



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 08:49 AM UTC

PDB ID : 8W4R / pdb_00008w4r
Title : Crystal structure of PDE4D complexed with CVT-313
Authors : Liu, J.Y.; Li, M.J.; Xu, Y.C.
Deposited on : 2023-08-24
Resolution : 1.37 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

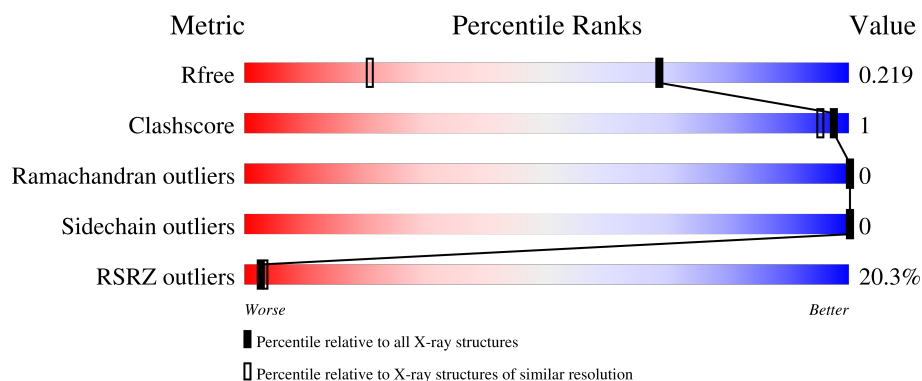
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.37 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	4403 (1.40-1.36)
Clashscore	190562	4528 (1.40-1.36)
Ramachandran outliers	187476	4459 (1.40-1.36)
Sidechain outliers	187428	4458 (1.40-1.36)
RSRZ outliers	180081	4399 (1.40-1.36)

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	349	10% 91% 7%
1	B	349	28% 91% 7%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5412 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 cAMP-specific 3',5'-cyclic phosphodiesterase 4D.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2584	1636	441	493	14			
1	B	323	Total	C	N	O	S	0	0	0
			2528	1605	435	474	14			

There are 42 discrepancies between the modelled and reference sequences:

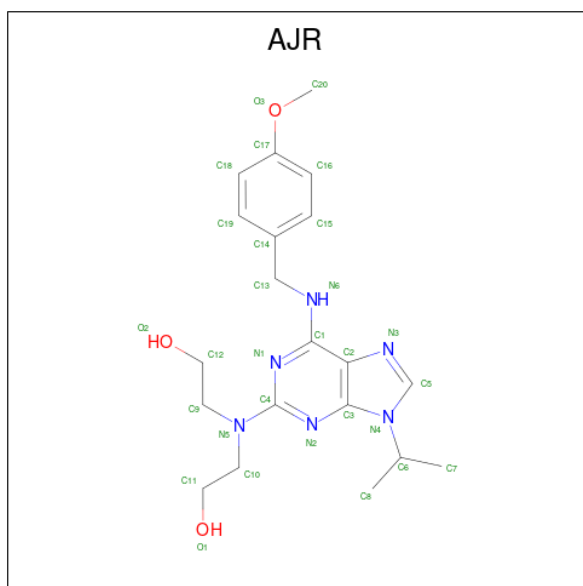
Chain	Residue	Modelled	Actual	Comment	Reference
A	65	MET	-	expression tag	UNP Q08499
A	66	GLY	-	expression tag	UNP Q08499
A	67	SER	-	expression tag	UNP Q08499
A	68	SER	-	expression tag	UNP Q08499
A	69	HIS	-	expression tag	UNP Q08499
A	70	HIS	-	expression tag	UNP Q08499
A	71	HIS	-	expression tag	UNP Q08499
A	72	HIS	-	expression tag	UNP Q08499
A	73	HIS	-	expression tag	UNP Q08499
A	74	HIS	-	expression tag	UNP Q08499
A	75	SER	-	expression tag	UNP Q08499
A	76	SER	-	expression tag	UNP Q08499
A	77	GLY	-	expression tag	UNP Q08499
A	78	LEU	-	expression tag	UNP Q08499
A	79	VAL	-	expression tag	UNP Q08499
A	80	PRO	-	expression tag	UNP Q08499
A	81	ARG	-	expression tag	UNP Q08499
A	82	GLY	-	expression tag	UNP Q08499
A	83	SER	-	expression tag	UNP Q08499
A	84	HIS	-	expression tag	UNP Q08499
A	85	MET	-	expression tag	UNP Q08499
B	65	MET	-	expression tag	UNP Q08499
B	66	GLY	-	expression tag	UNP Q08499
B	67	SER	-	expression tag	UNP Q08499
B	68	SER	-	expression tag	UNP Q08499

