



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 08:15 AM UTC

PDB ID : 3I8V / pdb_00003i8v
Title : Crystal structure of human PDE4a with 4-(3-butoxy-4-methoxyphenyl)methyl-2-imidazolidone
Authors : Cheng, R.K.Y.; Crawley, L.; Barker, J.; Wood, M.; Felicetti, B.; Whittaker, M.
Deposited on : 2009-07-10
Resolution : 2.25 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

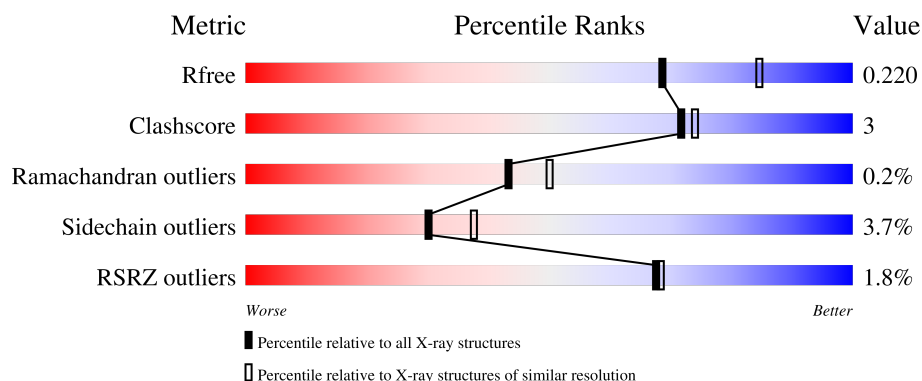
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

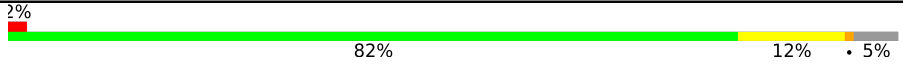
The reported resolution of this entry is 2.25 Å.

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	1898 (2.26-2.26)
Clashscore	190562	2005 (2.26-2.26)
Ramachandran outliers	187476	1965 (2.26-2.26)
Sidechain outliers	187428	1966 (2.26-2.26)
RSRZ outliers	180081	1898 (2.26-2.26)

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	354	
1	B	354	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5833 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 4A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	335	Total	C	N	O	S	0	0	0
			2708	1712	460	515	21			
1	B	334	Total	C	N	O	S	0	2	0
			2713	1718	457	517	21			

There are 42 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	269	MET	-	expression tag	UNP P27815
A	270	GLY	-	expression tag	UNP P27815
A	271	SER	-	expression tag	UNP P27815
A	272	SER	-	expression tag	UNP P27815
A	273	HIS	-	expression tag	UNP P27815
A	274	HIS	-	expression tag	UNP P27815
A	275	HIS	-	expression tag	UNP P27815
A	276	HIS	-	expression tag	UNP P27815
A	277	HIS	-	expression tag	UNP P27815
A	278	HIS	-	expression tag	UNP P27815
A	279	SER	-	expression tag	UNP P27815
A	280	SER	-	expression tag	UNP P27815
A	281	GLY	-	expression tag	UNP P27815
A	282	LEU	-	expression tag	UNP P27815
A	283	VAL	-	expression tag	UNP P27815
A	284	PRO	-	expression tag	UNP P27815
A	285	ARG	-	expression tag	UNP P27815
A	286	GLY	-	expression tag	UNP P27815
A	287	SER	-	expression tag	UNP P27815
A	288	HIS	-	expression tag	UNP P27815
A	289	MET	-	expression tag	UNP P27815
B	269	MET	-	expression tag	UNP P27815
B	270	GLY	-	expression tag	UNP P27815
B	271	SER	-	expression tag	UNP P27815
B	272	SER	-	expression tag	UNP P27815

