



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 05:57 PM UTC

PDB ID : 8RVK / pdb_00008rvk
Title : Maltodextrin phosphorylase (MalP) in complex with a alpha-1,2-cyclophellitol analogue
Authors : Bennett, M.; Ofman, T.P.; Overkleeft, H.S.; Davies, G.J.
Deposited on : 2024-02-01
Resolution : 2.18 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

<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

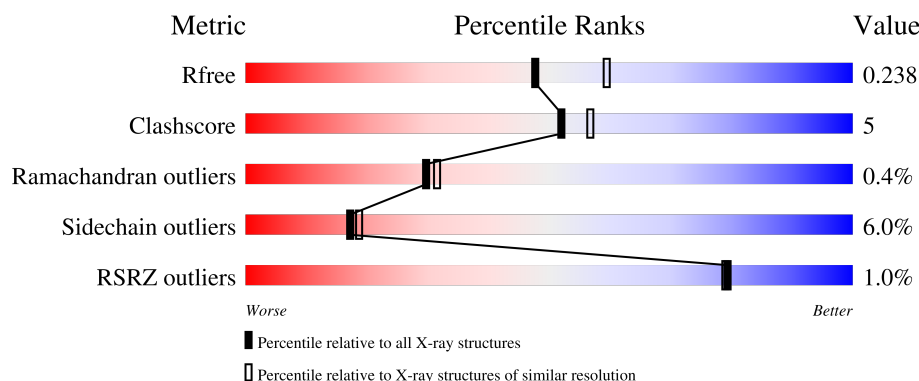
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.18 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	8975 (2.20-2.16)
Clashscore	190562	9786 (2.20-2.16)
Ramachandran outliers	187476	9664 (2.20-2.16)
Sidechain outliers	187428	9664 (2.20-2.16)
RSRZ outliers	180081	8979 (2.20-2.16)

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	797	82% 14% ..
1	B	797	81% 15% ..

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
4	PEG	B	821	-	-	X	-
5	SO4	A	820	-	-	X	-

2 Entry composition [i](#)

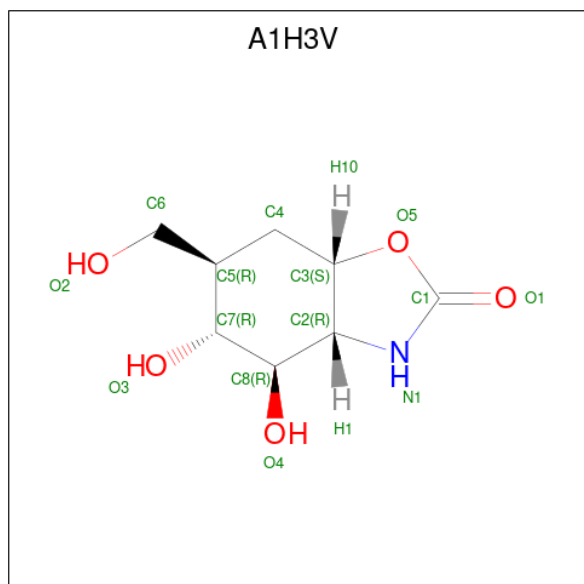
There are 6 unique types of molecules in this entry. The entry contains 13558 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Maltodextrin phosphorylase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	796	Total	C	N	O	P	S	0	0	0
			6332	4045	1103	1163	1	20			
1	B	795	Total	C	N	O	P	S	0	2	0
			6315	4039	1100	1155	1	20			

- Molecule 2 is (3 {a} {R},4 {R},5 {R},6 {R},7 {a} {S})-6-(hydroxymethyl)-4,5-bis(oxidany l)-3 {a},4,5,6,7,7 {a}-hexahydro-3 {H}-1,3-benzoxazol-2-one (CCD ID: A1H3V) (formula: C₈H₁₃NO₅) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

- Molecule 4 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	A	1	Total	C	O	0	0
			7	4	3		
4	A	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		
4	B	1	Total	C	O	0	0
			7	4	3		