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Chain	Residue	Modelled	Actual	Comment	Reference
B	69	HIS	-	expression tag	UNP Q08499
B	70	HIS	-	expression tag	UNP Q08499
B	71	HIS	-	expression tag	UNP Q08499
B	72	HIS	-	expression tag	UNP Q08499
B	73	HIS	-	expression tag	UNP Q08499
B	74	HIS	-	expression tag	UNP Q08499
B	75	SER	-	expression tag	UNP Q08499
B	76	SER	-	expression tag	UNP Q08499
B	77	GLY	-	expression tag	UNP Q08499
B	78	LEU	-	expression tag	UNP Q08499
B	79	VAL	-	expression tag	UNP Q08499
B	80	PRO	-	expression tag	UNP Q08499
B	81	ARG	-	expression tag	UNP Q08499
B	82	GLY	-	expression tag	UNP Q08499
B	83	SER	-	expression tag	UNP Q08499
B	84	HIS	-	expression tag	UNP Q08499
B	85	MET	-	expression tag	UNP Q08499

- Molecule 2 is 2,2'-[6-[(4-methoxyphenyl)methyl]amino}-9-(propan-2-yl)-9H-purin-2-yl]azanediy]di(ethan-1-ol) (CCD ID: AJR) (formula: C₂₀H₂₈N₆O₃) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			29	20	6	3		
2	B	1	Total	C	N	O	0	0
			29	20	6	3		

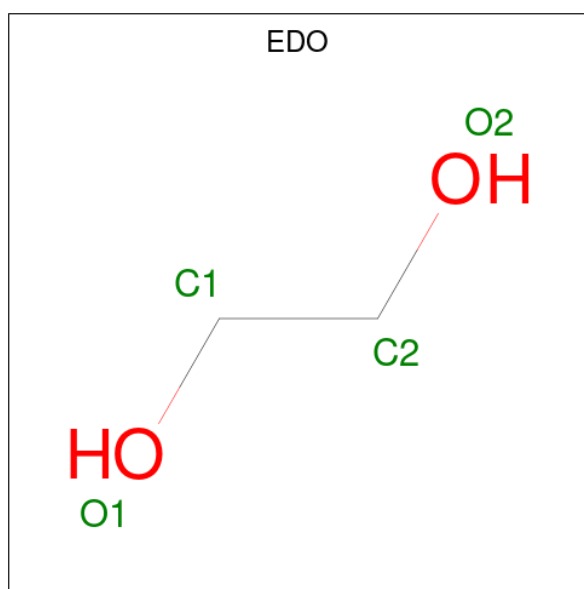
- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Mg	0	0
			1	1		
3	B	1	Total	Mg	0	0
			1	1		

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		
4	B	1	Total	Zn	0	0
			1	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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

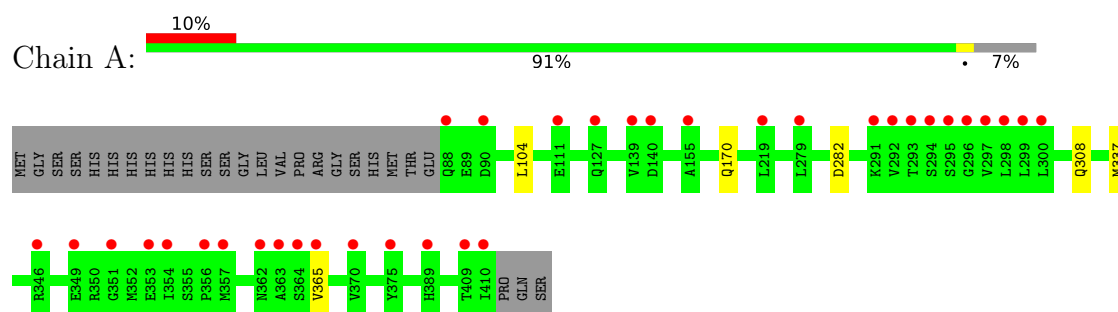
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	128	Total	O	0	0
			128	128		
6	B	78	Total	O	0	0
			78	78		