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Chain	Residue	Modelled	Actual	Comment	Reference
B	273	HIS	-	expression tag	UNP P27815
B	274	HIS	-	expression tag	UNP P27815
B	275	HIS	-	expression tag	UNP P27815
B	276	HIS	-	expression tag	UNP P27815
B	277	HIS	-	expression tag	UNP P27815
B	278	HIS	-	expression tag	UNP P27815
B	279	SER	-	expression tag	UNP P27815
B	280	SER	-	expression tag	UNP P27815
B	281	GLY	-	expression tag	UNP P27815
B	282	LEU	-	expression tag	UNP P27815
B	283	VAL	-	expression tag	UNP P27815
B	284	PRO	-	expression tag	UNP P27815
B	285	ARG	-	expression tag	UNP P27815
B	286	GLY	-	expression tag	UNP P27815
B	287	SER	-	expression tag	UNP P27815
B	288	HIS	-	expression tag	UNP P27815
B	289	MET	-	expression tag	UNP P27815

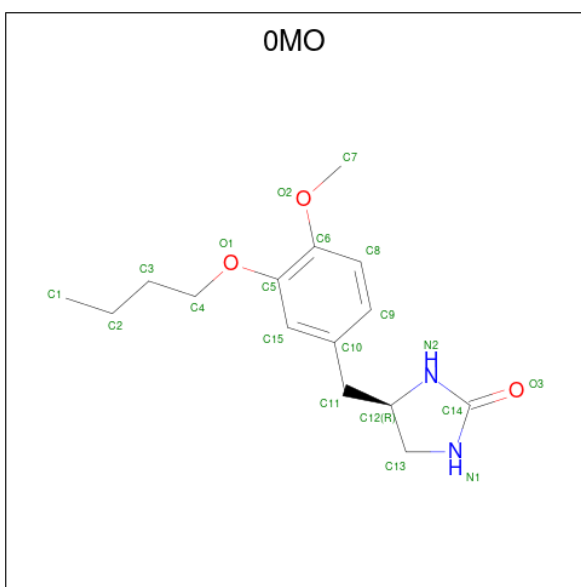
- Molecule 2 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

- 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 (4R)-4-(3-butoxy-4-methoxybenzyl)imidazolidin-2-one (CCD ID: 0MO) (formula: C₁₅H₂₂N₂O₃).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			20	15	2	3		
4	B	1	Total	C	N	O	0	0
			20	15	2	3		

- Molecule 5 is GLYCEROL (CCD ID: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			6	3	3		
5	B	1	Total	C	O	0	0
			6	3	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 6 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Co	0	0
			1	1		

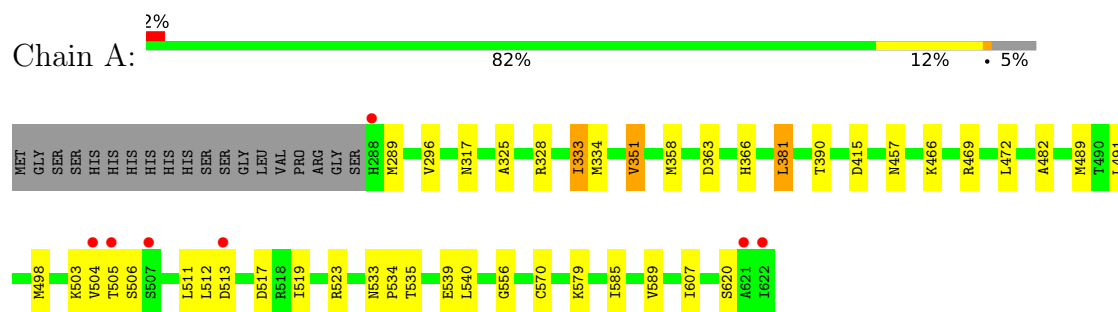
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	172	Total	O	0	0
			172	172		
7	B	177	Total	O	0	0
			177	177		