- Molecule 5 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

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

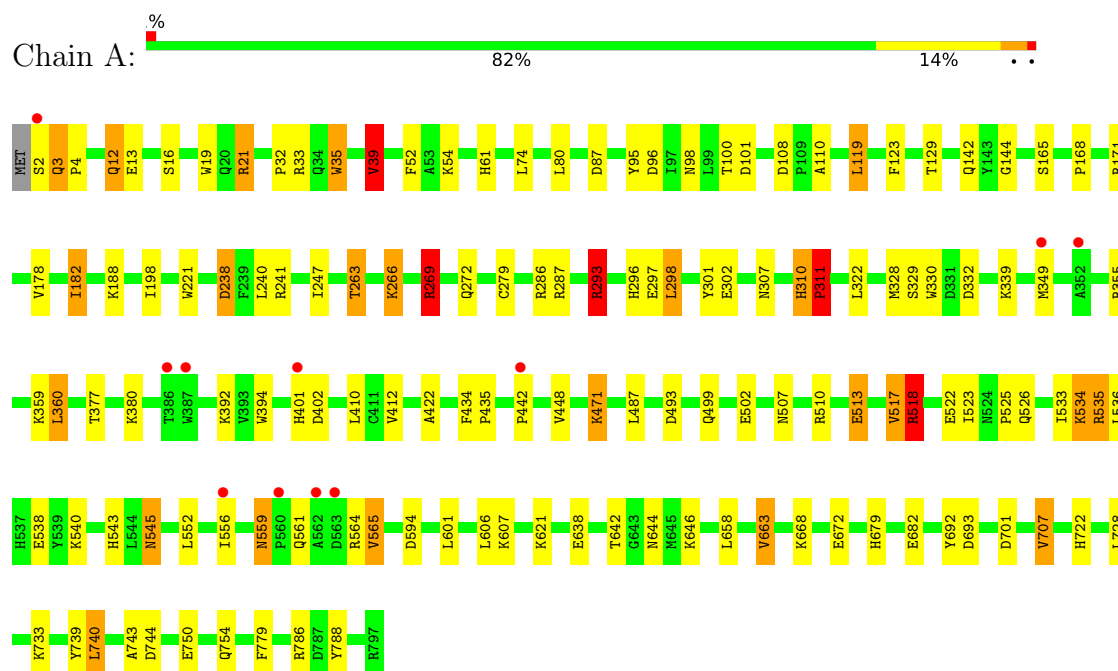
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	320	Total	O	0	0
			320	320		
6	B	309	Total	O	0	0
			309	309		

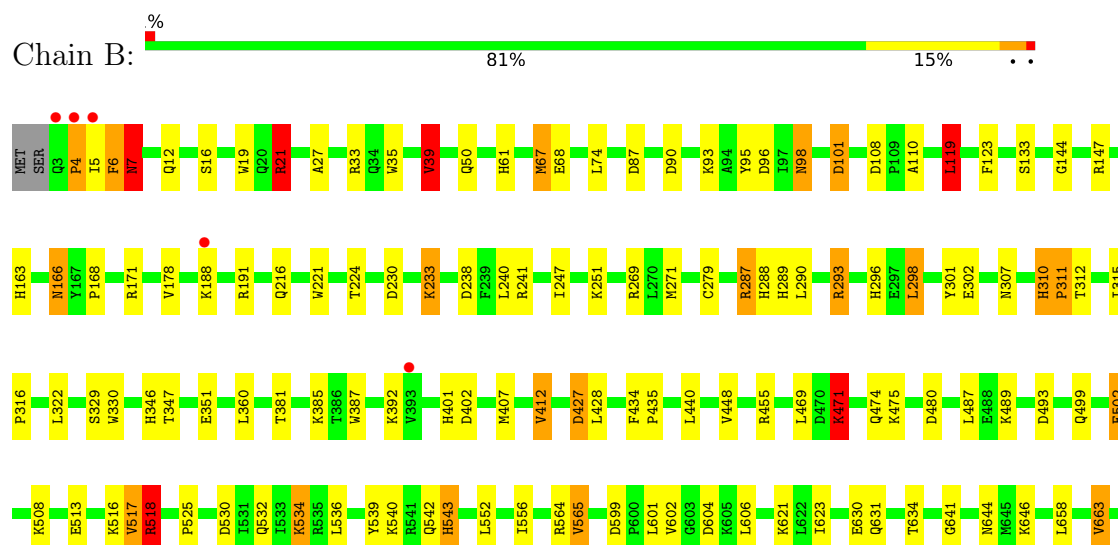
3 Residue-property plots

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: Maltodextrin phosphorylase