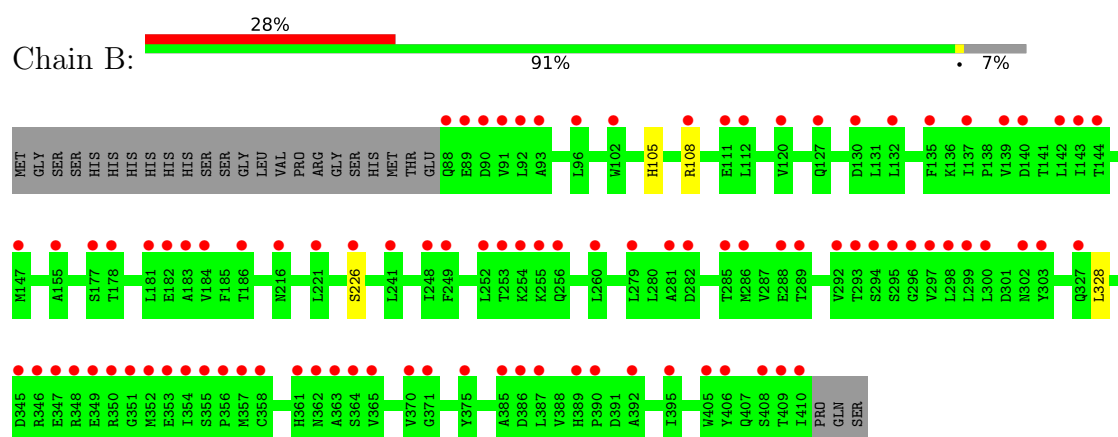
3 Residue-property plots [i](#)

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: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.63Å 80.71Å 163.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.33 – 1.37 30.33 – 1.37	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.33-1.37) 99.7 (30.33-1.37)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.08 (at 1.37Å)	Xtriage
Refinement program	PHENIX 1.17.1_3660	Depositor
R, R_{free}	0.206 , 0.215 0.210 , 0.219	Depositor DCC
R_{free} test set	8184 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.478	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 35.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5412	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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, AJR, EDO, MG

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	0.23	0/2637	0.43	0/3589
1	B	0.22	0/2581	0.42	0/3521
All	All	0.23	0/5218	0.42	0/7110

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	2584	0	2512	3	0
1	B	2528	0	2429	5	0
2	A	29	0	0	0	0
2	B	29	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	A	20	0	30	0	0
5	B	12	0	18	0	0
6	A	128	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	78	0	0	1	0
All	All	5412	0	4989	8	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 1.

All (8) 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:105:HIS:HA	1:B:108:ARG:HH21	1.67	0.60
1:A:337:MET:SD	1:A:365:VAL:HG21	2.43	0.58
1:B:108:ARG:HH22	1:B:328:LEU:HD21	1.70	0.56
1:A:282:ASP:HB3	1:A:308:GLN:NE2	2.21	0.55
1:B:108:ARG:H	1:B:108:ARG:NE	2.11	0.48
1:A:104:LEU:HD22	1:A:170:GLN:HG3	2.00	0.43
1:B:226:SER:HB3	6:B:620:HOH:O	2.20	0.41
1:B:108:ARG:NH2	1:B:328:LEU:HD21	2.35	0.41

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	321/349 (92%)	318 (99%)	3 (1%)	0	100	100
1	B	321/349 (92%)	318 (99%)	3 (1%)	0	100	100
All	All	642/698 (92%)	636 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	287/318 (90%)	287 (100%)	0	100	100
1	B	273/318 (86%)	273 (100%)	0	100	100
All	All	560/636 (88%)	560 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	250	GLN
1	A	308	GLN
1	A	407	GLN
1	B	210	GLN
1	B	393	GLN

