



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 03:10 AM UTC

PDB ID : 8WDN / pdb_00008wdn
Title : Crystal structure of PDE4D complexed with 7b-1
Authors : Liu, J.Y.; Li, M.J.; Xu, Y.C.
Deposited on : 2023-09-15
Resolution : 1.55 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

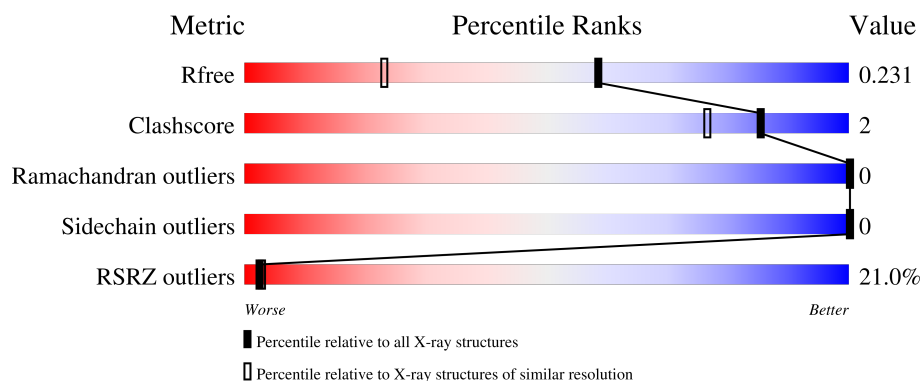
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.55 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	2145 (1.56-1.56)
Clashscore	190562	2189 (1.56-1.56)
Ramachandran outliers	187476	2153 (1.56-1.56)
Sidechain outliers	187428	2150 (1.56-1.56)
RSRZ outliers	180081	2146 (1.56-1.56)

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	5% 91% 7%
1	B	349	34% 83% 9% 7%

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 5470 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	324	Total	C	N	O	S	0	0	0
			2614	1653	446	501	14			
1	B	324	Total	C	N	O	S	0	0	0
			2591	1640	442	495	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

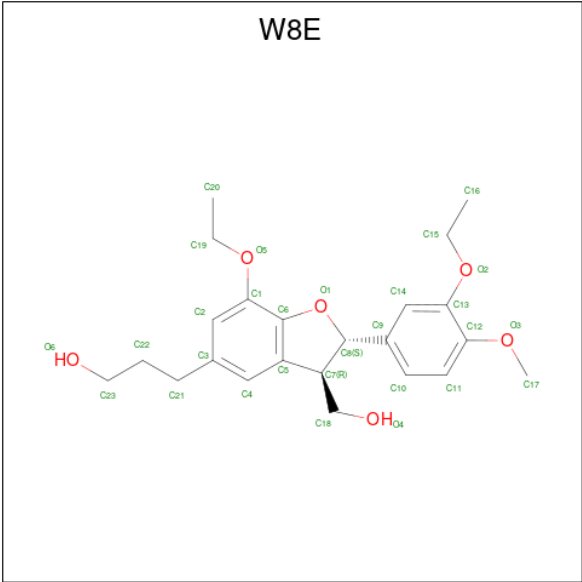
- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- Molecule 4 is 3-[(2 {S},3 {R})-7-ethoxy-2-(3-ethoxy-4-methoxy-phenyl)-3-(hydroxymethyl)-2,3-dihydro-1-benzofuran-5-yl]propan-1-ol (CCD ID: W8E) (formula: C₂₃H₃₀O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			29	23	6		
4	B	1	Total	C	O	0	0
			29	23	6		

- 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		

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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		

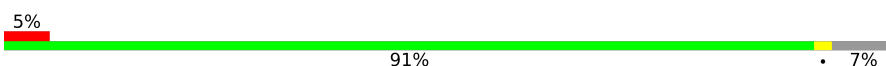
- Molecule 6 is water.