• Molecule 1: Maltodextrin phosphorylase



E667	K668	E672	H679	E682	K696	V707	D718	L728	I731	Q734	Y739	L740	V741	M742	K743	D744	Q762	F779	Y788	K796	R797
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4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	110.50Å 119.79Å 150.75Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	71.50 – 2.18 71.50 – 2.18	Depositor EDS
% Data completeness (in resolution range)	100.0 (71.50-2.18) 100.0 (71.50-2.18)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.06 (at 1.90Å)	Xtriage
Refinement program	REFMAC 5.8.0425	Depositor
R, R_{free}	0.177 , 0.229 0.186 , 0.238	Depositor DCC
R_{free} test set	2018 reflections (1.26%)	wwPDB-VP
Wilson B-factor (Å ²)	29.4	Xtriage
Anisotropy	0.373	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.2	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	0.96	EDS
Total number of atoms	13558	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.36% 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, A1H3V, SO4, PEG, LLP

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	1.01	5/6457 (0.1%)	1.52	64/8772 (0.7%)
1	B	0.96	1/6440 (0.0%)	1.46	55/8752 (0.6%)
All	All	0.98	6/12897 (0.0%)	1.49	119/17524 (0.7%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	7
1	B	0	7
All	All	0	14

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	311	PRO	CA-CB	-6.20	1.45	1.53
1	A	21	ARG	NE-CZ	6.09	1.39	1.33
1	A	310	HIS	CE1-NE2	-5.37	1.27	1.32
1	A	241	ARG	NE-CZ	5.35	1.39	1.33
1	A	33	ARG	NE-CZ	5.26	1.38	1.33

The worst 5 of 119 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	502	GLU	CB-CG-CD	10.37	130.22	112.60
1	A	12	GLN	CB-CA-C	-9.40	94.88	110.85
1	A	513	GLU	CB-CG-CD	9.03	127.95	112.60
1	A	238	ASP	CA-CB-CG	8.46	121.06	112.60

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	796	LYS	CB-CA-C	8.33	123.42	109.84

There are no chirality outliers.

5 of 14 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	21	ARG	Sidechain
1	A	269	ARG	Sidechain
1	A	293	ARG	Sidechain
1	A	355	ARG	Sidechain
1	A	4	PRO	Peptide

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	6332	0	6152	62	0
1	B	6315	0	6117	67	0
2	A	14	0	0	0	0
3	A	56	0	84	7	0
3	B	68	0	102	4	0
4	A	21	0	30	1	0
4	B	28	0	39	7	0
5	A	40	0	0	2	0
5	B	55	0	0	1	0
6	A	320	0	0	11	1
6	B	309	0	0	9	1
All	All	13558	0	12524	130	1

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 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:B:502:GLU:HG3	4:B:821:PEG:H41	1.50	0.93

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:HIS:HD2	3:B:806:EDO:O1	1.62	0.83
1:A:559:ASN:HA	1:A:561:GLN:NE2	1.95	0.80
1:B:502:GLU:CG	4:B:821:PEG:H41	2.13	0.78
1:A:238:ASP:OD1	6:A:901:HOH:O	2.02	0.77

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
6:A:1165:HOH:O	6:B:1117:HOH:O[4_545]	2.14	0.06

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	793/797 (100%)	760 (96%)	30 (4%)	3 (0%)	30	31
1	B	794/797 (100%)	768 (97%)	22 (3%)	4 (0%)	24	25
All	All	1587/1594 (100%)	1528 (96%)	52 (3%)	7 (0%)	30	31

5 of 7 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	7	ASN
1	B	6	PHE
1	A	3	GLN
1	A	422	ALA
1	B	311	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	643/667 (96%)	606 (94%)	37 (6%)	18	20
1	B	635/667 (95%)	596 (94%)	39 (6%)	17	18
All	All	1278/1334 (96%)	1202 (94%)	76 (6%)	17	19

5 of 76 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	471	LYS
1	B	668	LYS
1	B	517	VAL
1	B	565	VAL
1	B	740	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 31 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	50	GLN
1	B	499	GLN
1	B	98	ASN
1	B	545	ASN
1	B	401	HIS

