



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:42 PM UTC

PDB ID : 5XR8 / pdb_00005xr8
Title : Crystal structure of the human CB1 in complex with agonist AM841
Authors : Hua, T.; Vemuri, K.; Nikas, P.S.; Laprairie, R.B.; Wu, Y.; Qu, L.; Pu, M.; Korde, A.; Shan, J.; Ho, J.H.; Han, G.W.; Ding, K.; Li, X.; Liu, H.; Hanson, M.A.; Zhao, S.; Bohn, L.M.; Makriyannis, A.; Stevens, R.C.; Liu, Z.J.
Deposited on : 2017-06-07
Resolution : 2.95 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

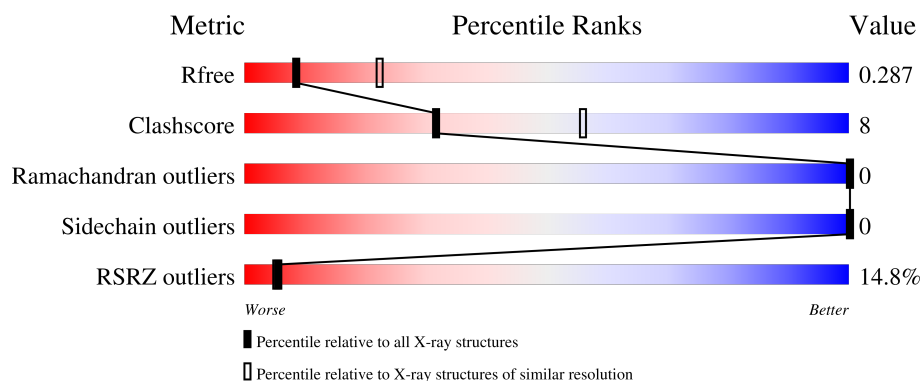
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	1130 (2.98-2.94)
Clashscore	190562	1157 (2.98-2.94)
Ramachandran outliers	187476	1101 (2.98-2.94)
Sidechain outliers	187428	1101 (2.98-2.94)
RSRZ outliers	180081	1130 (2.98-2.94)

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	438	15% 86% 11% ..

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 3410 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.

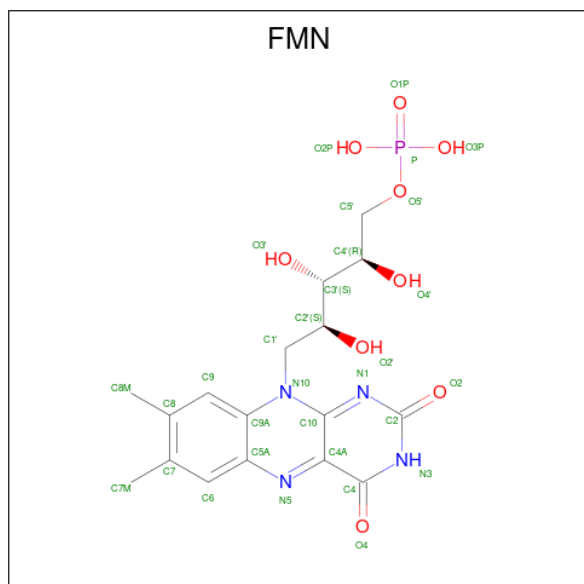
- Molecule 1 is a protein called Cannabinoid receptor 1,Flavodoxin,Cannabinoid receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3314	2163	535	594	22			

There are 6 discrepancies between the modelled and reference sequences:

