0.13	20,24,29,31	0
4	KFT	A	1106	17/17	0.97	0.08	14,16,38,41	0
5	ZN	A	1110	1/1	0.99	0.03	14,14,14,14	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.



6.5 Other polymers ⓘ

There are no such residues in this entry.