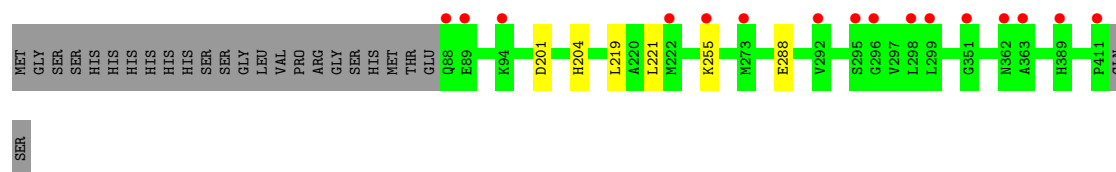
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	118	Total	O	0	0
			118	118		
6	B	69	Total	O	0	0
			69	69		

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.

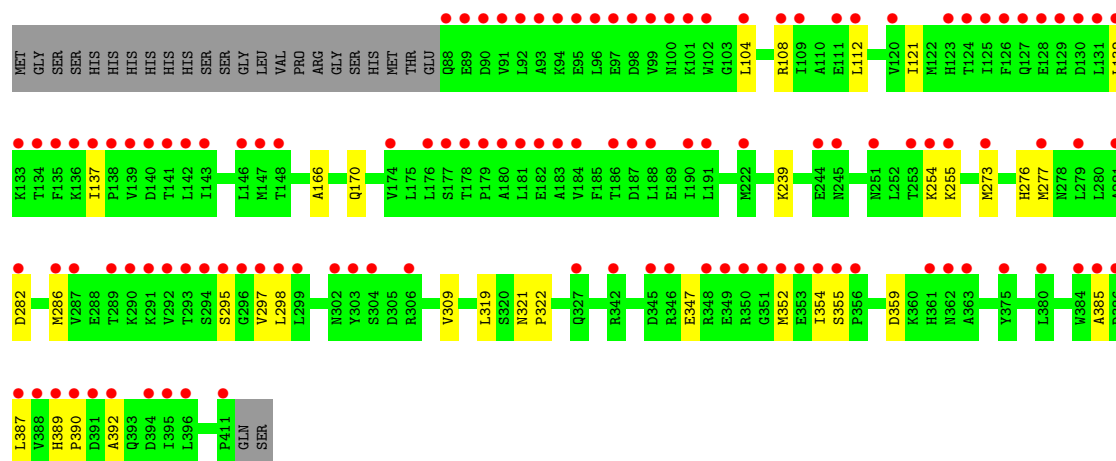
- Molecule 1: cAMP-specific 3',5'-cyclic phosphodiesterase 4D

Chain A: 



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

Chain B: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	57.97Å 80.41Å 163.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	36.42 – 1.55 36.42 – 1.55	Depositor EDS
% Data completeness (in resolution range)	100.0 (36.42-1.55) 100.0 (36.42-1.55)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.22 (at 1.55Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.208 , 0.231 0.209 , 0.231	Depositor DCC
R_{free} test set	5557 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	22.4	Xtriage
Anisotropy	0.294	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 37.0	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	5470	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.00% 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: W8E, EDO, MG, ZN

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	0.27	0/2668	0.49	0/3628
1	B	0.22	0/2645	0.42	0/3601
All	All	0.25	0/5313	0.45	0/7229

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	2614	0	2556	3	1
1	B	2591	0	2516	21	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	29	0	0	0	0
4	B	29	0	0	0	0
5	A	8	0	12	0	0
5	B	8	0	12	0	0
6	A	118	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	69	0	0	1	0
All	All	5470	0	5096	23	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 2.