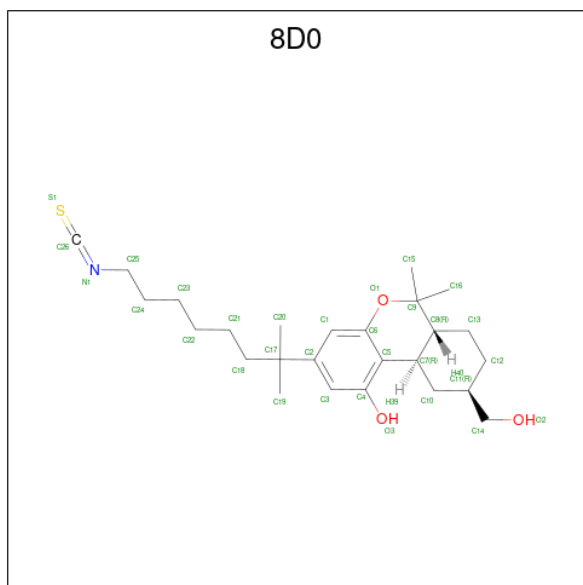
Chain	Residue	Modelled	Actual	Comment	Reference
A	210	ALA	THR	engineered mutation	UNP P21554
A	273	LYS	GLU	engineered mutation	UNP P21554
A	283	VAL	THR	engineered mutation	UNP P21554
A	307	ALA	-	linker	UNP P21554
A	403	TRP	TYR	engineered mutation	UNP P00323
A	462	GLU	ARG	engineered mutation	UNP P21554

- Molecule 2 is FLAVIN MONONUCLEOTIDE (CCD ID: FMN) (formula: $C_{17}H_{21}N_4O_9P$).



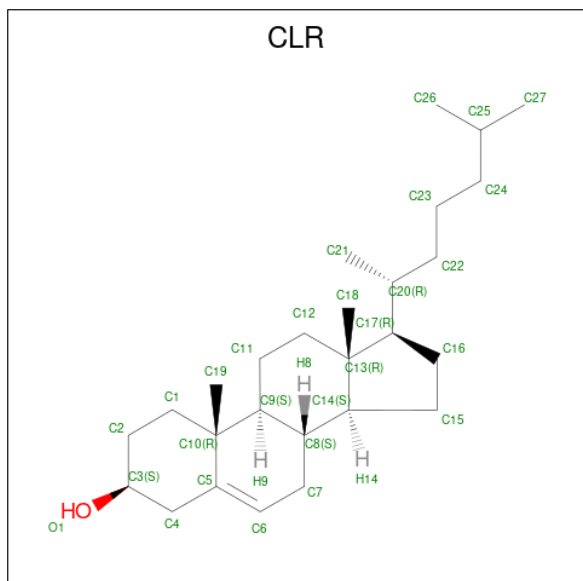
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is (6 {a} {R},9 {R},10 {a} {R})-9-(hydroxymethyl)-3-(8-isothiocyanato-2-methyl-octan-2-yl)-6,6-dimethyl-6 {a},7,8,9,10,10 {a}-hexahydrobenzo[c]chromen-1-ol (CCD ID: 8D0) (formula: C₂₆H₃₉NO₃S).



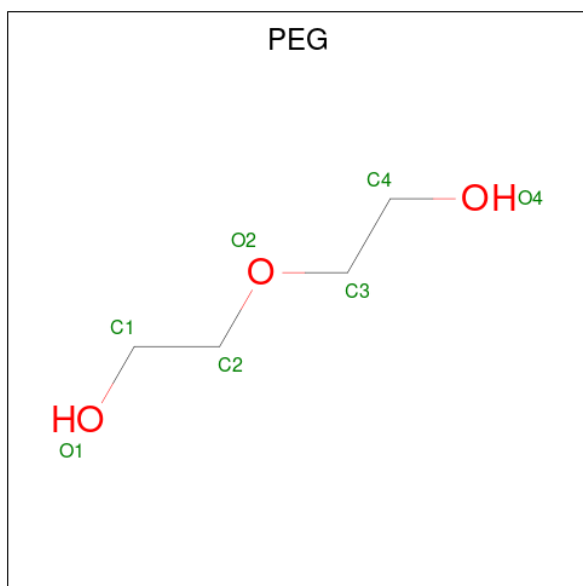
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			29	25	1	3		

- Molecule 4 is CHOLESTEROL (CCD ID: CLR) (formula: C₂₇H₄₆O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			28	27	1		

- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



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

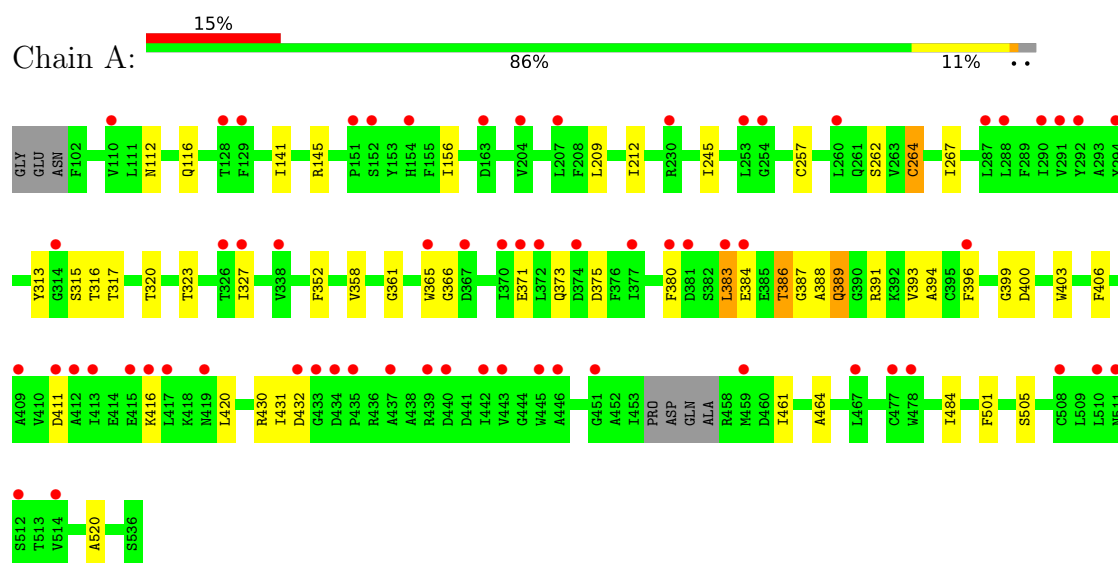
- Molecule 6 is water.

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

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: Cannabinoid receptor 1,Flavodoxin,Cannabinoid receptor 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2 ₁	Depositor
Cell constants a, b, c, α , β , γ	66.83Å 73.61Å 139.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.48 – 2.95 49.48 – 2.95	Depositor EDS
% Data completeness (in resolution range)	88.2 (49.48-2.95) 85.6 (49.48-2.95)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.64 (at 2.96Å)	Xtriage
Refinement program	PHENIX 1.10.1 _2155	Depositor
R, R_{free}	0.255 , 0.274 0.265 , 0.287	Depositor DCC
R_{free} test set	621 reflections (4.11%)	wwPDB-VP
Wilson B-factor (Å ²)	100.8	Xtriage
Anisotropy	0.163	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 79.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	3410	wwPDB-VP
Average B, all atoms (Å ²)	130.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.55% 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: CLR, PEG, 8D0, FMN

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	0.18	0/3389	0.38	4/4613 (0.1%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	264	CYS	N-CA-C	7.04	119.61	110.53
1	A	386	THR	N-CA-C	-5.83	102.79	110.43
1	A	389	GLN	N-CA-C	5.18	117.05	108.13
1	A	383	LEU	N-CA-C	5.12	116.86	111.28

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	3314	0	3298	55	0
2	A	31	0	19	3	0
3	A	29	0	0	1	0
4	A	28	0	46	1	0
5	A	7	0	10	0	0
6	A	1	0	0	0	0
All	All	3410	0	3373	55	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 8.