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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
1	LLP	B	646	1	23,24,25	0.92	1 (4%)	25,32,34	1.32	2 (8%)
1	LLP	A	646	1	23,24,25	0.88	1 (4%)	25,32,34	1.76	5 (20%)

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	LLP	B	646	1	-	2/16/17/19	0/1/1/1
1	LLP	A	646	1	-	0/16/17/19	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	646	LLP	P-OP2	-3.01	1.43	1.54
1	B	646	LLP	P-OP2	-2.78	1.44	1.54

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	646	LLP	OP2-P-OP4	-4.93	93.80	106.67
1	A	646	LLP	OP4-P-OP1	3.71	116.46	106.44
1	B	646	LLP	CD-CE-NZ	3.65	120.50	110.83
1	A	646	LLP	CD-CE-NZ	3.11	119.06	110.83
1	B	646	LLP	C3-C2-N1	-2.49	117.81	120.96

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	B	646	LLP	C4-C4'-NZ-CE
1	B	646	LLP	C6-C5-C5'-OP4

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

58 ligands 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	$\# Z > 2$
5	SO4	A	824	-	4,4,4	0.34	0	6,6,6	0.51	0
5	SO4	A	820	-	4,4,4	0.29	0	6,6,6	0.26	0
5	SO4	A	822	-	4,4,4	0.32	0	6,6,6	0.48	0
5	SO4	A	826	-	4,4,4	0.27	0	6,6,6	0.29	0
3	EDO	B	806	-	3,3,3	0.45	0	2,2,2	0.09	0
3	EDO	B	810	-	3,3,3	0.20	0	2,2,2	0.13	0
5	SO4	A	819	-	4,4,4	0.36	0	6,6,6	0.17	0
5	SO4	B	827	-	4,4,4	0.19	0	6,6,6	0.30	0
5	SO4	A	825	-	4,4,4	0.54	0	6,6,6	0.44	0
5	SO4	B	832	-	4,4,4	0.58	0	6,6,6	0.43	0
4	PEG	B	819	-	6,6,6	0.33	0	5,5,5	0.27	0
3	EDO	B	816	-	3,3,3	0.31	0	2,2,2	0.20	0
3	EDO	B	817	-	3,3,3	0.14	0	2,2,2	0.28	0
3	EDO	A	813	-	3,3,3	0.40	0	2,2,2	0.23	0
4	PEG	B	801	-	6,6,6	0.84	0	5,5,5	0.52	0
3	EDO	B	814	-	3,3,3	0.70	0	2,2,2	0.34	0
3	EDO	A	812	-	3,3,3	0.27	0	2,2,2	0.25	0
5	SO4	B	830	-	4,4,4	0.34	0	6,6,6	0.29	0
3	EDO	A	807	-	3,3,3	0.51	0	2,2,2	0.50	0
3	EDO	B	802	-	3,3,3	0.87	0	2,2,2	0.71	0
4	PEG	A	806	-	6,6,6	0.74	0	5,5,5	0.44	0
5	SO4	B	828	-	4,4,4	0.66	0	6,6,6	0.54	0
3	EDO	B	812	-	3,3,3	0.31	0	2,2,2	0.32	0
3	EDO	A	815	-	3,3,3	0.55	0	2,2,2	0.13	0
4	PEG	A	818	-	6,6,6	0.26	0	5,5,5	0.29	0
5	SO4	B	826	-	4,4,4	0.34	0	6,6,6	0.07	0
5	SO4	B	824	-	4,4,4	0.18	0	6,6,6	0.23	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	A	817	-	3,3,3	0.21	0	2,2,2	0.28	0
4	PEG	B	821	-	6,6,6	0.61	0	5,5,5	0.50	0
3	EDO	B	803	-	3,3,3	0.15	0	2,2,2	0.51	0
3	EDO	B	818	-	3,3,3	0.32	0	2,2,2	0.38	0
5	SO4	B	825	-	4,4,4	0.25	0	6,6,6	0.23	0