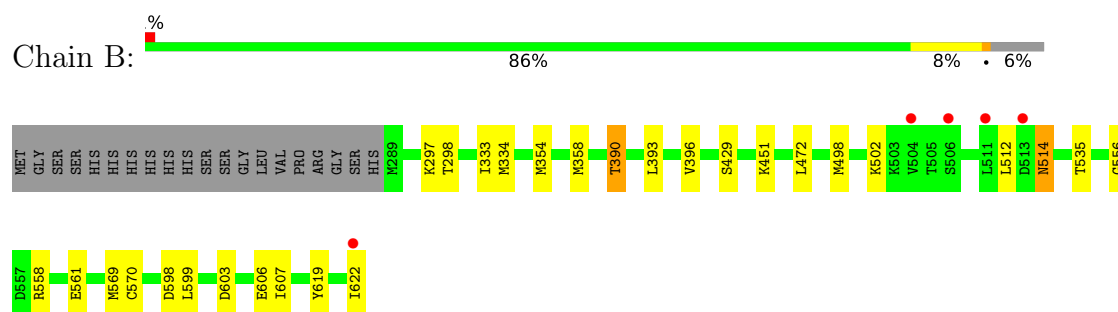
3 Residue-property plots [i](#)

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 4A



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.41Å 105.41Å 165.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.33 – 2.25 45.33 – 2.25	Depositor EDS
% Data completeness (in resolution range)	99.9 (45.33-2.25) 99.9 (45.33-2.25)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.56 (at 2.24Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.187 , 0.222 0.185 , 0.220	Depositor DCC
R_{free} test set	2262 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	38.3	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 27.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5833	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 3.30% 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: GOL, MG, ZN, CO, CSS, OMO

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	0.66	0/2756	0.85	1/3736 (0.0%)
1	B	0.65	0/2767	0.85	1/3751 (0.0%)
All	All	0.66	0/5523	0.85	2/7487 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	603	ASP	N-CA-C	5.15	117.63	111.71
1	A	351	VAL	CB-CA-C	-5.04	105.53	111.97

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	2708	0	2648	21	0
1	B	2713	0	2656	17	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	20	0	22	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	20	0	22	0	0
5	A	6	0	8	3	0
5	B	12	0	16	0	0
6	A	1	0	0	0	0
7	A	172	0	0	3	0
7	B	177	0	0	1	0
All	All	5833	0	5372	36	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 (36) 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:415:ASP:OD1	5:A:3:GOL:H2	1.76	0.84
1:B:498:MET:HE1	1:B:599:LEU:CD1	2.29	0.63
1:A:366:HIS:HE1	5:A:3:GOL:H32	1.71	0.56
1:B:334:MET:HB3	1:B:358:MET:SD	2.47	0.55
1:B:396:VAL:HG11	1:B:512:LEU:HD12	1.87	0.55
1:B:498:MET:HE1	1:B:599:LEU:HD11	1.89	0.55
1:A:539:GLU:HB2	7:A:83:HOH:O	2.09	0.51
1:B:535:THR:HB	1:B:607:ILE:HG23	1.93	0.50
1:A:519:ILE:O	1:A:523:ARG:HG3	2.11	0.49
1:A:334:MET:HB3	1:A:358:MET:SD	2.52	0.49
1:A:457:ASN:ND2	7:A:16:HOH:O	2.38	0.48
1:B:498:MET:HE1	1:B:599:LEU:HD13	1.94	0.47
1:B:514:ASN:HD22	1:B:514:ASN:N	2.12	0.47
1:A:535:THR:HB	1:A:607:ILE:HG23	1.97	0.46
1:A:556:GLY:HA3	1:A:570:CYS:O	2.15	0.46
1:B:619:TYR:HA	1:B:622:ILE:HD12	1.98	0.46
1:B:297:LYS:HG3	1:B:298:THR:N	2.31	0.46
1:A:585:ILE:HA	1:A:589:VAL:HB	1.99	0.45
7:A:652:HOH:O	1:B:429:SER:HB2	2.16	0.45
1:B:390:THR:HG22	1:B:393:LEU:HD12	2.00	0.43
1:A:498:MET:HB3	1:A:498:MET:HE2	1.69	0.43
1:A:415:ASP:CG	5:A:3:GOL:H2	2.42	0.43
1:B:514:ASN:N	1:B:514:ASN:ND2	2.67	0.43
1:A:296:VAL:HG21	1:A:325:ALA:HB1	2.01	0.42
1:A:505:THR:CG2	1:A:511:LEU:HD12	2.49	0.42
1:A:505:THR:HG22	1:A:511:LEU:HD12	2.00	0.42
1:A:512:LEU:HD22	1:A:517:ASP:HB3	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:ASP:OD1	1:B:558:ARG:HD3	2.19	0.42
1:B:354:MET:HG3	1:B:358:MET:HE2	2.02	0.42
1:A:317:ASN:ND2	1:A:540:LEU:HD21	2.34	0.41
1:B:502:LYS:NZ	7:B:669:HOH:O	2.52	0.41
1:A:328:ARG:NH2	1:B:561:GLU:OE1	2.50	0.41
1:A:533:ASN:HB2	1:A:534:PRO:HD3	2.01	0.41
1:A:482:ALA:HB1	1:A:491:LEU:HD21	2.02	0.41
1:A:333:ILE:HG23	1:A:381:LEU:HD13	2.03	0.41
1:B:556:GLY:HA3	1:B:570:CYS:O	2.21	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	332/354 (94%)	328 (99%)	3 (1%)	1 (0%)	36	40
1	B	333/354 (94%)	328 (98%)	5 (2%)	0	100	100
All	All	665/708 (94%)	656 (99%)	8 (1%)	1 (0%)	43	50