All (55) 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:257:CYS:SG	1:A:264:CYS:SG	1.34	1.16
1:A:257:CYS:CB	1:A:264:CYS:SG	2.36	1.14
1:A:383:LEU:HD12	1:A:416:LYS:HD3	1.67	0.77
1:A:257:CYS:SG	1:A:264:CYS:CB	2.75	0.72
1:A:484:ILE:HG21	1:A:501:PHE:HB2	1.73	0.71
1:A:388:ALA:HB1	1:A:420:LEU:HD12	1.72	0.70
1:A:387:GLY:HA3	1:A:391:ARG:HH21	1.57	0.70
1:A:380:PHE:O	1:A:383:LEU:HG	1.93	0.69
1:A:383:LEU:O	1:A:386:THR:N	2.27	0.67
1:A:388:ALA:O	1:A:389:GLN:HG3	1.95	0.65
1:A:388:ALA:HB1	1:A:420:LEU:CD1	2.25	0.65
1:A:352:PHE:O	1:A:391:ARG:NH1	2.30	0.64
1:A:383:LEU:HD12	1:A:416:LYS:CD	2.26	0.64
1:A:257:CYS:HB3	1:A:264:CYS:SG	2.36	0.63
1:A:383:LEU:O	1:A:386:THR:HB	1.99	0.61
1:A:406:PHE:HE1	1:A:432:ASP:HB3	1.67	0.59
1:A:366:GLY:N	2:A:1201:FMN:N5	2.52	0.57
1:A:406:PHE:CE1	1:A:432:ASP:HB3	2.40	0.57
1:A:388:ALA:O	1:A:389:GLN:CG	2.53	0.56
1:A:315:SER:HB3	1:A:320:THR:HB	1.87	0.56
1:A:112:ASN:O	1:A:116:GLN:N	2.37	0.55
1:A:387:GLY:HA3	1:A:391:ARG:HE	1.72	0.54
1:A:317:THR:HB	2:A:1201:FMN:O3P	2.11	0.51
1:A:388:ALA:C	1:A:389:GLN:HG3	2.36	0.51
1:A:156:ILE:HD11	1:A:520:ALA:HB2	1.92	0.51
1:A:432:ASP:OD1	1:A:432:ASP:N	2.44	0.50
1:A:313:TYR:HA	1:A:361:GLY:O	2.11	0.50
1:A:316:THR:HB	1:A:365:TRP:CZ2	2.47	0.50
1:A:400:ASP:HB3	1:A:403:TRP:HD1	1.77	0.49
1:A:501:PHE:O	1:A:505:SER:N	2.44	0.49
1:A:141:ILE:O	1:A:145:ARG:N	2.39	0.49
1:A:267:ILE:O	3:A:1202:8D0:O2	2.30	0.49
1:A:257:CYS:HA	1:A:262:SER:HB2	1.95	0.48
1:A:387:GLY:HA3	1:A:391:ARG:NH2	2.24	0.47
1:A:383:LEU:O	1:A:384:GLU:C	2.58	0.46
1:A:400:ASP:HB3	1:A:403:TRP:CD1	2.50	0.46
1:A:245:ILE:HD11	4:A:1203:CLR:H232	1.96	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:383:LEU:O	1:A:386:THR:CB	2.63	0.45
1:A:358:VAL:O	1:A:393:VAL:HG23	2.16	0.45
1:A:257:CYS:SG	1:A:264:CYS:CA	3.05	0.45
1:A:399:GLY:N	1:A:431:ILE:O	2.50	0.45
1:A:393:VAL:HG22	1:A:394:ALA:N	2.31	0.44
1:A:373:GLN:HG3	1:A:375:ASP:H	1.82	0.44
1:A:209:LEU:O	1:A:212:ILE:HG13	2.18	0.44
1:A:461:ILE:HA	1:A:464:ALA:HB3	1.99	0.43
1:A:323:THR:O	1:A:327:ILE:N	2.43	0.43
1:A:361:GLY:HA3	1:A:396:PHE:CE2	2.53	0.43
1:A:411:ASP:CG	1:A:430:ARG:HH22	2.27	0.42
1:A:393:VAL:CG2	1:A:394:ALA:N	2.82	0.41
1:A:352:PHE:C	1:A:391:ARG:NH1	2.78	0.41
1:A:361:GLY:HA2	1:A:396:PHE:O	2.20	0.41
1:A:365:TRP:O	1:A:371:GLU:HB2	2.21	0.41
1:A:316:THR:OG1	1:A:373:GLN:OE1	2.32	0.40
1:A:352:PHE:HB3	1:A:391:ARG:HD3	2.01	0.40
1:A:315:SER:HA	2:A:1201:FMN:O2P	2.21	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	427/438 (98%)	412 (96%)	15 (4%)	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	351/369 (95%)	351 (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. There are no such sidechains identified.