5	SO4	B	831	-	4,4,4	0.46	0	6,6,6	0.82	0
4	PEG	B	820	-	6,6,6	0.72	0	5,5,5	0.54	0
5	SO4	B	823	-	4,4,4	0.18	0	6,6,6	0.43	0
3	EDO	B	815	-	3,3,3	0.53	0	2,2,2	0.81	0
3	EDO	A	808	-	3,3,3	0.45	0	2,2,2	0.71	0
4	PEG	A	804	-	6,6,6	0.54	0	5,5,5	0.56	0
5	SO4	A	823	-	4,4,4	0.52	0	6,6,6	0.53	0
3	EDO	A	810	-	3,3,3	0.16	0	2,2,2	0.21	0
3	EDO	A	816	-	3,3,3	0.48	0	2,2,2	0.38	0
3	EDO	B	813	-	3,3,3	0.68	0	2,2,2	0.36	0
5	SO4	A	821	-	4,4,4	0.31	0	6,6,6	0.30	0
3	EDO	B	805	-	3,3,3	0.24	0	2,2,2	0.30	0
2	A1H3V	A	801	-	15,15,15	1.85	2 (13%)	17,22,22	1.73	5 (29%)
3	EDO	A	814	-	3,3,3	0.87	0	2,2,2	0.66	0
3	EDO	B	804	-	3,3,3	1.44	0	2,2,2	1.00	0
3	EDO	B	808	-	3,3,3	0.90	0	2,2,2	0.81	0
3	EDO	A	802	-	3,3,3	0.82	0	2,2,2	0.07	0
3	EDO	B	807	-	3,3,3	0.34	0	2,2,2	0.30	0
3	EDO	A	809	-	3,3,3	0.51	0	2,2,2	0.51	0
3	EDO	B	811	-	3,3,3	0.76	0	2,2,2	0.43	0
5	SO4	B	829	-	4,4,4	0.43	0	6,6,6	0.45	0
5	SO4	B	822	-	4,4,4	0.51	0	6,6,6	0.33	0
3	EDO	A	805	-	3,3,3	0.58	0	2,2,2	0.89	0
3	EDO	A	803	-	3,3,3	0.52	0	2,2,2	0.55	0
3	EDO	A	811	-	3,3,3	0.65	0	2,2,2	0.90	0
3	EDO	B	809	-	3,3,3	0.84	0	2,2,2	0.76	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
3	EDO	B	806	-	-	1/1/1/1	-
3	EDO	B	810	-	-	1/1/1/1	-
4	PEG	B	819	-	-	1/4/4/4	-
3	EDO	B	816	-	-	1/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	B	817	-	-	0/1/1/1	-
3	EDO	A	813	-	-	0/1/1/1	-
4	PEG	B	801	-	-	2/4/4/4	-
3	EDO	B	814	-	-	1/1/1/1	-
3	EDO	A	812	-	-	0/1/1/1	-
3	EDO	A	807	-	-	1/1/1/1	-
3	EDO	B	802	-	-	0/1/1/1	-
4	PEG	A	806	-	-	3/4/4/4	-
3	EDO	B	812	-	-	1/1/1/1	-
3	EDO	A	815	-	-	1/1/1/1	-
4	PEG	A	818	-	-	3/4/4/4	-
3	EDO	A	817	-	-	1/1/1/1	-
4	PEG	B	821	-	-	3/4/4/4	-
3	EDO	B	803	-	-	0/1/1/1	-
3	EDO	B	818	-	-	1/1/1/1	-
4	PEG	B	820	-	-	2/4/4/4	-
3	EDO	B	815	-	-	1/1/1/1	-
3	EDO	A	808	-	-	0/1/1/1	-
4	PEG	A	804	-	-	1/4/4/4	-
3	EDO	A	810	-	-	1/1/1/1	-
3	EDO	A	816	-	-	1/1/1/1	-
3	EDO	B	813	-	-	1/1/1/1	-
3	EDO	B	805	-	-	1/1/1/1	-
2	A1H3V	A	801	-	-	0/2/30/30	0/2/2/2
3	EDO	A	814	-	-	0/1/1/1	-
3	EDO	B	804	-	-	0/1/1/1	-
3	EDO	B	808	-	-	1/1/1/1	-
3	EDO	A	802	-	-	1/1/1/1	-
3	EDO	B	807	-	-	0/1/1/1	-
3	EDO	A	809	-	-	1/1/1/1	-
3	EDO	B	811	-	-	1/1/1/1	-
3	EDO	A	805	-	-	0/1/1/1	-
3	EDO	A	803	-	-	0/1/1/1	-
3	EDO	A	811	-	-	1/1/1/1	-
3	EDO	B	809	-	-	1/1/1/1	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	801	A1H3V	C2-N1	5.93	1.56	1.45
2	A	801	A1H3V	C8-C2	2.27	1.57	1.53