All (23) 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:276:HIS:CD2	1:B:277:MET:HE3	2.33	0.62
1:B:298:LEU:HD11	1:B:387:LEU:HG	1.85	0.58
1:A:221:LEU:HD21	1:B:239:LYS:HD2	1.96	0.48
1:B:282:ASP:O	1:B:286:MET:HG3	2.14	0.48
1:B:385:ALA:HA	1:B:392:ALA:HB3	1.94	0.48
1:B:321:ASN:HB2	1:B:322:PRO:HD3	1.97	0.47
1:B:273:MET:HE1	1:B:319:LEU:HD11	1.96	0.47
1:B:277:MET:HE2	1:B:277:MET:HA	1.95	0.47
1:B:121:ILE:HD12	1:B:166:ALA:HB1	1.98	0.45
1:B:104:LEU:HD22	1:B:170:GLN:HG3	1.98	0.44
1:B:347:GLU:O	1:B:352:MET:N	2.46	0.43
1:B:254:LYS:HE3	6:B:764:HOH:O	2.19	0.43
1:B:255:LYS:HA	1:B:255:LYS:HD3	1.72	0.42
1:B:132:LEU:O	1:B:137:ILE:N	2.47	0.42
1:B:347:GLU:OE2	1:B:355:SER:OG	2.29	0.41
1:A:201:ASP:O	1:A:204:HIS:HB2	2.20	0.41
1:B:389:HIS:HA	1:B:390:PRO:HA	1.75	0.41
1:B:354:ILE:HG21	1:B:359:ASP:HB2	2.00	0.41
1:B:108:ARG:NH2	1:B:112:LEU:HD21	2.35	0.41
1:B:254:LYS:HE2	1:B:254:LYS:HB3	1.77	0.41
1:B:286:MET:HE1	1:B:309:VAL:HG23	2.02	0.41
1:A:219:LEU:HD23	1:A:219:LEU:HA	1.96	0.41
1:B:295:SER:OG	1:B:297:VAL:HG23	2.21	0.41

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)
1:A:255:LYS:NZ	1:A:288:GLU:OE1[3_555]	2.06	0.14

5.3 Torsion angles

5.3.1 Protein backbone

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	322/349 (92%)	316 (98%)	6 (2%)	0	100	100
1	B	322/349 (92%)	318 (99%)	4 (1%)	0	100	100
All	All	644/698 (92%)	634 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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	294/318 (92%)	294 (100%)	0	100	100
1	B	288/318 (91%)	288 (100%)	0	100	100
All	All	582/636 (92%)	582 (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 (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	258	GLN
1	A	321	ASN
1	A	407	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 10 ligands modelled in this entry, 4 are monoatomic - leaving 6 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	A	604	-	3,3,3	0.38	0	2,2,2	0.52	0
5	EDO	A	605	-	3,3,3	0.37	0	2,2,2	0.37	0
4	W8E	B	603	-	31,31,31	0.31	0	39,42,42	1.06	4 (10%)
4	W8E	A	603	-	31,31,31	0.32	0	39,42,42	0.92	3 (7%)
5	EDO	B	604	-	3,3,3	0.42	0	2,2,2	0.43	0
5	EDO	B	605	-	3,3,3	0.44	0	2,2,2	0.33	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	A	604	-	-	0/1/1/1	-
5	EDO	A	605	-	-	0/1/1/1	-
4	W8E	B	603	-	-	0/18/30/30	0/3/3/3
4	W8E	A	603	-	-	1/18/30/30	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	EDO	B	604	-	-	0/1/1/1	-
5	EDO	B	605	-	-	0/1/1/1	-

There are no bond length outliers.

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	603	W8E	C6-O1-C8	2.76	108.36	105.96
4	A	603	W8E	C6-O1-C8	2.41	108.05	105.96
4	B	603	W8E	O5-C1-C6	2.39	121.02	115.07
4	A	603	W8E	C5-C7-C8	2.35	102.91	101.41
4	B	603	W8E	C5-C7-C8	2.32	102.89	101.41
4	B	603	W8E	C2-C1-C6	-2.18	117.80	120.22
4	A	603	W8E	C2-C1-C6	-2.04	117.95	120.22

There are no chirality outliers.

