



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 02:00 PM UTC

PDB ID : 7B6B / pdb_00007b6b
Title : The carbohydrate binding module family 48 (CBM48) and carboxy-terminal carbohydrate esterase family 1 (CE1) domains of the multidomain esterase DmCE1B from *Dysgonomonas mossii* in complex with methyl ferulate
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Deposited on : 2020-12-07
Resolution : 1.41 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)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

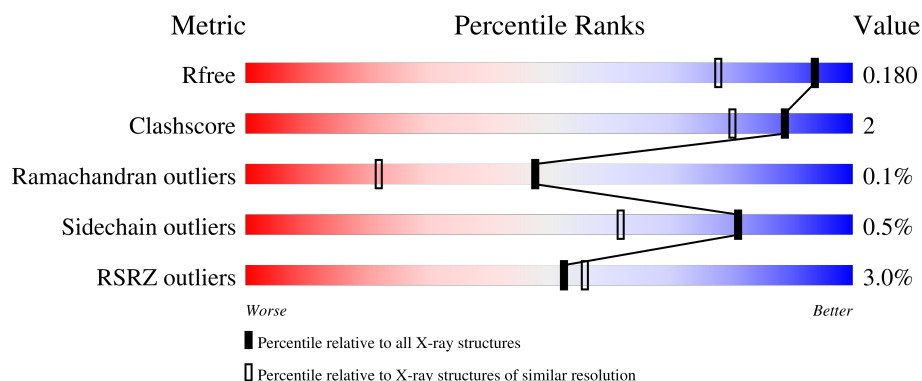
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

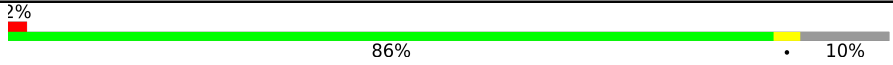
The reported resolution of this entry is 1.41 Å.

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	4041 (1.44-1.40)
Clashscore	190562	4154 (1.44-1.40)
Ramachandran outliers	187476	4083 (1.44-1.40)
Sidechain outliers	187428	4082 (1.44-1.40)
RSRZ outliers	180081	4039 (1.44-1.40)

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	386	
1	B	386	

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6449 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 Carbohydrate Esterase family 1 protein with an N-terminal carbohydrate binding module family 48.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	346	Total	C	N	O	S	0	9	0
			2813	1795	478	528	12			
1	B	345	Total	C	N	O	S	0	16	0
			2870	1832	487	538	13			

There are 42 discrepancies between the modelled and reference sequences:

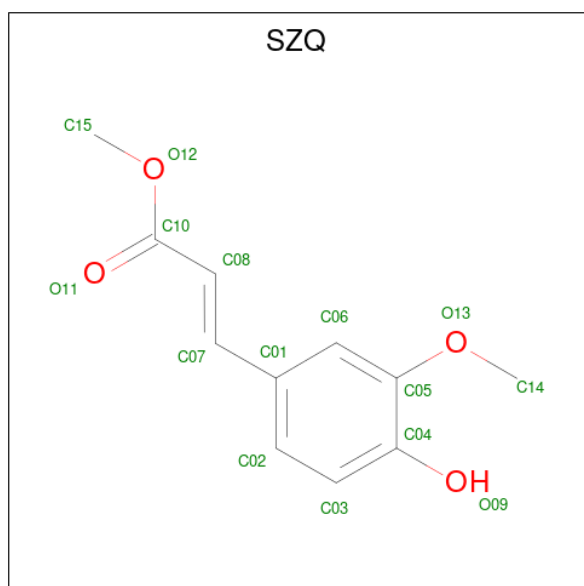
Chain	Residue	Modelled	Actual	Comment	Reference
A	271	MET	-	initiating methionine	UNP F8X1N1
A	272	GLY	-	expression tag	UNP F8X1N1
A	273	SER	-	expression tag	UNP F8X1N1
A	274	SER	-	expression tag	UNP F8X1N1
A	275	HIS	-	expression tag	UNP F8X1N1
A	276	HIS	-	expression tag	UNP F8X1N1
A	277	HIS	-	expression tag	UNP F8X1N1
A	278	HIS	-	expression tag	UNP F8X1N1
A	279	HIS	-	expression tag	UNP F8X1N1
A	280	HIS	-	expression tag	UNP F8X1N1
A	281	SER	-	expression tag	UNP F8X1N1
A	282	SER	-	expression tag	UNP F8X1N1
A	283	GLU	-	expression tag	UNP F8X1N1
A	284	ASN	-	expression tag	UNP F8X1N1
A	285	LEU	-	expression tag	UNP F8X1N1
A	286	TYR	-	expression tag	UNP F8X1N1
A	287	PHE	-	expression tag	UNP F8X1N1
A	288	GLN	-	expression tag	UNP F8X1N1
A	289	GLY	-	expression tag	UNP F8X1N1
A	290	HIS	-	expression tag	UNP F8X1N1
A	291	SER	-	expression tag	UNP F8X1N1
B	271	MET	-	initiating methionine	UNP F8X1N1
B	272	GLY	-	expression tag	UNP F8X1N1
B	273	SER	-	expression tag	UNP F8X1N1