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	506	SER

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	300/316 (95%)	286 (95%)	14 (5%)	23	26
1	B	301/316 (95%)	293 (97%)	8 (3%)	39	49
All	All	601/632 (95%)	579 (96%)	22 (4%)	30	37

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	289	MET
1	A	333	ILE
1	A	351	VAL
1	A	381	LEU
1	A	390	THR
1	A	466	LYS
1	A	469	ARG
1	A	472	LEU
1	A	489	MET
1	A	503	LYS
1	A	504	VAL
1	A	513	ASP
1	A	579	LYS
1	A	620	SER
1	B	333	ILE
1	B	390	THR
1	B	451	LYS
1	B	472	LEU
1	B	514	ASN
1	B	569	MET
1	B	598	ASP
1	B	606	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	288	HIS
1	A	290	ASN
1	A	422	GLN
1	A	457	ASN
1	A	462	GLN
1	A	514	ASN

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Mol	Chain	Res	Type
1	A	524	ASN
1	A	533	ASN
1	B	290	ASN
1	B	310	ASN
1	B	366	HIS
1	B	457	ASN
1	B	462	GLN
1	B	524	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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	CSS	A	320	1	4,6,7	0.80	0	2,6,8	0.55	0
1	CSS	B	320	1	4,6,7	0.92	0	2,6,8	0.79	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
1	CSS	A	320	1	-	0/1/5/7	-
1	CSS	B	320	1	-	0/1/5/7	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

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](#)

Of 10 ligands modelled in this entry, 5 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	0MO	B	2	-	20,21,21	1.09	1 (5%)	25,27,27	2.53	8 (32%)
5	GOL	A	3	-	5,5,5	0.35	0	5,5,5	0.31	0
5	GOL	B	625	-	5,5,5	0.33	0	5,5,5	0.34	0
4	0MO	A	1	-	20,21,21	1.24	3 (15%)	25,27,27	3.35	7 (28%)
5	GOL	B	624	-	5,5,5	0.27	0	5,5,5	1.00	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	0MO	B	2	-	-	2/11/20/20	0/2/2/2
5	GOL	A	3	-	-	2/4/4/4	-
5	GOL	B	625	-	-	0/4/4/4	-
4	0MO	A	1	-	-	3/11/20/20	0/2/2/2
5	GOL	B	624	-	-	2/4/4/4	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1	0MO	C6-C5	4.03	1.49	1.40
4	B	2	0MO	C6-C5	3.92	1.48	1.40
4	A	1	0MO	C12-N2	-2.43	1.43	1.46
4	A	1	0MO	C11-C12	-2.16	1.49	1.53

