



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:45 AM UTC

PDB ID : 8WDO / pdb_00008wdo
Title : Crystal structure of PDE4D complexed with DCN
Authors : Liu, J.Y.; Li, M.J.; Xu, Y.C.
Deposited on : 2023-09-15
Resolution : 1.67 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

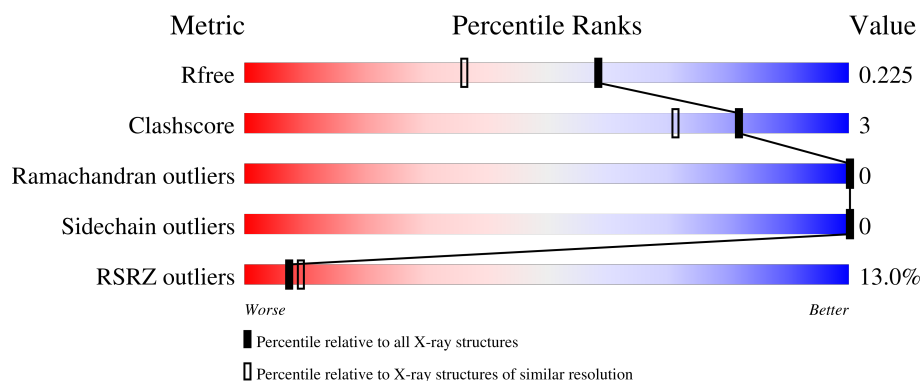
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.67 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	1054 (1.68-1.68)
Clashscore	190562	1078 (1.68-1.68)
Ramachandran outliers	187476	1068 (1.68-1.68)
Sidechain outliers	187428	1067 (1.68-1.68)
RSRZ outliers	180081	1055 (1.68-1.68)

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	4% 88% 5% 7%
1	B	349	20% 86% 7% 7%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 5354 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
			2591	1641	443	493	14			
1	B	324	Total	C	N	O	S	0	0	0
			2561	1624	438	485	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

Continued on next page...

Continued from previous page...

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

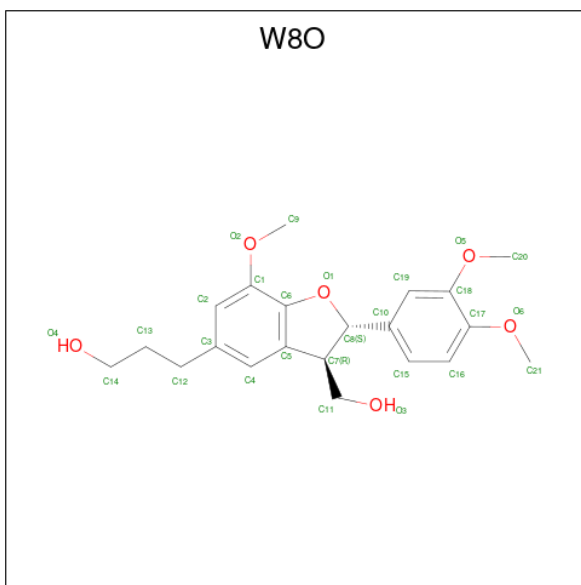
- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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})-2-(3,4-dimethoxyphenyl)-3-(hydroxymethyl)-7-methoxy-2,3-dihydro-1-benzofuran-5-yl]propan-1-ol (CCD ID: W8O) (formula: C₂₁H₂₆O₆) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			27	21	6		
4	B	1	Total	C	O	0	0
			27	21	6		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

Continued on next page...

Continued from previous page...

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

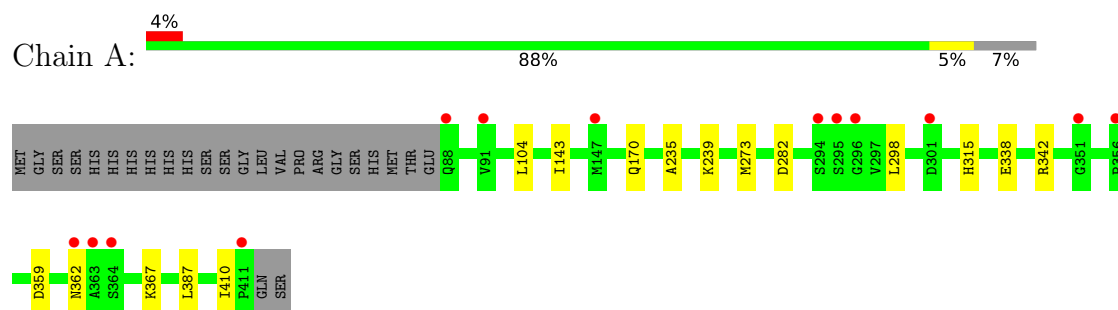
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	80	Total	O	0	0
			80	80		
6	B	52	Total	O	0	0
			52	52		