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Chain	Residue	Modelled	Actual	Comment	Reference
B	274	SER	-	expression tag	UNP F8X1N1
B	275	HIS	-	expression tag	UNP F8X1N1
B	276	HIS	-	expression tag	UNP F8X1N1
B	277	HIS	-	expression tag	UNP F8X1N1
B	278	HIS	-	expression tag	UNP F8X1N1
B	279	HIS	-	expression tag	UNP F8X1N1
B	280	HIS	-	expression tag	UNP F8X1N1
B	281	SER	-	expression tag	UNP F8X1N1
B	282	SER	-	expression tag	UNP F8X1N1
B	283	GLU	-	expression tag	UNP F8X1N1
B	284	ASN	-	expression tag	UNP F8X1N1
B	285	LEU	-	expression tag	UNP F8X1N1
B	286	TYR	-	expression tag	UNP F8X1N1
B	287	PHE	-	expression tag	UNP F8X1N1
B	288	GLN	-	expression tag	UNP F8X1N1
B	289	GLY	-	expression tag	UNP F8X1N1
B	290	HIS	-	expression tag	UNP F8X1N1
B	291	SER	-	expression tag	UNP F8X1N1

- Molecule 2 is Trans-methylferulate (CCD ID: SZQ) (formula: $C_{11}H_{12}O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			15	11	4		
2	A	1	Total	C	O	0	0
			15	11	4		

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Cl 1 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

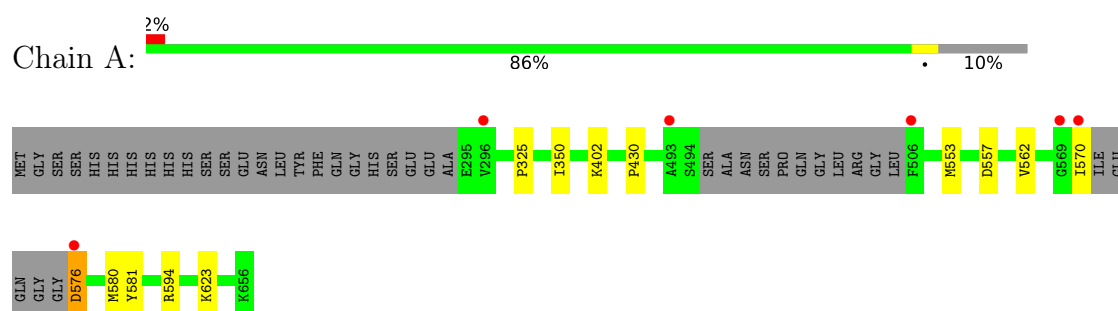
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	389	Total O 389 389	0	0
5	B	334	Total O 334 334	0	0

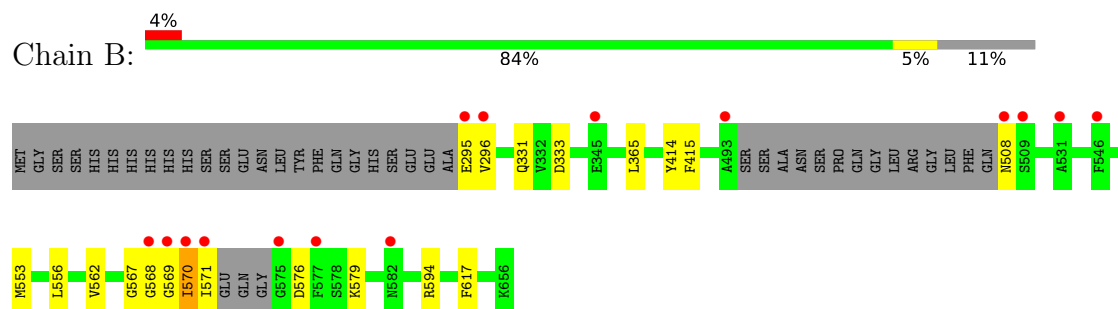
3 Residue-property plots [i](#)