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 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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	$\# Z > 2$
5	EDO	B	505	-	3,3,3	0.41	0	2,2,2	0.47	0
5	EDO	A	506	-	3,3,3	0.40	0	2,2,2	0.41	0
5	EDO	B	506	-	3,3,3	0.36	0	2,2,2	0.22	0
2	AJR	A	501	-	31,31,31	0.43	0	41,42,42	0.47	0
5	EDO	A	504	-	3,3,3	0.50	0	2,2,2	0.38	0
5	EDO	A	507	-	3,3,3	0.27	0	2,2,2	0.56	0
5	EDO	A	508	-	3,3,3	0.42	0	2,2,2	0.20	0
2	AJR	B	501	-	31,31,31	0.42	0	41,42,42	0.45	0
5	EDO	B	504	-	3,3,3	0.50	0	2,2,2	0.37	0
5	EDO	A	505	-	3,3,3	0.41	0	2,2,2	0.43	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
5	EDO	B	505	-	-	0/1/1/1	-
5	EDO	A	506	-	-	1/1/1/1	-
5	EDO	B	506	-	-	0/1/1/1	-
2	AJR	A	501	-	-	0/21/21/21	0/3/3/3
5	EDO	A	504	-	-	0/1/1/1	-
5	EDO	A	507	-	-	0/1/1/1	-
5	EDO	A	508	-	-	0/1/1/1	-
2	AJR	B	501	-	-	0/21/21/21	0/3/3/3
5	EDO	B	504	-	-	0/1/1/1	-
5	EDO	A	505	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

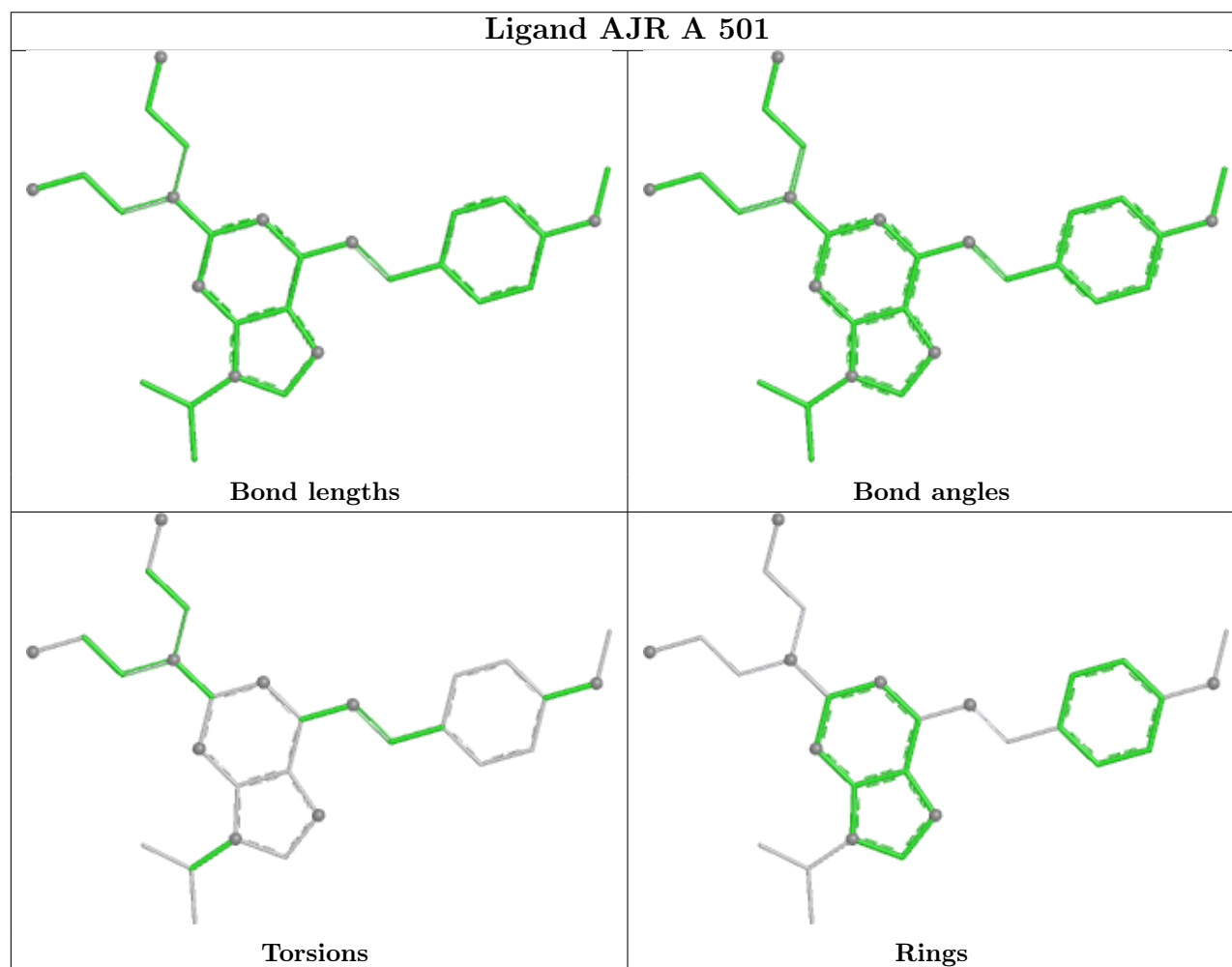
All (1) torsion outliers are listed below:

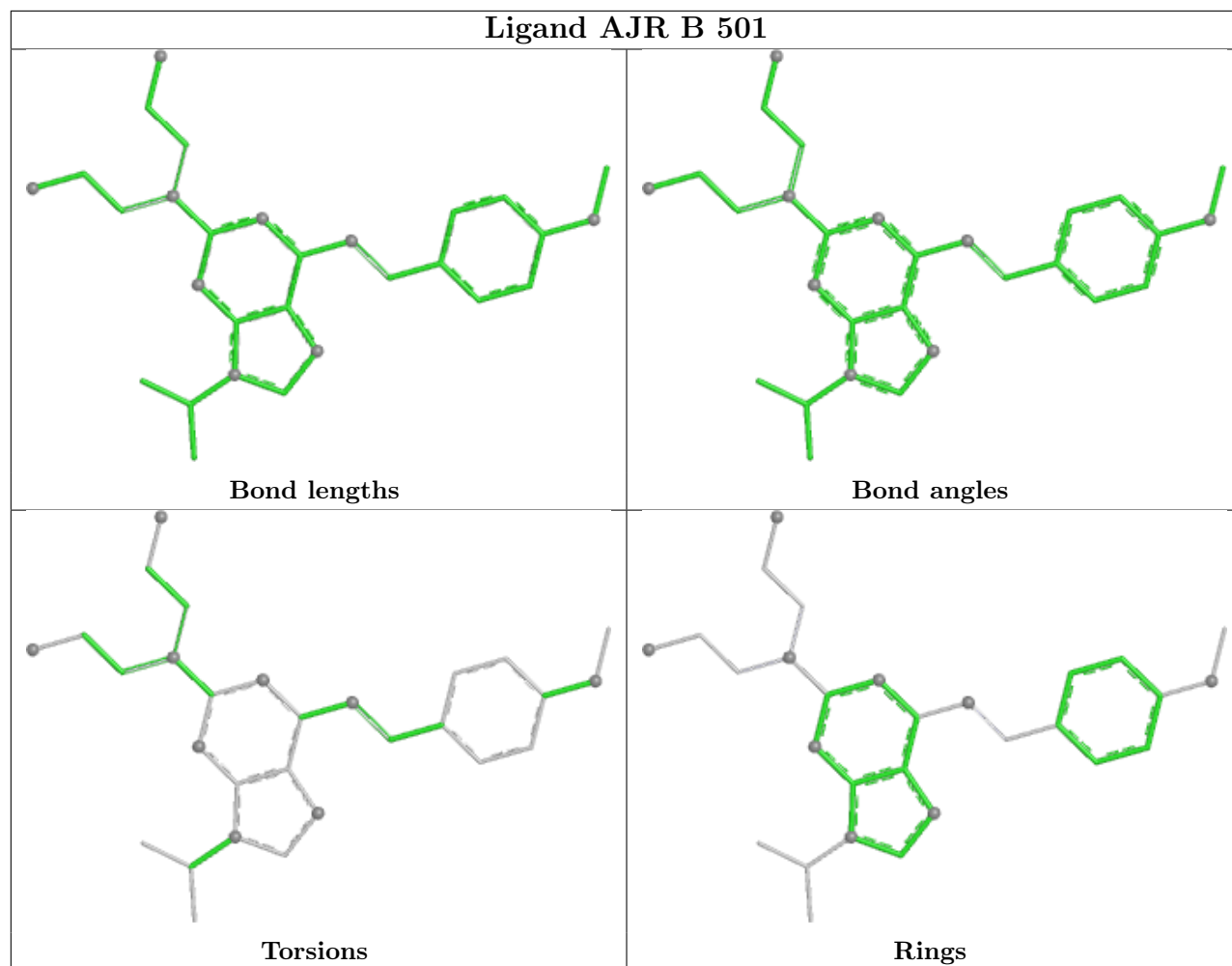
Mol	Chain	Res	Type	Atoms
5	A	506	EDO	O1-C1-C2-O2