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	801	A1H3V	C3-O5-C1	3.25	111.87	109.11
2	A	801	A1H3V	O3-C7-C5	-3.22	104.64	110.01
2	A	801	A1H3V	C7-C8-C2	3.07	114.88	110.40
2	A	801	A1H3V	O4-C8-C2	2.84	115.23	109.58
2	A	801	A1H3V	C5-C4-C3	2.12	118.22	112.50

There are no chirality outliers.

5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	801	PEG	O2-C3-C4-O4
4	B	821	PEG	O2-C3-C4-O4
4	B	820	PEG	O2-C3-C4-O4
4	A	806	PEG	O1-C1-C2-O2
3	A	802	EDO	O1-C1-C2-O2

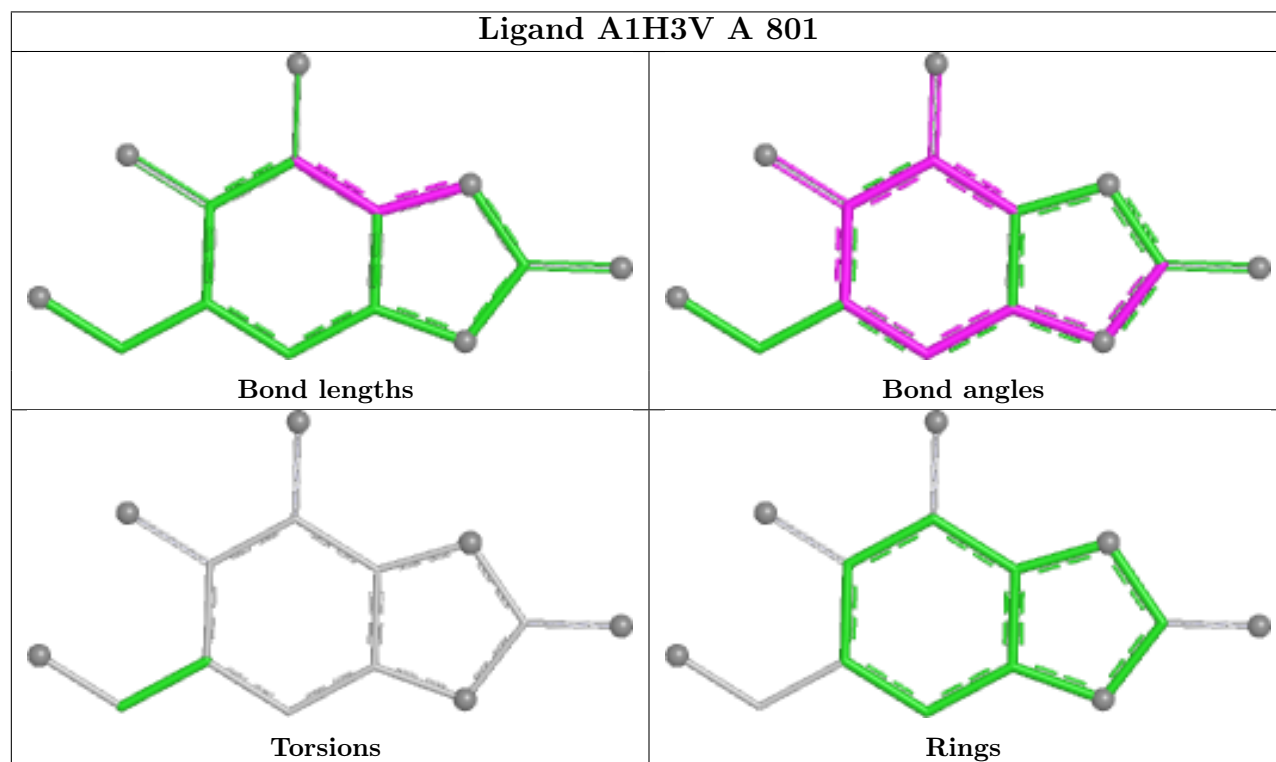
There are no ring outliers.