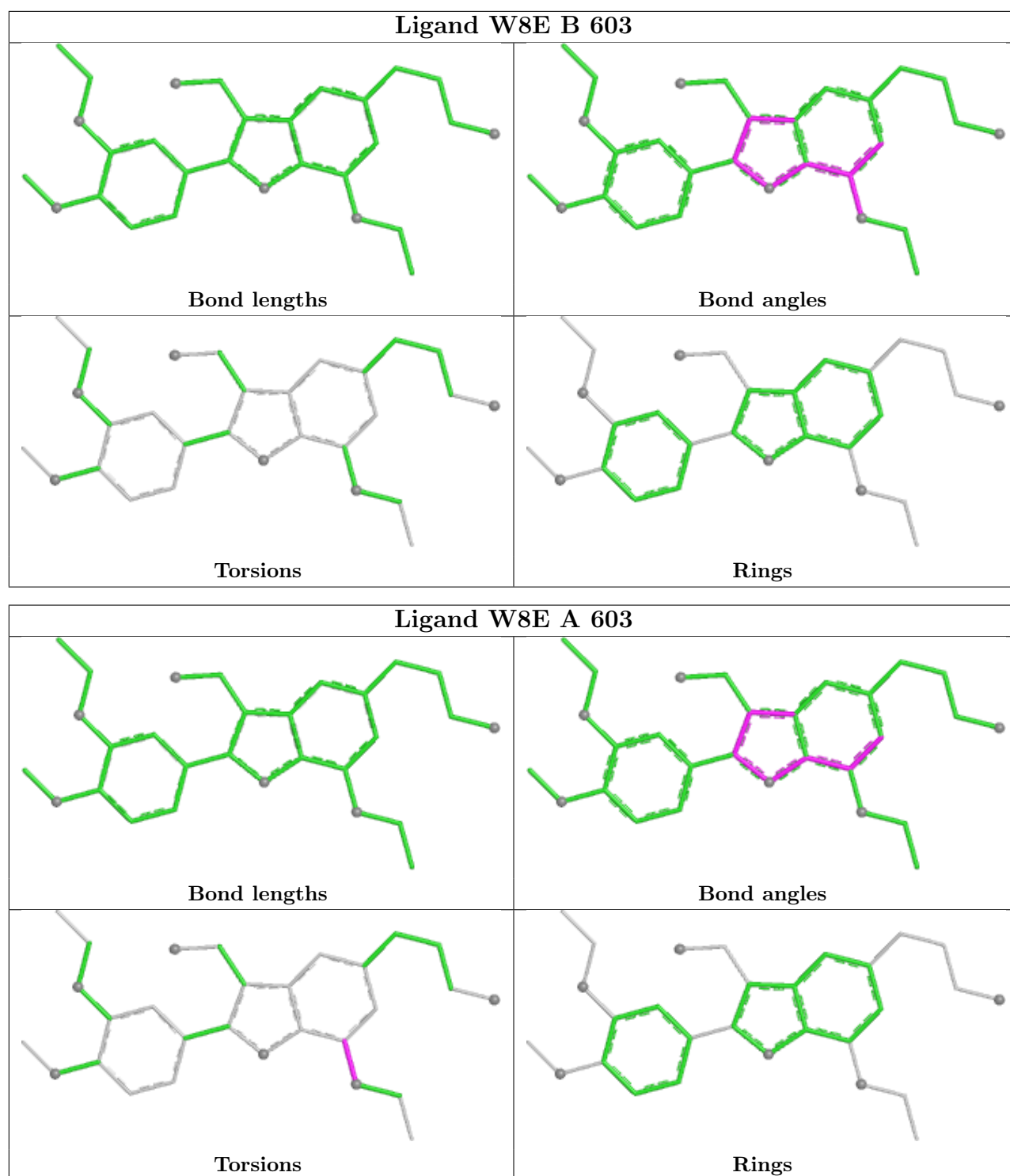
All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	603	W8E	C6-C1-O5-C19