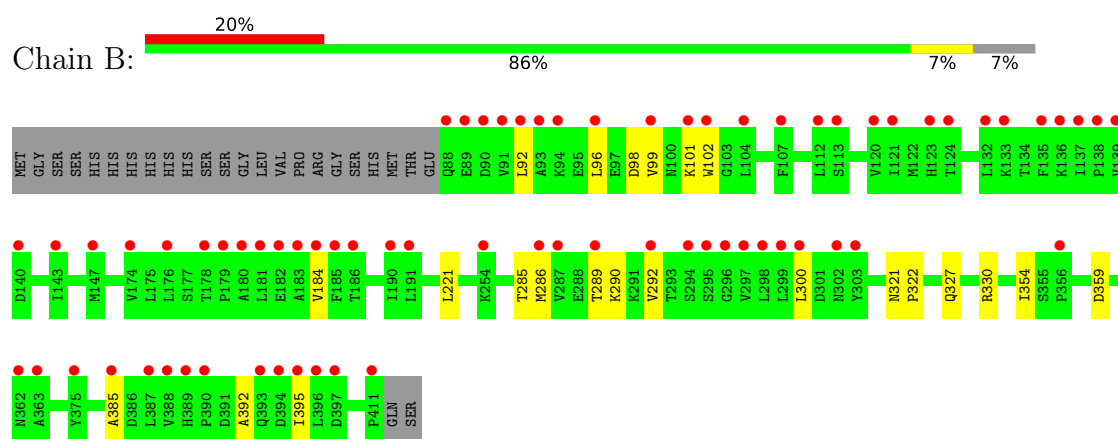
3 Residue-property plots [i](#)

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	57.50Å 80.03Å 163.15Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.79 – 1.67 40.79 – 1.67	Depositor EDS
% Data completeness (in resolution range)	96.8 (40.79-1.67) 96.8 (40.79-1.67)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.27 (at 1.67Å)	Xtriage
Refinement program	PHENIX 1.17.1 _3660	Depositor
R, R_{free}	0.197 , 0.226 0.198 , 0.225	Depositor DCC
R_{free} test set	4200 reflections (4.74%)	wwPDB-VP
Wilson B-factor (Å ²)	26.1	Xtriage
Anisotropy	0.240	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 36.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5354	wwPDB-VP
Average B, all atoms (Å ²)	38.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.28% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: EDO, ZN, W8O, 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	0.43	0/2644	0.57	0/3597
1	B	0.37	0/2615	0.54	0/3565
All	All	0.40	0/5259	0.56	0/7162

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 [i](#)

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	2591	0	2525	12	0
1	B	2561	0	2474	16	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	27	0	0	1	0
4	B	27	0	0	0	0
5	A	4	0	6	0	0
5	B	8	0	12	0	0
6	A	80	0	0	1	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	B	52	0	0	0	0
All	All	5354	0	5017	26	0