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: Carbohydrate Esterase family 1 protein with an N-terminal carbohydrate binding module family 48



- Molecule 1: Carbohydrate Esterase family 1 protein with an N-terminal carbohydrate binding module family 48



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	73.26Å 50.51Å 90.15Å 90.00° 100.14° 90.00°	Depositor
Resolution (Å)	43.90 – 1.41 43.90 – 1.41	Depositor EDS
% Data completeness (in resolution range)	98.2 (43.90-1.41) 98.3 (43.90-1.41)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.14 (at 1.41Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.161 , 0.179 0.162 , 0.180	Depositor DCC
R_{free} test set	9254 reflections (7.37%)	wwPDB-VP
Wilson B-factor (Å ²)	16.2	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 36.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	6449	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.46% 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: EDO, CL, SZQ

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	0.66	2/2881 (0.1%)	0.71	1/3897 (0.0%)
1	B	0.41	1/2939 (0.0%)	0.56	3/3973 (0.1%)
All	All	0.55	3/5820 (0.1%)	0.64	4/7870 (0.1%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	567	GLY	C-O	-6.96	1.16	1.24
1	A	430	PRO	C-O	-6.69	1.15	1.23
1	A	325	PRO	C-O	-5.41	1.17	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	568	GLY	O-C-N	7.28	132.16	122.70
1	B	568	GLY	CA-C-N	6.58	134.31	121.41
1	B	568	GLY	C-N-CA	6.58	134.31	121.41
1	A	576	ASP	CA-CB-CG	-5.08	107.52	112.60

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	2813	0	2723	7	0
1	B	2870	0	2778	14	0
2	A	30	0	0	0	0
3	A	1	0	0	0	0
4	A	4	0	6	1	0
4	B	8	0	12	3	0
5	A	389	0	0	0	0
5	B	334	0	0	1	0
All	All	6449	0	5519	21	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 2.

All (21) 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:576:ASP:N	1:A:576:ASP:OD1	2.11	0.80
1:B:415:PHE:H	4:B:701:EDO:H21	1.60	0.67
1:A:402:LYS:HB3	4:A:704:EDO:H22	1.78	0.66
1:B:571:ILE:HD11	1:B:617:PHE:HA	1.81	0.63
1:B:415:PHE:H	4:B:701:EDO:C2	2.15	0.60
1:B:576:ASP:HB3	1:B:579:LYS:HE3	1.91	0.53
1:A:557:ASP:OD1	1:A:594:ARG:NH1	2.42	0.52
1:A:553:MET:HE3	1:A:562[B]:VAL:HG21	1.92	0.52
1:B:333:ASP:HB2	1:B:365:LEU:HD21	1.92	0.52
1:B:508:ASN:ND2	5:B:812:HOH:O	2.43	0.49
1:B:331:GLN:HB2	1:B:365:LEU:HB2	1.94	0.49
1:A:553:MET:CE	1:A:562[B]:VAL:HG21	2.45	0.47
1:B:576:ASP:CB	1:B:579:LYS:HE3	2.46	0.45
1:B:553:MET:HE3	1:B:562:VAL:HG21	1.98	0.45
1:B:556:LEU:HB3	1:B:594[B]:ARG:NH2	2.31	0.44
1:B:570:ILE:HD13	1:B:570:ILE:HA	1.73	0.43
1:B:414:TYR:HA	4:B:701:EDO:H22	2.01	0.43
1:A:350:ILE:HD12	1:A:350:ILE:HA	1.93	0.42
1:A:580:MET:HE2	1:A:581:TYR:CZ	2.56	0.40
1:B:556:LEU:HD12	1:B:556:LEU:HA	1.86	0.40
1:B:295:GLU:HG2	1:B:296:VAL:HG23	2.02	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	349/386 (90%)	341 (98%)	8 (2%)	0	100	100
1	B	355/386 (92%)	346 (98%)	8 (2%)	1 (0%)	36	17
All	All	704/772 (91%)	687 (98%)	16 (2%)	1 (0%)	48	22