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

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	324/349 (92%)	0.38	16 (4%) 35 42	15, 25, 45, 66	0
1	B	324/349 (92%)	1.78	120 (37%) 1 1	18, 35, 82, 132	0
All	All	648/698 (92%)	1.08	136 (20%) 2 3	15, 29, 68, 132	0

All (136) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	ALA	9.9
1	B	91	VAL	9.5
1	B	93	ALA	8.0
1	B	297	VAL	7.6
1	B	390	PRO	6.9
1	B	92	LEU	6.8
1	B	179	PRO	6.8
1	B	132	LEU	6.4
1	B	180	ALA	6.4
1	B	184	VAL	6.3
1	B	388	VAL	6.1
1	B	99	VAL	6.0
1	B	182	GLU	6.0
1	B	96	LEU	5.9
1	B	88	GLN	5.9
1	B	112	LEU	5.7
1	B	292	VAL	5.5
1	B	139	VAL	5.2
1	B	295	SER	5.1
1	B	181	LEU	5.1
1	B	389	HIS	5.0
1	B	354	ILE	4.9
1	B	296	GLY	4.8
1	B	134	THR	4.7

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Mol	Chain	Res	Type	RSRZ
1	B	298	LEU	4.6
1	B	127	GLN	4.6
1	B	133	LYS	4.5
1	B	294	SER	4.5
1	B	363	ALA	4.5
1	B	94	LYS	4.4
1	B	411	PRO	4.4
1	B	90	ASP	4.3
1	B	293	THR	4.3
1	B	391	ASP	4.3
1	B	137	ILE	4.2
1	B	351	GLY	4.2
1	B	342	ARG	4.2
1	B	385	ALA	4.2
1	B	178	THR	4.1
1	B	124	THR	4.0
1	B	289	THR	4.0
1	A	292	VAL	4.0
1	B	349	GLU	4.0
1	B	392	ALA	4.0
1	B	286	MET	3.9
1	B	131	LEU	3.9
1	B	387	LEU	3.9
1	B	353	GLU	3.8
1	B	143	ILE	3.7
1	B	350	ARG	3.7
1	B	362	ASN	3.6
1	A	295	SER	3.5
1	B	130	ASP	3.4
1	B	348	ARG	3.4
1	B	138	PRO	3.4
1	B	352	MET	3.4
1	B	123	HIS	3.3
1	B	128	GLU	3.3
1	B	386	ASP	3.3
1	B	120	VAL	3.3
1	B	97	GLU	3.3
1	A	298	LEU	3.2
1	B	299	LEU	3.2
1	B	186	THR	3.2
1	B	100	ASN	3.2
1	B	142	LEU	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	140	ASP	3.2
1	B	302	ASN	3.1
1	B	395	ILE	3.1
1	B	102	TRP	3.1
1	A	363	ALA	3.1
1	B	95	GLU	3.0
1	B	254	LYS	3.0
1	B	135	PHE	3.0
1	B	98	ASP	3.0
1	A	411	PRO	3.0
1	B	303	TYR	2.9
1	B	174	VAL	2.9
1	B	287	VAL	2.9
1	B	191	LEU	2.9
1	B	109	ILE	2.9
1	B	222	MET	2.8
1	B	176	LEU	2.8
1	B	279	LEU	2.8
1	A	88	GLN	2.8
1	B	327	GLN	2.8
1	B	253	THR	2.8
1	B	147	MET	2.7
1	B	126	PHE	2.7
1	A	351	GLY	2.7
1	B	245	ASN	2.6
1	B	356	PRO	2.6
1	B	190	ILE	2.6
1	B	89	GLU	2.6
1	B	108	ARG	2.6
1	A	299	LEU	2.6
1	B	290	LYS	2.6
1	B	244	GLU	2.5
1	B	361	HIS	2.5
1	A	94	LYS	2.5
1	B	141	THR	2.5
1	A	255	LYS	2.4
1	B	129	ARG	2.4
1	B	177	SER	2.3
1	B	146	LEU	2.3
1	B	394	ASP	2.3
1	B	136	LYS	2.3
1	B	148	THR	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	375	TYR	2.3
1	A	362	ASN	2.3
1	B	345	ASP	2.3
1	B	384	TRP	2.2
1	B	281	ALA	2.2
1	A	389	HIS	2.2
1	B	291	LYS	2.2
1	B	251	ASN	2.2
1	B	188	LEU	2.2
1	A	222	MET	2.2
1	B	125	ILE	2.2
1	B	255	LYS	2.2
1	B	355	SER	2.2
1	B	104	LEU	2.1
1	B	396	LEU	2.1
1	A	89	GLU	2.1
1	B	282	ASP	2.1
1	B	306	ARG	2.1
1	A	296	GLY	2.1
1	B	187	ASP	2.1
1	B	304	SER	2.1
1	B	346	ARG	2.1
1	B	277	MET	2.1
1	B	101	LYS	2.0
1	B	380	LEU	2.0
1	A	273	MET	2.0
1	B	273	MET	2.0
1	B	111	GLU	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,