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

All (26) 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:239:LYS:HG2	1:B:221:LEU:HD21	1.79	0.63
1:A:367:LYS:HG2	1:A:410:ILE:HD13	1.80	0.63
1:B:184:VAL:HG11	1:B:300:LEU:HD12	1.83	0.60
1:A:273:MET:HE2	4:A:603:W8O:C9	2.34	0.58
1:B:102:TRP:CD1	1:B:395:ILE:HD12	2.42	0.54
1:B:92:LEU:O	1:B:96:LEU:HG	2.08	0.53
1:B:96:LEU:O	1:B:99:VAL:HG13	2.09	0.52
1:B:290:LYS:HE3	1:B:292:VAL:HG11	1.92	0.52
1:B:385:ALA:HA	1:B:392:ALA:HB3	1.93	0.51
1:A:359:ASP:OD2	1:A:362:ASN:ND2	2.43	0.51
1:A:239:LYS:HG2	1:B:221:LEU:CD2	2.40	0.50
1:A:338:GLU:O	1:A:342:ARG:HG3	2.12	0.50
1:A:298:LEU:HD11	1:A:387:LEU:HG	1.94	0.50
1:B:290:LYS:HE3	1:B:292:VAL:CG1	2.43	0.49
1:B:286:MET:HE3	1:B:286:MET:HB2	1.67	0.46
1:A:235:ALA:O	1:A:239:LYS:HG3	2.16	0.46
1:A:273:MET:HE1	1:A:315:HIS:HE1	1.81	0.45
1:B:327:GLN:HE22	1:B:330:ARG:HH11	1.66	0.44
1:A:104:LEU:HD22	1:A:170:GLN:HG3	1.98	0.43
1:B:354:ILE:HG21	1:B:359:ASP:HB2	2.00	0.43
1:B:98:ASP:OD1	1:B:101:LYS:NZ	2.45	0.42
1:B:321:ASN:HB2	1:B:322:PRO:HD3	2.03	0.41
1:B:184:VAL:CG1	1:B:300:LEU:HD12	2.49	0.41
1:B:285:THR:O	1:B:289:THR:HG23	2.21	0.41
1:A:143:ILE:HD13	1:A:143:ILE:HA	1.92	0.40
1:A:282:ASP:OD2	6:A:701:HOH:O	2.22	0.40

There are no symmetry-related clashes.

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%)	315 (98%)	7 (2%)	0	100	100
1	B	322/349 (92%)	318 (99%)	4 (1%)	0	100	100
All	All	644/698 (92%)	633 (98%)	11 (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	288/318 (91%)	288 (100%)	0	100	100
1	B	281/318 (88%)	281 (100%)	0	100	100
All	All	569/636 (90%)	569 (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 (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	88	GLN
1	A	308	GLN
1	A	321	ASN
1	A	331	GLN
1	A	407	GLN
1	B	210	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	278	ASN
1	B	308	GLN
1	B	321	ASN
1	B	327	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 9 ligands modelled in this entry, 4 are 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	$\# Z > 2$
4	W8O	B	603	-	29,29,29	0.30	0	37,40,40	1.07	3 (8%)
5	EDO	B	605	-	3,3,3	0.41	0	2,2,2	0.32	0
4	W8O	A	603	-	29,29,29	0.36	0	37,40,40	1.10	3 (8%)
5	EDO	A	604	-	3,3,3	0.40	0	2,2,2	0.29	0
5	EDO	B	604	-	3,3,3	0.39	0	2,2,2	0.46	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
4	W8O	B	603	-	-	1/16/28/28	0/3/3/3
5	EDO	B	605	-	-	0/1/1/1	-
4	W8O	A	603	-	-	2/16/28/28	0/3/3/3
5	EDO	A	604	-	-	0/1/1/1	-
5	EDO	B	604	-	-	0/1/1/1	-

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	603	W8O	C6-O1-C8	3.53	109.02	105.96
4	A	603	W8O	C6-O1-C8	2.99	108.56	105.96
4	B	603	W8O	C5-C7-C8	2.79	103.19	101.41
4	A	603	W8O	C5-C7-C8	2.37	102.93	101.41
4	A	603	W8O	C2-C1-C6	-2.35	117.61	120.22
4	B	603	W8O	C2-C1-C6	-2.34	117.62	120.22

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	603	W8O	C3-C12-C13-C14
4	A	603	W8O	O3-C11-C7-C8
4	A	603	W8O	C13-C12-C3-C4