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	569	GLY

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	296/321 (92%)	294 (99%)	2 (1%)	76	52
1	B	303/321 (94%)	302 (100%)	1 (0%)	86	71
All	All	599/642 (93%)	596 (100%)	3 (0%)	81	62

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

Mol	Chain	Res	Type
1	A	570	ILE
1	A	623	LYS
1	B	570	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	459	ASN
1	A	648	ASN
1	B	615	ASN
1	B	648	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 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	SZQ	A	701	-	15,15,15	1.71	4 (26%)	19,19,19	2.21	5 (26%)
4	EDO	B	702	-	3,3,3	0.40	0	2,2,2	0.43	0
2	SZQ	A	702	-	15,15,15	1.41	3 (20%)	19,19,19	1.52	3 (15%)
4	EDO	A	704	-	3,3,3	0.38	0	2,2,2	0.32	0
4	EDO	B	701	-	3,3,3	0.24	0	2,2,2	0.36	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	SZQ	A	701	-	-	0/9/9/9	0/1/1/1
4	EDO	B	702	-	-	1/1/1/1	-
2	SZQ	A	702	-	-	2/9/9/9	0/1/1/1
4	EDO	A	704	-	-	1/1/1/1	-
4	EDO	B	701	-	-	0/1/1/1	-

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	701	SZQ	O11-C10	-3.40	1.14	1.21
2	A	701	SZQ	C08-C10	2.65	1.54	1.48
2	A	702	SZQ	O12-C10	2.53	1.40	1.34
2	A	701	SZQ	O12-C15	-2.47	1.39	1.45
2	A	702	SZQ	O13-C05	2.20	1.40	1.37
2	A	701	SZQ	O13-C05	2.18	1.40	1.37
2	A	702	SZQ	O12-C15	-2.09	1.40	1.45

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	701	SZQ	O12-C10-C08	6.05	121.42	111.39
2	A	701	SZQ	O12-C10-O11	-3.87	116.54	123.02
2	A	702	SZQ	O12-C10-C08	3.51	117.21	111.39
2	A	701	SZQ	C01-C07-C08	-3.28	119.76	126.92
2	A	701	SZQ	C15-O12-C10	2.96	121.01	115.91
2	A	702	SZQ	O13-C05-C04	2.73	118.64	114.55
2	A	702	SZQ	C01-C07-C08	-2.65	121.14	126.92
2	A	701	SZQ	C06-C05-C04	-2.39	117.64	120.04

There are no chirality outliers.

All (4) torsion outliers are listed below:

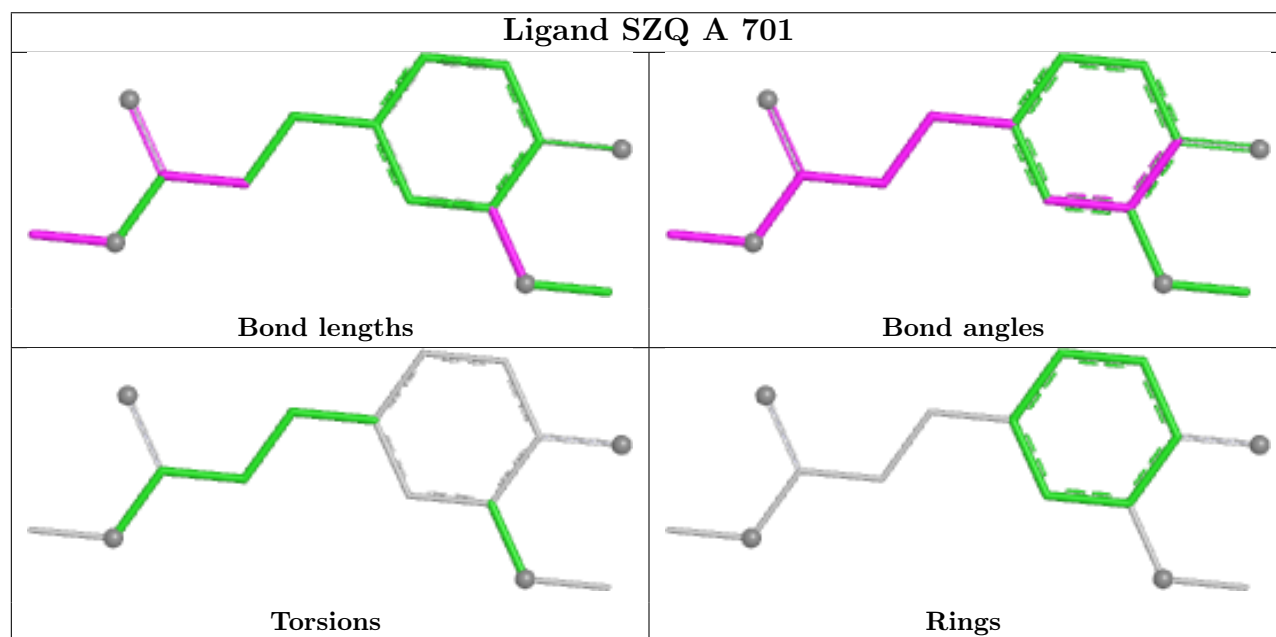
Mol	Chain	Res	Type	Atoms
2	A	702	SZQ	C06-C05-O13-C14
2	A	702	SZQ	C04-C05-O13-C14
4	B	702	EDO	O1-C1-C2-O2
4	A	704	EDO	O1-C1-C2-O2