There are no ring outliers.

No monomer is involved in short contacts.

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	323/349 (92%)	0.92	35 (10%) 11 13	16, 27, 40, 50	0
1	B	323/349 (92%)	1.59	96 (29%) 1 1	18, 35, 48, 60	0
All	All	646/698 (92%)	1.25	131 (20%) 3 3	16, 30, 45, 60	0

All (131) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	294	SER	7.0
1	B	410	ILE	6.6
1	B	295	SER	6.0
1	B	183	ALA	5.9
1	B	354	ILE	5.8
1	A	410	ILE	5.4
1	A	295	SER	5.0
1	B	292	VAL	4.9
1	B	108	ARG	4.6
1	B	253	THR	4.5
1	A	349	GLU	4.4
1	A	362	ASN	4.4
1	B	296	GLY	4.4
1	B	89	GLU	4.2
1	A	363	ALA	4.2
1	B	254	LYS	4.1
1	B	375	TYR	4.1
1	B	362	ASN	4.1
1	B	353	GLU	4.1
1	B	286	MET	4.0
1	A	90	ASP	4.0
1	B	349	GLU	4.0
1	A	293	THR	3.9
1	B	93	ALA	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	390	PRO	3.8
1	A	351	GLY	3.8
1	A	297	VAL	3.7
1	B	91	VAL	3.7
1	B	351	GLY	3.6
1	B	299	LEU	3.6
1	A	292	VAL	3.6
1	B	363	ALA	3.5
1	B	302	ASN	3.4
1	B	139	VAL	3.4
1	B	297	VAL	3.4
1	B	178	THR	3.4
1	A	294	SER	3.3
1	B	303	TYR	3.3
1	B	127	GLN	3.3
1	B	289	THR	3.2
1	B	298	LEU	3.2
1	A	365	VAL	3.2
1	B	88	GLN	3.2
1	B	346	ARG	3.2
1	B	405	TRP	3.2
1	B	140	ASP	3.2
1	A	409	THR	3.2
1	A	296	GLY	3.2
1	B	216	ASN	3.1
1	B	409	THR	3.1
1	A	354	ILE	3.1
1	B	300	LEU	3.1
1	A	353	GLU	3.1
1	B	90	ASP	3.1
1	A	357	MET	3.0
1	B	221	LEU	3.0
1	B	356	PRO	3.0
1	B	387	LEU	3.0
1	B	285	THR	2.9
1	B	352	MET	2.9
1	B	130	ASP	2.9
1	B	281	ALA	2.9
1	B	389	HIS	2.9
1	B	181	LEU	2.8
1	B	184	VAL	2.8
1	B	355	SER	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	112	LEU	2.8
1	B	279	LEU	2.8
1	B	143	ILE	2.8
1	B	252	LEU	2.7
1	A	356	PRO	2.7
1	B	96	LEU	2.7
1	B	142	LEU	2.7
1	B	392	ALA	2.7
1	B	255	LYS	2.7
1	B	186	THR	2.6
1	B	155	ALA	2.6
1	A	127	GLN	2.6
1	B	248	ILE	2.6
1	A	140	ASP	2.5
1	B	226	SER	2.5
1	A	298	LEU	2.5
1	B	92	LEU	2.5
1	B	132	LEU	2.5
1	B	385	ALA	2.5
1	B	371	GLY	2.5
1	A	139	VAL	2.5
1	B	364	SER	2.4
1	B	361	HIS	2.4
1	B	408	SER	2.4
1	A	279	LEU	2.4
1	A	300	LEU	2.4
1	B	370	VAL	2.4
1	B	288	GLU	2.4
1	B	293	THR	2.4
1	B	348	ARG	2.4
1	B	365	VAL	2.4
1	A	389	HIS	2.4
1	B	358	CYS	2.4
1	B	135	PHE	2.4
1	A	291	LYS	2.3
1	A	219	LEU	2.3
1	B	347	GLU	2.3
1	B	120	VAL	2.3
1	B	182	GLU	2.3
1	B	241	LEU	2.3
1	A	370	VAL	2.3
1	B	357	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	137	ILE	2.2
1	A	364	SER	2.2
1	A	375	TYR	2.2
1	A	88	GLN	2.2
1	A	299	LEU	2.2
1	B	256	GLN	2.2
1	A	111	GLU	2.2
1	B	147	MET	2.2
1	B	260	LEU	2.1
1	B	350	ARG	2.1
1	B	406	TYR	2.1
1	A	346	ARG	2.1
1	B	102	TRP	2.1
1	B	177	SER	2.1
1	B	395	ILE	2.1
1	B	327	GLN	2.1
1	B	282	ASP	2.1
1	B	386	ASP	2.1
1	A	155	ALA	2.1
1	B	249	PHE	2.1
1	B	111	GLU	2.0
1	B	345	ASP	2.0
1	B	144	THR	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](#)