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 ⓘ

4 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	FMN	A	1201	-	33,33,33	0.17	0	48,50,50	0.33	0
5	PEG	A	1204	-	6,6,6	0.50	0	5,5,5	0.26	0
4	CLR	A	1203	-	31,31,31	0.66	1 (3%)	48,48,48	1.43	8 (16%)
3	8D0	A	1202	-	31,31,33	1.01	1 (3%)	45,46,48	0.94	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
2	FMN	A	1201	-	-	0/18/18/18	0/3/3/3
5	PEG	A	1204	-	-	1/4/4/4	-
4	CLR	A	1203	-	-	2/10/68/68	0/4/4/4
3	8D0	A	1202	-	-	9/16/44/46	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1203	CLR	C10-C9	-2.28	1.52	1.56
3	A	1202	8D0	O1-C9	-2.16	1.43	1.47

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1203	CLR	C19-C10-C9	-3.42	107.82	111.66
4	A	1203	CLR	C13-C17-C20	-2.87	115.06	119.50
4	A	1203	CLR	C14-C8-C9	-2.52	105.79	109.09
4	A	1203	CLR	C3-C4-C5	-2.43	108.18	112.05
4	A	1203	CLR	C13-C14-C8	-2.25	111.22	114.41
4	A	1203	CLR	C4-C5-C6	-2.10	117.72	120.57
4	A	1203	CLR	C18-C13-C14	-2.04	107.98	111.68
4	A	1203	CLR	C21-C20-C22	-2.01	107.23	110.34

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1202	8D0	C10-C11-C14-O2
4	A	1203	CLR	C20-C22-C23-C24
3	A	1202	8D0	C21-C22-C23-C24
3	A	1202	8D0	C12-C11-C14-O2
5	A	1204	PEG	C1-C2-O2-C3
3	A	1202	8D0	C19-C17-C2-C1
3	A	1202	8D0	C18-C17-C2-C1
3	A	1202	8D0	C20-C17-C2-C3
3	A	1202	8D0	C18-C17-C2-C3
4	A	1203	CLR	C22-C23-C24-C25

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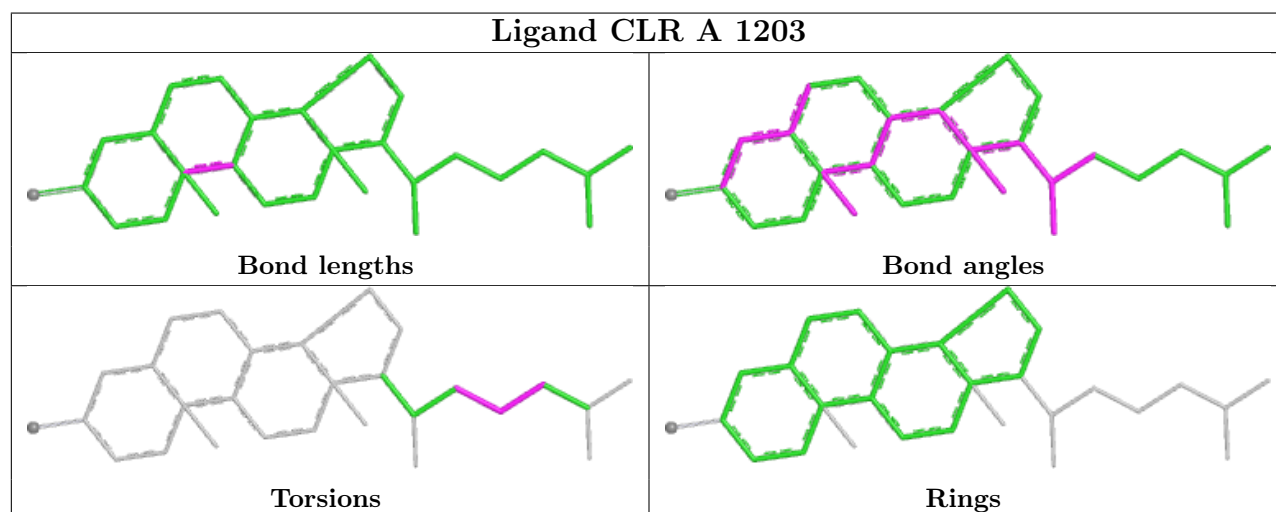
Mol	Chain	Res	Type	Atoms
3	A	1202	8D0	C19-C17-C2-C3
3	A	1202	8D0	C20-C17-C2-C1