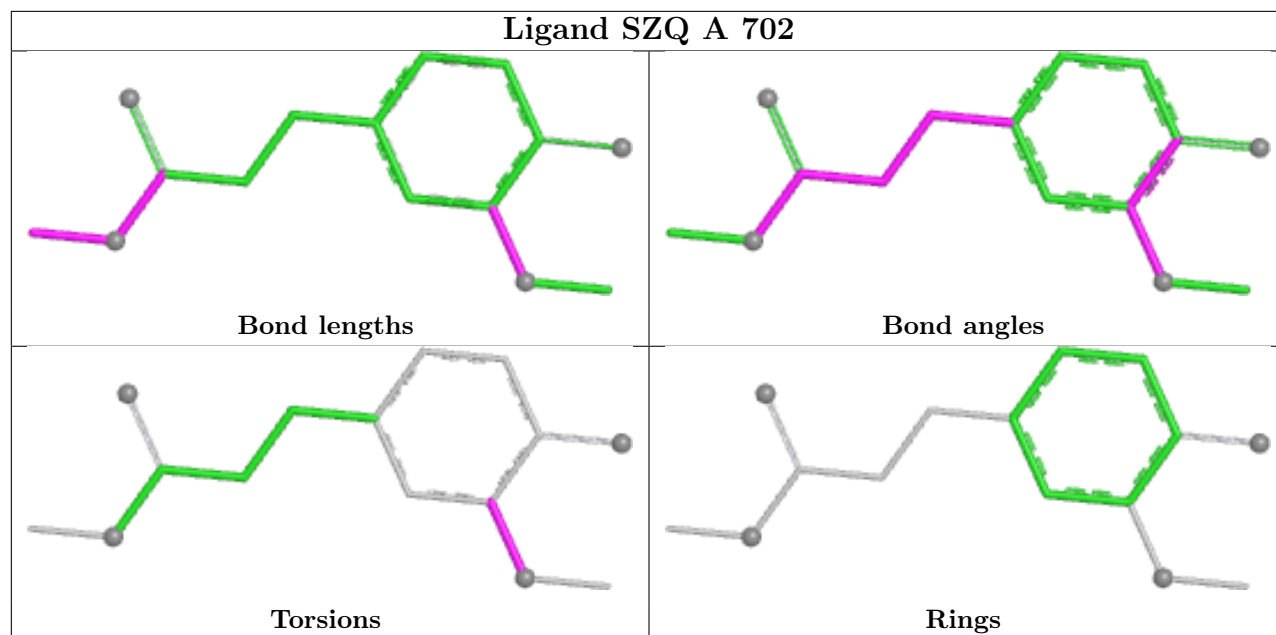
There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	704	EDO	1	0
4	B	701	EDO	3	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	346/386 (89%)	-0.03	6 (1%) 69 73	6, 16, 34, 63	9 (2%)
1	B	345/386 (89%)	0.15	15 (4%) 40 42	8, 18, 34, 58	16 (4%)
All	All	691/772 (89%)	0.06	21 (3%) 52 56	6, 17, 35, 63	25 (3%)