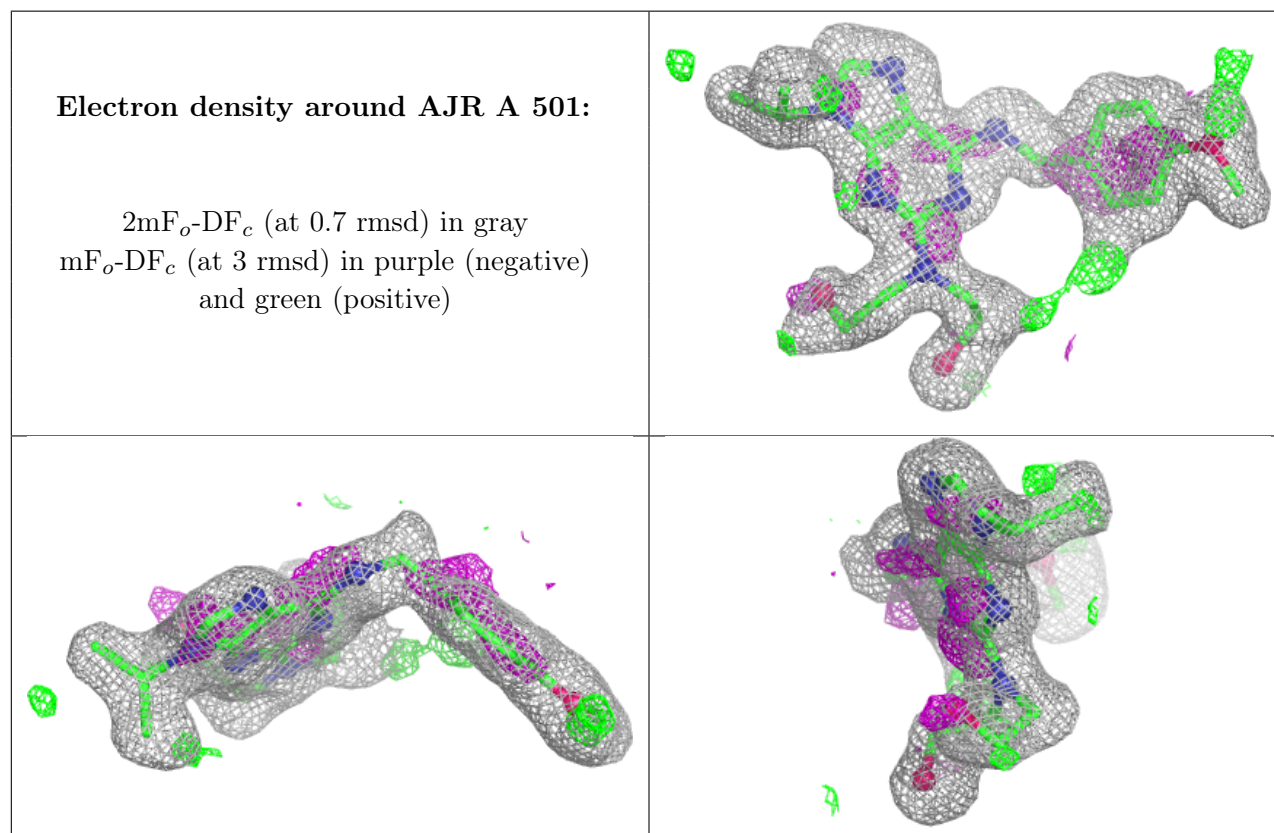
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists the number of atoms with occupancy less than 0.9.