12 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	820	SO4	2	0
3	B	806	EDO	2	0
5	B	832	SO4	1	0
3	B	814	EDO	1	0
3	A	807	EDO	1	0
4	B	821	PEG	6	0
4	B	820	PEG	1	0
3	B	815	EDO	1	0
4	A	804	PEG	1	0
3	A	816	EDO	2	0
3	A	802	EDO	2	0
3	A	803	EDO	2	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 [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	795/797 (99%)	-0.23	11 (1%) 73 73	23, 33, 56, 91	0
1	B	794/797 (99%)	-0.25	5 (0%) 85 84	16, 34, 54, 87	2 (0%)
All	All	1589/1594 (99%)	-0.24	16 (1%) 79 79	16, 34, 55, 91	2 (0%)

The worst 5 of 16 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	562	ALA	4.0
1	A	442	PRO	3.3
1	A	2	SER	3.2
1	B	3	GLN	3.2
1	B	4	PRO	3.2

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. 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(Å ²)	Q<0.9
1	LLP	A	646	24/25	0.97	0.06	22,27,33,38	0
1	LLP	B	646	24/25	0.97	0.05	22,26,35,42	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides 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. 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(Å ²)	Q<0.9
3	EDO	B	813	4/4	0.64	0.19	64,65,68,71	0
5	SO4	B	827	5/5	0.65	0.15	62,97,120,127	0
5	SO4	B	826	5/5	0.71	0.14	77,101,121,143	0
3	EDO	A	814	4/4	0.71	0.33	60,63,67,68	0
5	SO4	A	826	5/5	0.72	0.11	66,67,96,101	0
3	EDO	B	810	4/4	0.73	0.23	61,63,69,72	0
3	EDO	A	812	4/4	0.75	0.22	59,60,61,62	0
5	SO4	A	820	5/5	0.77	0.11	73,79,85,112	0
3	EDO	A	813	4/4	0.77	0.18	54,56,59,62	0
3	EDO	A	815	4/4	0.79	0.18	61,64,67,74	0
3	EDO	B	811	4/4	0.80	0.18	48,55,59,64	0
4	PEG	B	819	7/7	0.80	0.18	62,72,84,85	0
3	EDO	B	812	4/4	0.80	0.17	62,66,66,67	0
4	PEG	B	820	7/7	0.81	0.17	53,63,71,77	0
4	PEG	B	821	7/7	0.81	0.16	59,72,80,83	0
3	EDO	A	811	4/4	0.81	0.17	59,61,62,65	0
3	EDO	A	816	4/4	0.82	0.20	43,52,70,73	0
3	EDO	B	814	4/4	0.82	0.15	50,56,66,68	0
3	EDO	A	808	4/4	0.82	0.15	49,49,57,58	0
3	EDO	B	806	4/4	0.83	0.16	50,58,60,60	0
3	EDO	B	816	4/4	0.83	0.15	53,61,63,68	0
3	EDO	B	809	4/4	0.83	0.27	55,57,57,66	0
3	EDO	B	805	4/4	0.85	0.12	41,63,70,84	0
3	EDO	B	817	4/4	0.85	0.20	47,51,52,59	0
3	EDO	A	817	4/4	0.85	0.13	57,60,75,76	0
5	SO4	B	823	5/5	0.87	0.08	59,60,78,80	0
5	SO4	A	821	5/5	0.87	0.08	56,73,74,82	0
3	EDO	B	804	4/4	0.87	0.14	41,44,47,55	0
4	PEG	B	801	7/7	0.88	0.15	38,50,86,88	0
3	EDO	B	808	4/4	0.88	0.14	41,42,52,59	0
3	EDO	A	807	4/4	0.88	0.17	41,41,42,55	0
5	SO4	B	824	5/5	0.88	0.08	64,67,69,76	0
3	EDO	B	807	4/4	0.88	0.13	45,64,70,71	0
4	PEG	A	804	7/7	0.88	0.13	44,53,72,76	0
3	EDO	A	803	4/4	0.90	0.10	36,42,45,49	0
4	PEG	A	806	7/7	0.90	0.13	41,59,61,72	0
4	PEG	A	818	7/7	0.90	0.12	56,59,75,80	0