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	570	ILE	6.1
1	A	506	PHE	5.7
1	B	508	ASN	4.4
1	B	296	VAL	3.9
1	B	570	ILE	3.9
1	B	575	GLY	3.4
1	A	569	GLY	3.4
1	B	569	GLY	3.3
1	B	571	ILE	3.2
1	A	296	VAL	2.7
1	A	576	ASP	2.5
1	B	531	ALA	2.5
1	B	582	ASN	2.4
1	B	509	SER	2.3
1	B	568	GLY	2.2
1	B	493	ALA	2.1
1	A	493	ALA	2.1
1	B	295	GLU	2.1
1	B	546[A]	PHE	2.1
1	B	345	GLU	2.1
1	B	577	PHE	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](#)

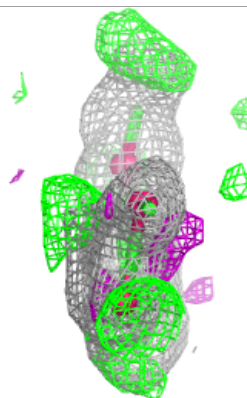
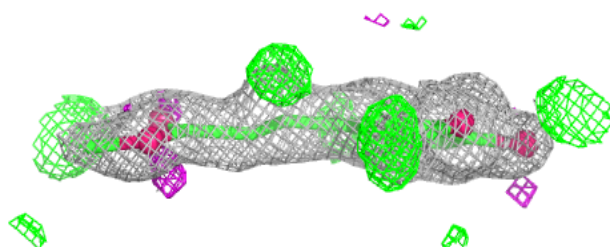
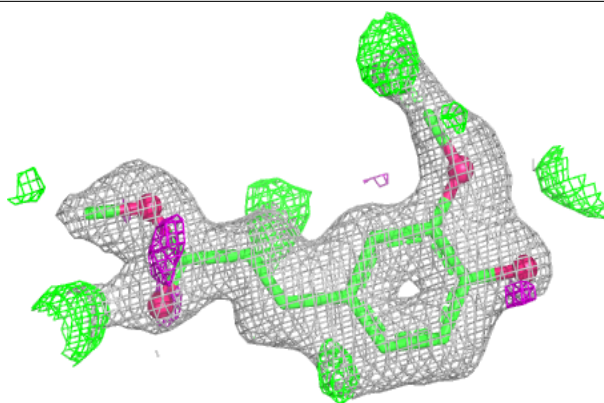
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
4	EDO	B	702	4/4	0.79	0.17	26,32,40,45	0
2	SZQ	A	701	15/15	0.80	0.14	20,30,38,39	0
4	EDO	B	701	4/4	0.90	0.11	16,23,24,33	0
2	SZQ	A	702	15/15	0.91	0.10	21,24,35,44	0
4	EDO	A	704	4/4	0.93	0.10	25,31,35,39	0
3	CL	A	703	1/1	0.98	0.09	21,21,21,21	0

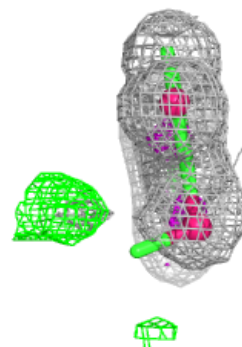
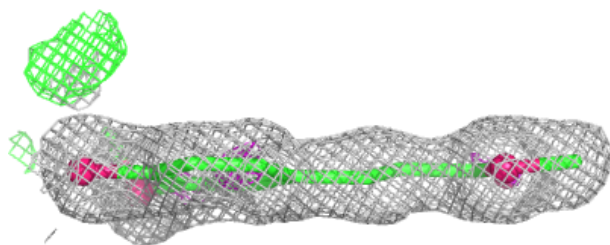
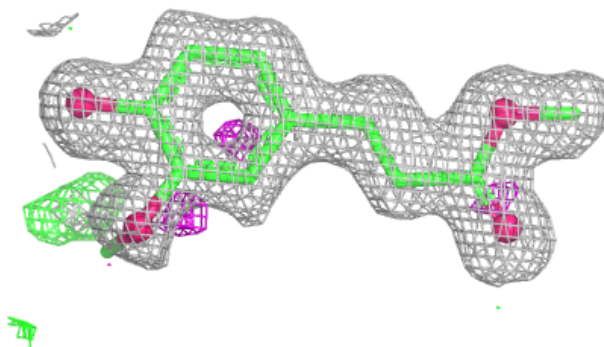
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around SZQ A 701:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around SZQ A 702:**

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.