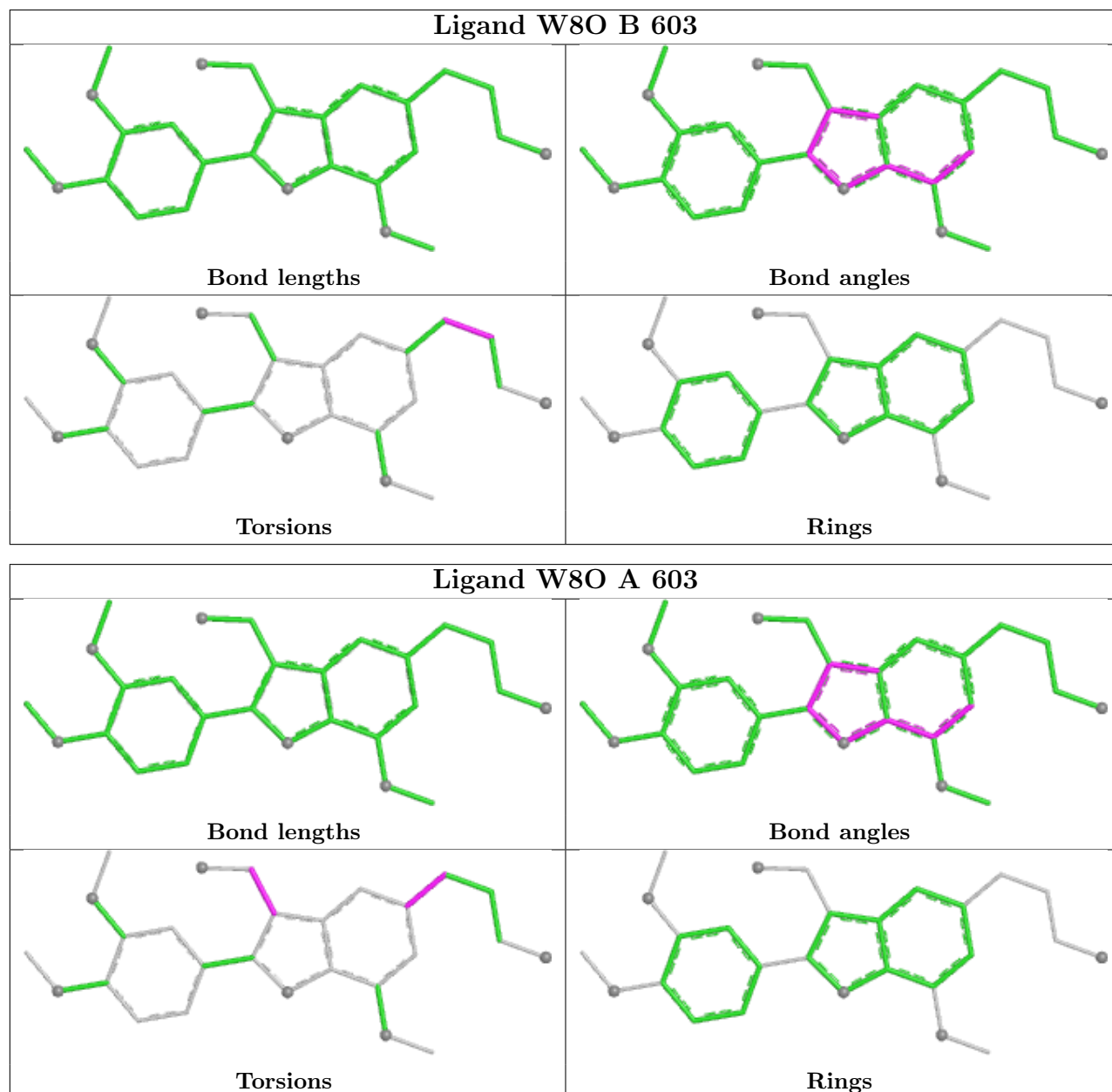
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	603	W8O	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and

any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	324/349 (92%)	0.24	13 (4%) 42 50	17, 30, 50, 62	0
1	B	324/349 (92%)	1.12	71 (21%) 2 3	20, 46, 73, 92	0
All	All	648/698 (92%)	0.68	84 (12%) 7 9	17, 37, 67, 92	0