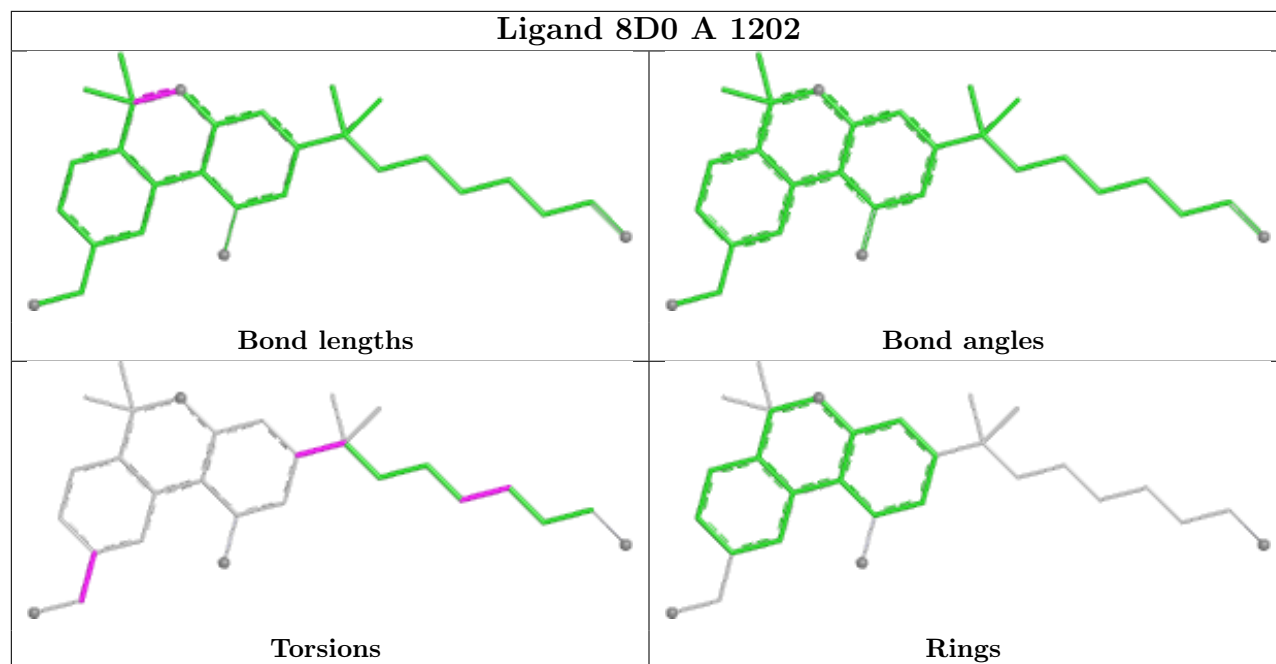
There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1201	FMN	3	0
4	A	1203	CLR	1	0
3	A	1202	8D0	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	431/438 (98%)	0.80	64 (14%) 5 5	80, 126, 184, 207	0