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1	0MO	C11-C12-N2	-14.67	97.97	112.95
4	B	2	0MO	C11-C12-N2	-9.46	103.29	112.95
4	B	2	0MO	C7-O2-C6	3.46	122.58	117.51
4	B	2	0MO	C11-C10-C15	-3.42	114.55	120.43
4	B	2	0MO	O1-C5-C6	3.33	122.63	115.75
4	A	1	0MO	O1-C5-C6	3.26	122.48	115.75
4	B	2	0MO	C13-C12-C11	-3.12	109.04	113.74
4	A	1	0MO	C7-O2-C6	3.11	122.08	117.51
4	A	1	0MO	O2-C6-C5	2.96	119.42	115.40
4	A	1	0MO	C11-C10-C15	-2.68	115.83	120.43
4	A	1	0MO	O3-C14-N2	-2.58	122.19	125.89
4	A	1	0MO	C9-C10-C15	2.21	121.60	118.55
4	B	2	0MO	O1-C5-C15	-2.16	118.83	123.49
4	B	2	0MO	O2-C6-C5	2.11	118.26	115.40
4	B	2	0MO	C9-C10-C15	2.01	121.32	118.55

There are no chirality outliers.

All (9) torsion outliers are listed below:

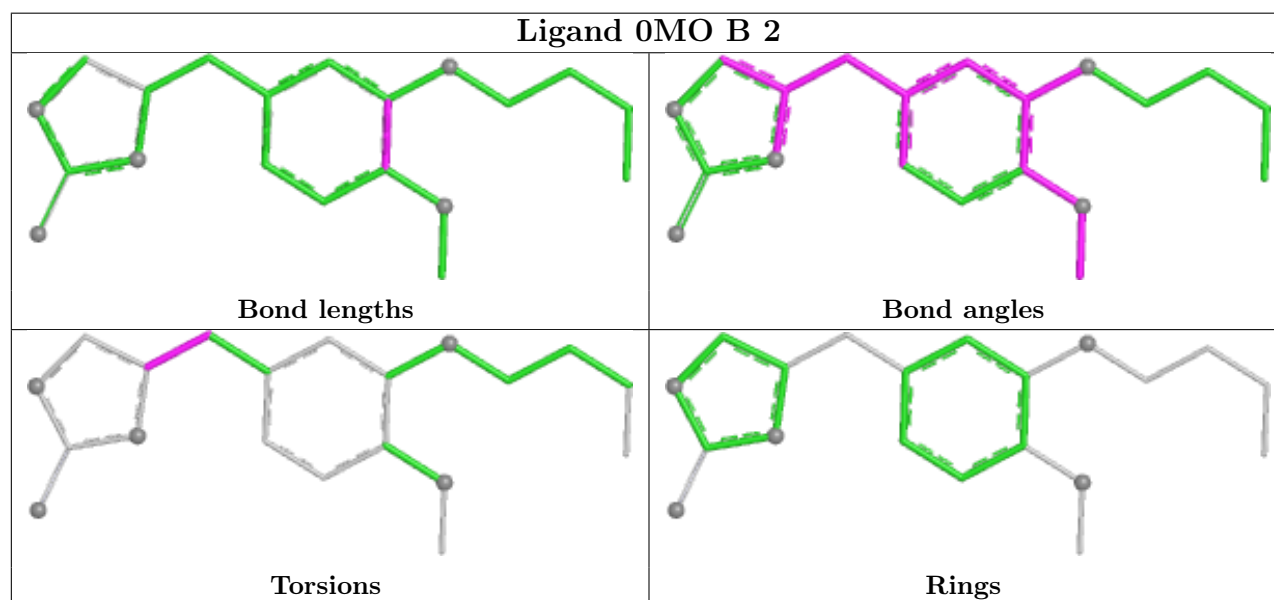
Mol	Chain	Res	Type	Atoms
4	A	1	0MO	C10-C11-C12-N2
4	A	1	0MO	C10-C11-C12-C13
4	B	2	0MO	C10-C11-C12-N2
4	B	2	0MO	C10-C11-C12-C13
5	B	624	GOL	O1-C1-C2-O2
5	B	624	GOL	O1-C1-C2-C3
5	A	3	GOL	C1-C2-C3-O3
5	A	3	GOL	O2-C2-C3-O3
4	A	1	0MO	C1-C2-C3-C4