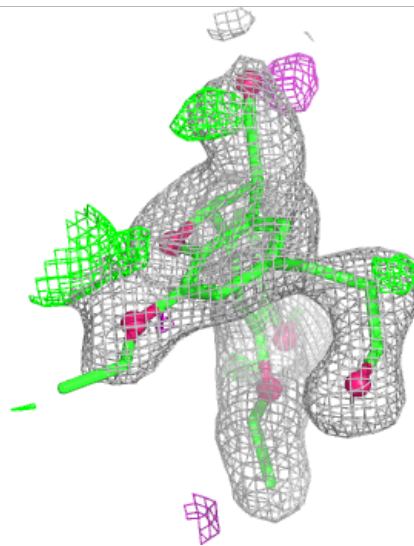
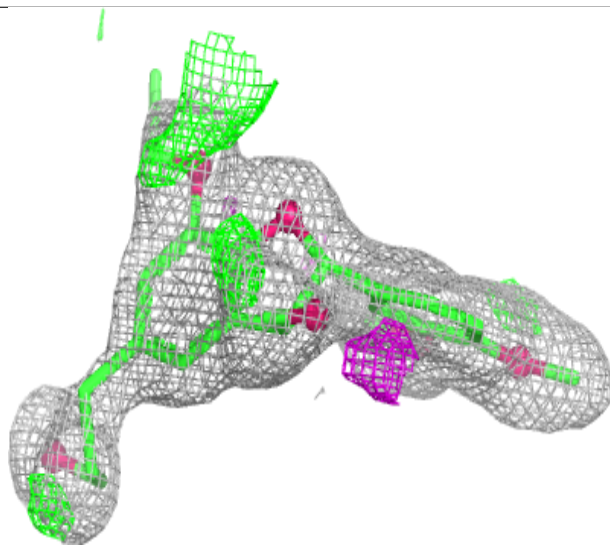
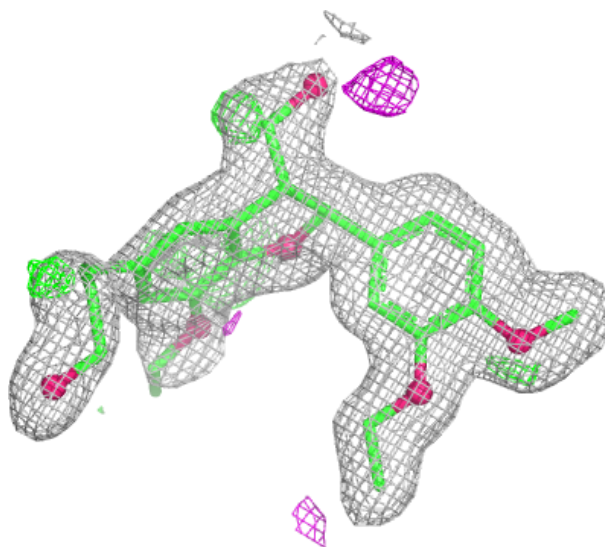
median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	B	605	4/4	0.85	0.19	42,49,55,59	0
5	EDO	A	604	4/4	0.88	0.14	36,40,41,42	0
4	W8E	B	603	29/29	0.89	0.14	21,32,54,60	0
5	EDO	B	604	4/4	0.90	0.13	35,39,42,44	0
4	W8E	A	603	29/29	0.91	0.12	19,31,49,52	0
5	EDO	A	605	4/4	0.91	0.13	31,38,38,41	0
2	MG	A	601	1/1	0.98	0.04	16,16,16,16	0
2	MG	B	601	1/1	0.99	0.02	17,17,17,17	0
3	ZN	A	602	1/1	0.99	0.03	18,18,18,18	0
3	ZN	B	602	1/1	0.99	0.05	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.