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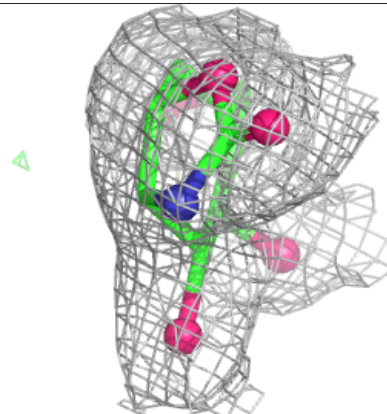
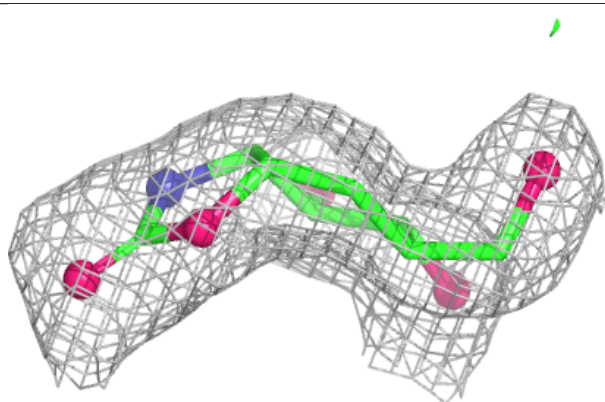
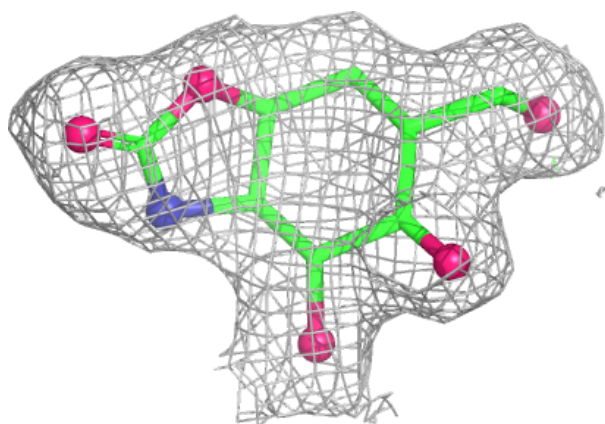
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	EDO	B	802	4/4	0.90	0.13	38,39,41,45	0
3	EDO	B	815	4/4	0.90	0.13	40,49,52,59	0
3	EDO	B	803	4/4	0.90	0.12	42,48,52,71	0
3	EDO	A	810	4/4	0.90	0.14	51,54,55,57	0
5	SO4	B	831	5/5	0.90	0.15	45,54,65,71	0
3	EDO	A	809	4/4	0.91	0.12	45,52,57,61	0
5	SO4	A	824	5/5	0.91	0.09	45,46,70,94	0
5	SO4	B	825	5/5	0.93	0.09	54,68,77,93	0
3	EDO	A	805	4/4	0.93	0.13	44,49,59,59	0
3	EDO	A	802	4/4	0.93	0.13	28,30,34,42	0
5	SO4	A	825	5/5	0.93	0.12	54,55,59,63	0
2	A1H3V	A	801	14/14	0.94	0.08	26,43,48,51	0
3	EDO	B	818	4/4	0.94	0.15	44,48,50,66	0
5	SO4	A	819	5/5	0.95	0.07	51,68,73,77	0
5	SO4	B	822	5/5	0.95	0.13	38,42,66,69	0
5	SO4	B	830	5/5	0.96	0.07	43,48,75,81	0
5	SO4	B	832	5/5	0.96	0.11	44,46,48,75	0
5	SO4	B	829	5/5	0.97	0.06	40,46,58,62	0
5	SO4	B	828	5/5	0.97	0.07	38,41,44,45	0
5	SO4	A	822	5/5	0.98	0.07	38,39,42,43	0
5	SO4	A	823	5/5	0.98	0.09	37,42,51,52	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 A1H3V A 801:

$2mF_o - DF_c$ (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.