All (84) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	183	ALA	5.8
1	B	112	LEU	5.4
1	B	184	VAL	5.0
1	B	90	ASP	5.0
1	A	411	PRO	4.7
1	B	88	GLN	4.3
1	B	297	VAL	4.1
1	B	99	VAL	4.0
1	B	91	VAL	3.9
1	B	94	LYS	3.5
1	B	363	ALA	3.5
1	B	179	PRO	3.5
1	B	182	GLU	3.4
1	B	390	PRO	3.4
1	B	298	LEU	3.4
1	B	294	SER	3.3
1	B	181	LEU	3.3
1	B	135	PHE	3.3
1	B	292	VAL	3.3
1	B	93	ALA	3.3
1	B	295	SER	3.2
1	B	96	LEU	3.1
1	B	137	ILE	3.0
1	B	385	ALA	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	289	THR	3.0
1	B	89	GLU	2.9
1	B	176	LEU	2.9
1	B	303	TYR	2.8
1	B	185	PHE	2.8
1	B	300	LEU	2.8
1	B	132	LEU	2.8
1	B	178	THR	2.8
1	B	104	LEU	2.7
1	B	299	LEU	2.7
1	A	356	PRO	2.7
1	B	388	VAL	2.7
1	B	296	GLY	2.7
1	A	362	ASN	2.6
1	B	124	THR	2.6
1	B	140	ASP	2.6
1	B	174	VAL	2.6
1	B	387	LEU	2.5
1	B	133	LYS	2.5
1	B	395	ILE	2.5
1	B	302	ASN	2.4
1	B	362	ASN	2.4
1	B	286	MET	2.4
1	B	411	PRO	2.4
1	A	295	SER	2.4
1	B	102	TRP	2.4
1	B	180	ALA	2.4
1	B	186	THR	2.4
1	B	113	SER	2.4
1	B	393	GLN	2.4
1	B	147	MET	2.4
1	A	296	GLY	2.3
1	B	396	LEU	2.3
1	B	121	ILE	2.3
1	A	91	VAL	2.3
1	B	394	ASP	2.3
1	B	139	VAL	2.3
1	A	147	MET	2.2
1	A	88	GLN	2.2
1	A	294	SER	2.2
1	B	254	LYS	2.2
1	B	191	LEU	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	123	HIS	2.2
1	A	351	GLY	2.1
1	B	136	LYS	2.1
1	B	190	ILE	2.1
1	B	287	VAL	2.1
1	B	138	PRO	2.1
1	B	143	ILE	2.1
1	B	120	VAL	2.1
1	B	397	ASP	2.1
1	B	92	LEU	2.1
1	B	389	HIS	2.1
1	B	375	TYR	2.1
1	A	363	ALA	2.0
1	B	101	LYS	2.0
1	B	356	PRO	2.0
1	B	107	PHE	2.0
1	A	301	ASP	2.0
1	A	364	SER	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
4	W8O	A	603	27/27	0.84	0.17	25,38,61,66	0
5	EDO	A	604	4/4	0.85	0.23	57,58,58,59	0
4	W8O	B	603	27/27	0.87	0.14	27,42,60,65	0
5	EDO	B	604	4/4	0.88	0.26	56,62,67,72	0
5	EDO	B	605	4/4	0.90	0.25	62,64,67,71	0

Continued on next page...

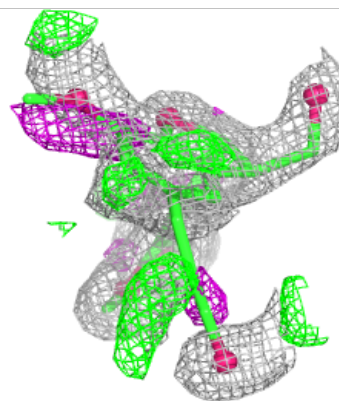
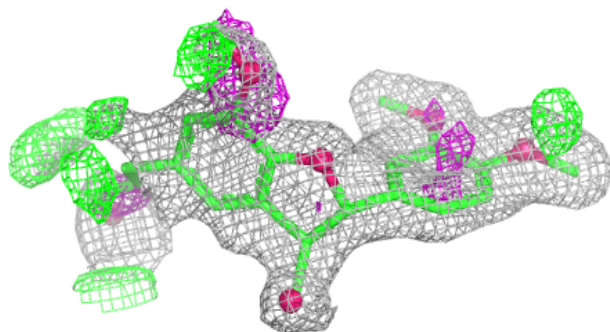
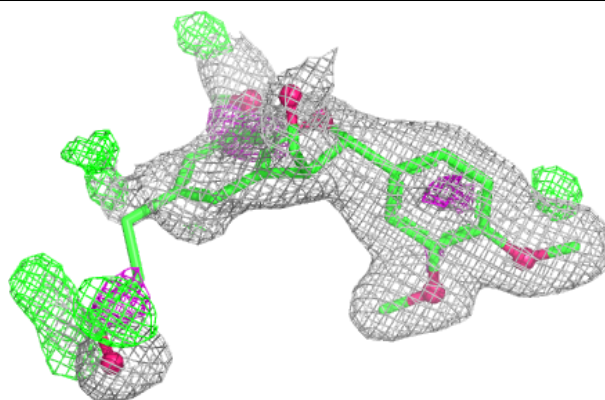
Continued from previous page...