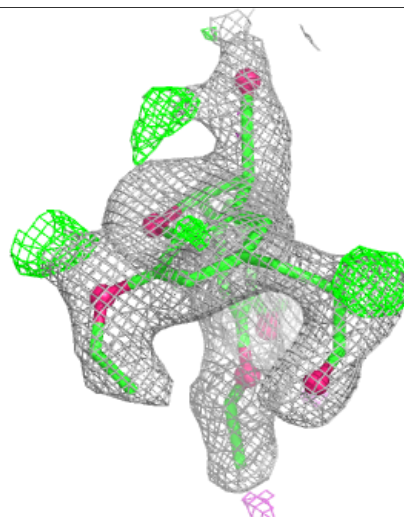
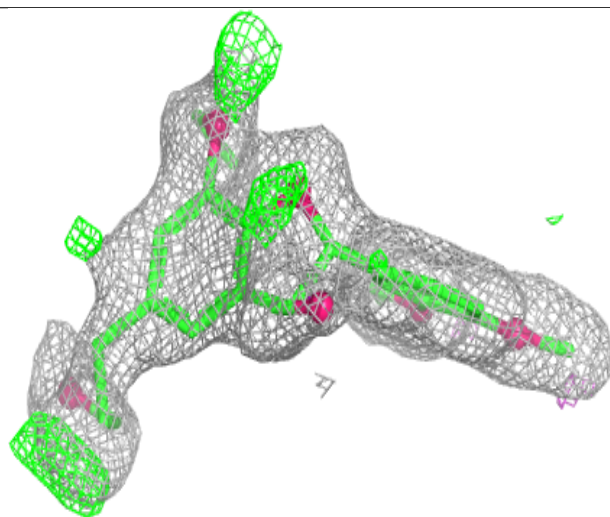
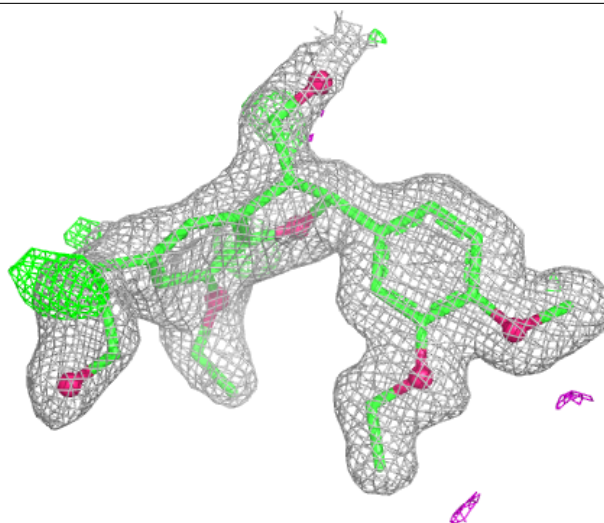
Electron density around W8E B 603:

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



Electron density around W8E A 603:

$2mF_o-DF_c$ (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.