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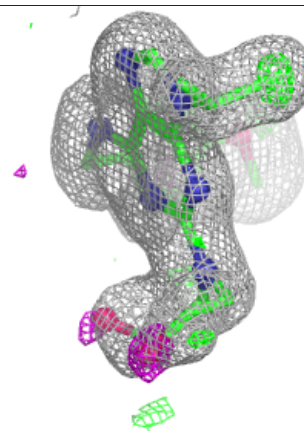
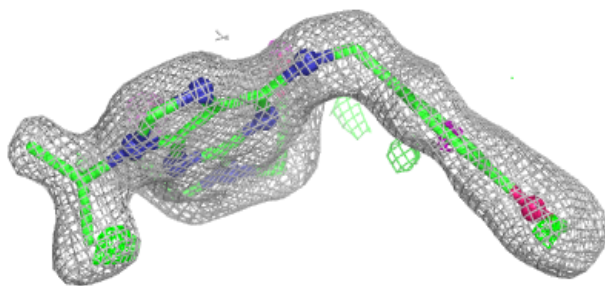
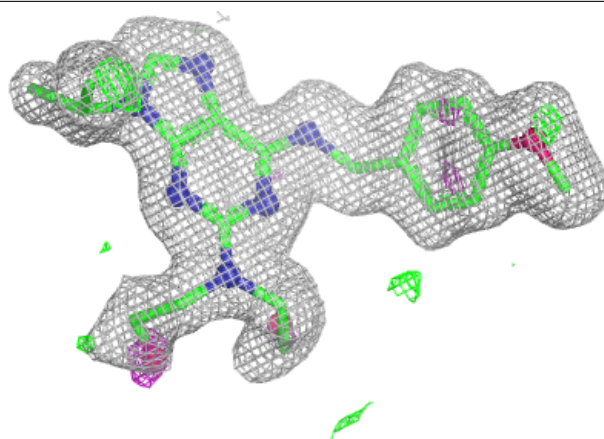
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	A	505	4/4	0.70	0.24	29,34,36,40	0
5	EDO	B	505	4/4	0.77	0.19	31,37,38,40	0
5	EDO	A	504	4/4	0.80	0.14	28,31,33,33	0
5	EDO	B	504	4/4	0.82	0.16	29,31,36,38	0
5	EDO	A	508	4/4	0.82	0.18	42,42,44,45	0
2	AJR	A	501	29/29	0.85	0.13	24,29,37,41	0
5	EDO	B	506	4/4	0.86	0.13	36,37,37,38	0
5	EDO	A	506	4/4	0.87	0.12	34,34,35,35	0
2	AJR	B	501	29/29	0.88	0.11	26,31,40,45	0
5	EDO	A	507	4/4	0.88	0.13	33,36,36,37	0
3	MG	B	502	1/1	0.98	0.07	18,18,18,18	0
3	MG	A	502	1/1	0.99	0.04	14,14,14,14	0
4	ZN	A	503	1/1	0.99	0.08	20,20,20,20	0
4	ZN	B	503	1/1	1.00	0.09	23,23,23,23	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 AJR B 501:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.