All (64) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	372	LEU	6.3
1	A	434	ASP	6.1
1	A	433	GLY	5.9
1	A	371	GLU	5.3
1	A	510	LEU	5.2
1	A	380	PHE	5.2
1	A	413	ILE	5.2
1	A	367	ASP	5.0
1	A	412	ALA	5.0
1	A	365	TRP	4.2
1	A	432	ASP	4.1
1	A	152	SER	4.1
1	A	478	TRP	4.0
1	A	377	ILE	3.7
1	A	260	LEU	3.4
1	A	451	GLY	3.3
1	A	439	ARG	3.3
1	A	294	TYR	3.2
1	A	508	CYS	3.2
1	A	204	VAL	3.1
1	A	154	HIS	3.0
1	A	253	LEU	3.0
1	A	287	LEU	2.9
1	A	384	GLU	2.9
1	A	163	ASP	2.9
1	A	440	ASP	2.9
1	A	442	ILE	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	290	ILE	2.8
1	A	417	LEU	2.8
1	A	511	ASN	2.8
1	A	151	PRO	2.8
1	A	129	PHE	2.7
1	A	381	ASP	2.7
1	A	370	ILE	2.7
1	A	409	ALA	2.6
1	A	288	LEU	2.6
1	A	374	ASP	2.6
1	A	446	ALA	2.6
1	A	396	PHE	2.6
1	A	512	SER	2.5
1	A	291	VAL	2.5
1	A	437	ALA	2.5
1	A	416	LYS	2.4
1	A	411	ASP	2.4
1	A	128	THR	2.4
1	A	207	LEU	2.4
1	A	419	ASN	2.4
1	A	477	CYS	2.4
1	A	110	VAL	2.4
1	A	230	ARG	2.4
1	A	445	TRP	2.4
1	A	514	VAL	2.3
1	A	292	TYR	2.3
1	A	326	THR	2.3
1	A	327	ILE	2.3
1	A	443	VAL	2.3
1	A	415	GLU	2.2
1	A	338	VAL	2.2
1	A	435	PRO	2.2
1	A	314	GLY	2.1
1	A	383	LEU	2.1
1	A	467	LEU	2.1
1	A	459	MET	2.0
1	A	254	GLY	2.0