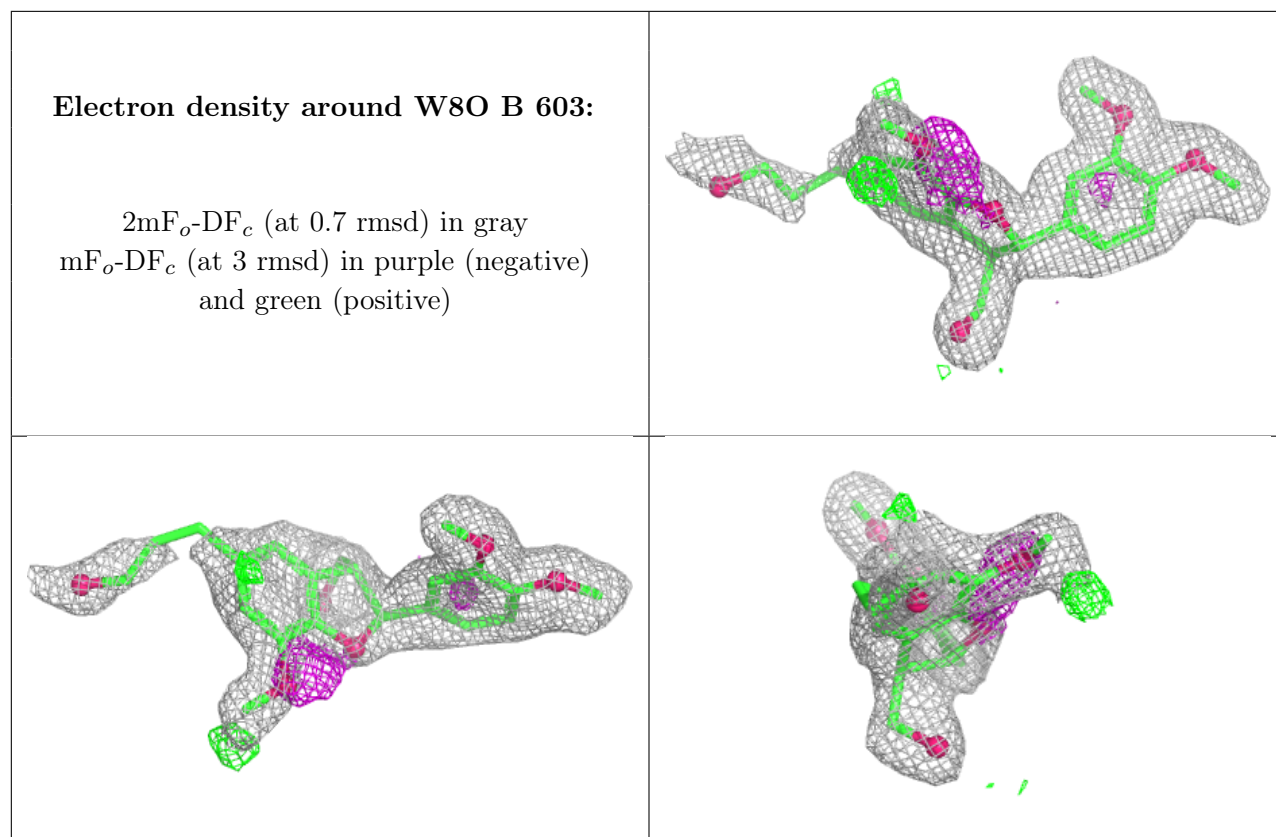
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	ZN	B	602	1/1	0.98	0.06	26,26,26,26	0
2	MG	A	601	1/1	0.99	0.02	18,18,18,18	0
2	MG	B	601	1/1	0.99	0.02	21,21,21,21	0
3	ZN	A	602	1/1	0.99	0.02	21,21,21,21	0

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 W8O 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.