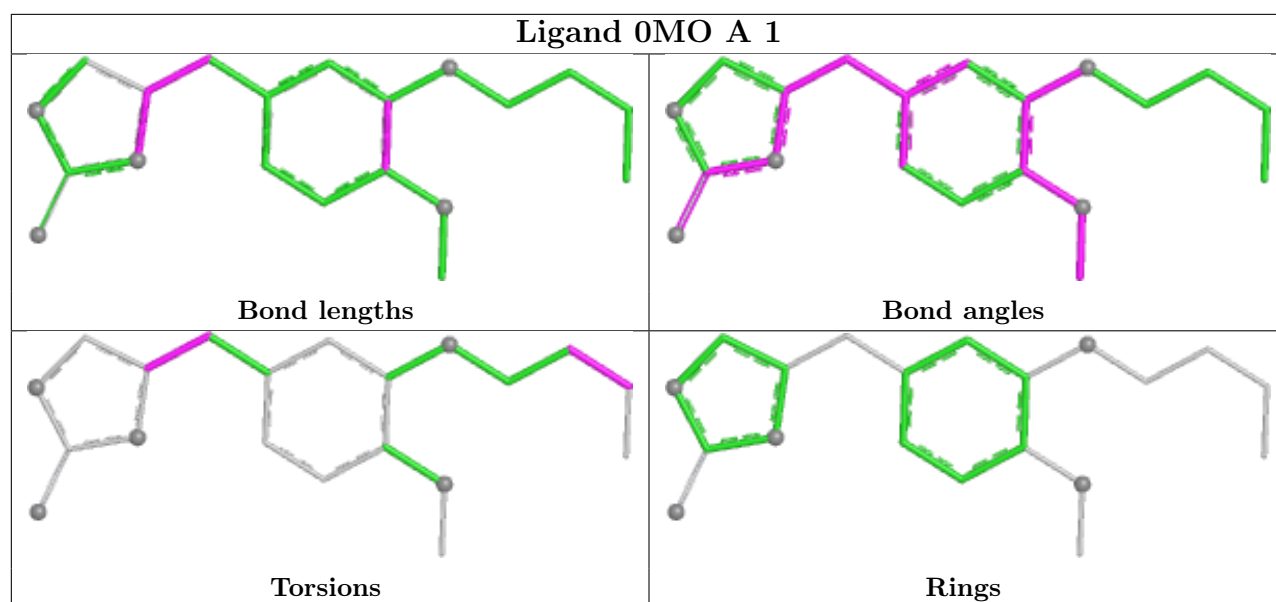
There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	3	GOL	3	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	334/354 (94%)	-0.09	7 (2%) 63 64	25, 35, 59, 75	0
1	B	333/354 (94%)	-0.14	5 (1%) 72 73	17, 36, 56, 70	2 (0%)
All	All	667/708 (94%)	-0.11	12 (1%) 67 68	17, 36, 58, 75	2 (0%)

All (12) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	507	SER	3.1
1	B	506	SER	2.8
1	B	622	ILE	2.8
1	A	513	ASP	2.5
1	A	504	VAL	2.2
1	A	621	ALA	2.1
1	B	504	VAL	2.1
1	B	511	LEU	2.1
1	A	288	HIS	2.1
1	A	505	THR	2.1
1	A	622	ILE	2.1
1	B	513	ASP	2.1