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

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

6.3 Carbohydrates [i](#)

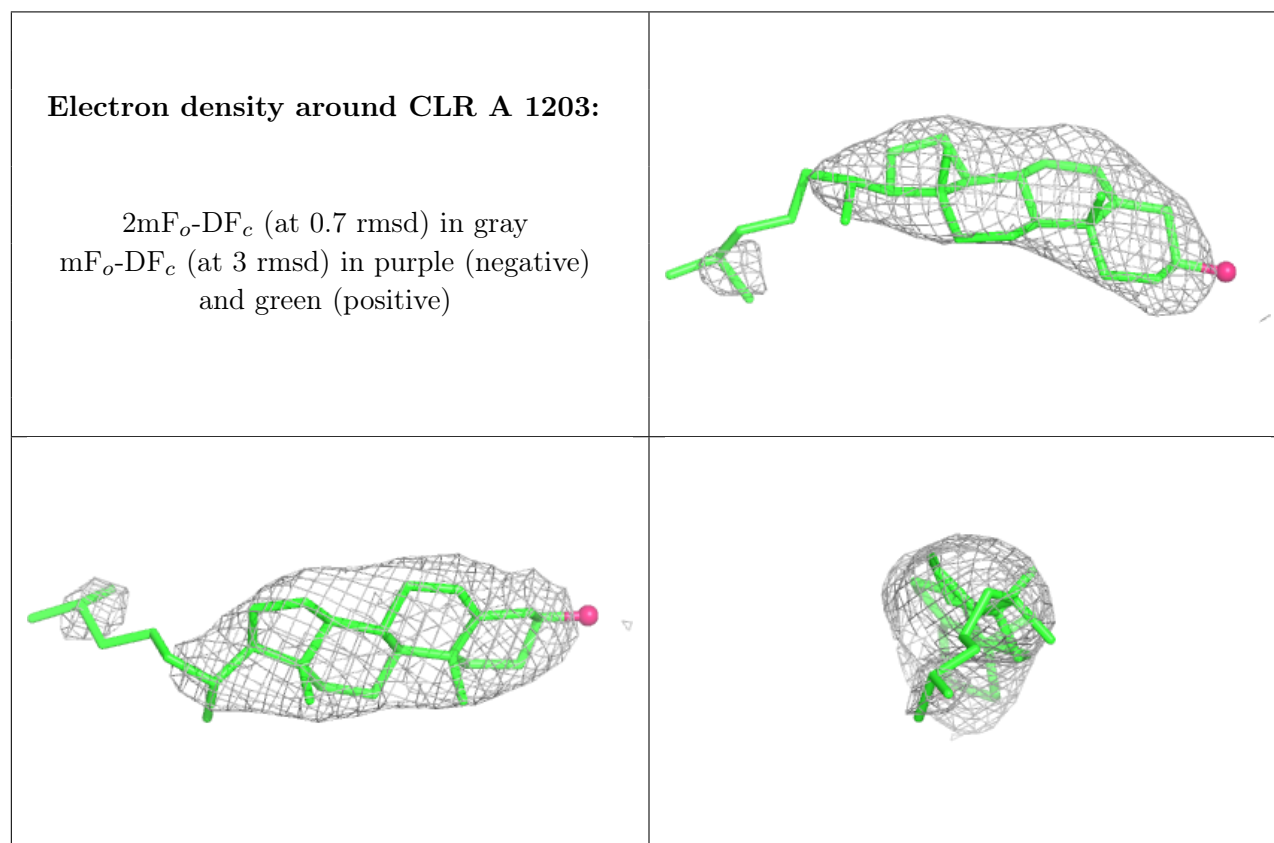
There are no oligosaccharides in this entry.

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.

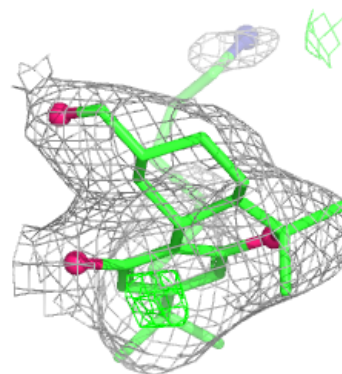
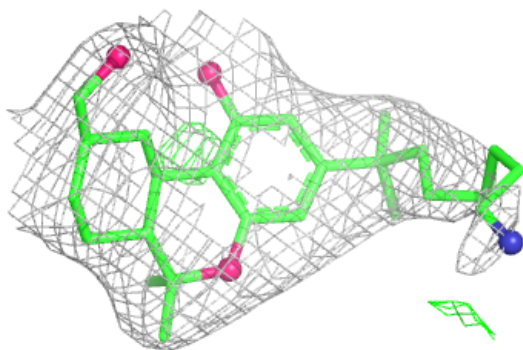
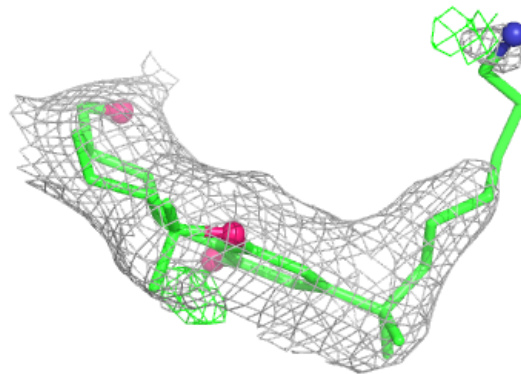
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	PEG	A	1204	7/7	0.83	0.15	84,109,114,116	0
2	FMN	A	1201	31/31	0.93	0.08	98,104,123,126	0
4	CLR	A	1203	28/28	0.94	0.14	91,103,110,116	0
3	8D0	A	1202	29/31	0.94	0.12	79,92,102,105	0

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 8D0 A 1202:

$2mF_o - DF_c$ (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.