6.2 Non-standard residues in protein, DNA, RNA chains

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	CSS	B	320	7/8	0.94	0.07	39,41,47,55	0
1	CSS	A	320	7/8	0.95	0.07	36,38,42,51	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

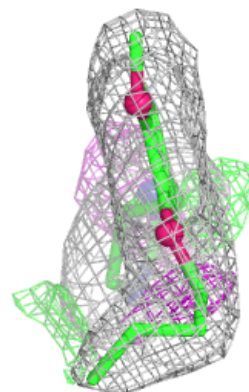
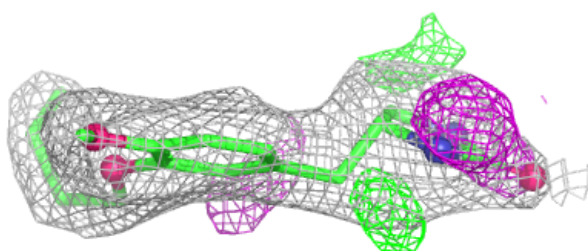
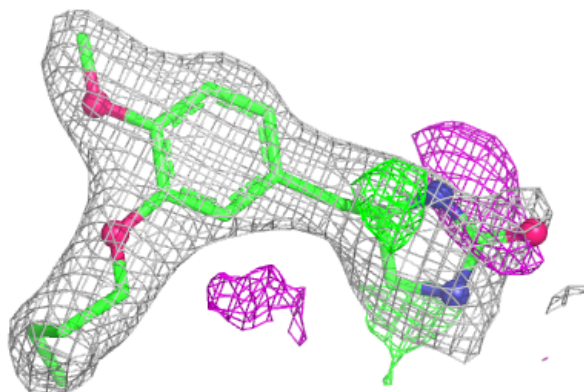
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	GOL	A	3	6/6	0.79	0.18	69,71,71,72	0
5	GOL	B	624	6/6	0.81	0.17	50,52,52,52	0
6	CO	A	624	1/1	0.85	0.13	110,110,110,110	0
5	GOL	B	625	6/6	0.86	0.19	77,78,79,79	0
4	OMO	A	1	20/20	0.87	0.14	37,43,54,55	0
4	OMO	B	2	20/20	0.91	0.12	38,42,55,56	0
3	MG	A	623	1/1	1.00	0.03	26,26,26,26	0
3	MG	B	623	1/1	1.00	0.01	24,24,24,24	0
2	ZN	A	2	1/1	1.00	0.02	31,31,31,31	0
2	ZN	B	1	1/1	1.00	0.01	33,33,33,33	0

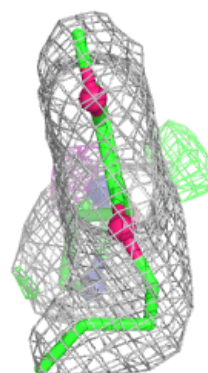
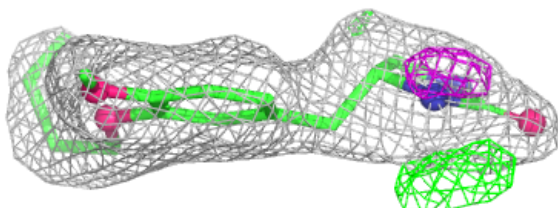
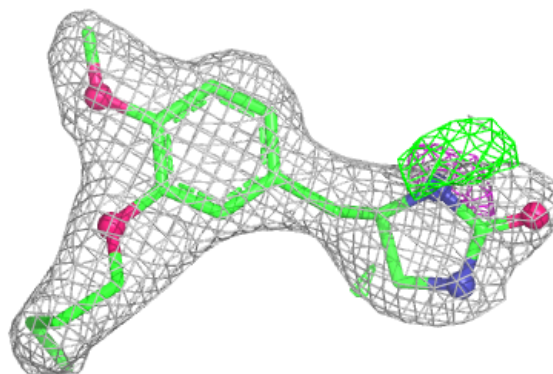
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around 0MO A 1:

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

**Electron density around 0MO B 2:**

$2mF_o-DF_c$ (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.