



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 10, 2017 – 09:28 PM EDT

PDB ID : 5XRA
Title : Crystal structure of the human CB1 in complex with agonist AM11542
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 : unknown
Resolution : 2.80 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

<http://wwpdb.org/validation/2016/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20030345
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20030345

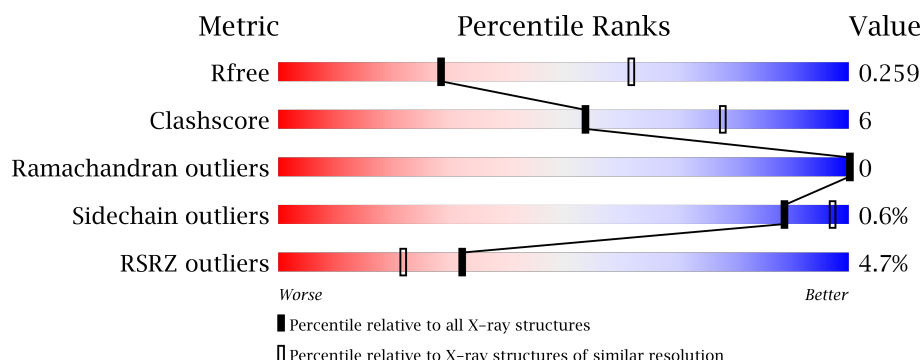
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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}	100719	2583 (2.80-2.80)
Clashscore	112137	3033 (2.80-2.80)
Ramachandran outliers	110173	2983 (2.80-2.80)
Sidechain outliers	110143	2985 (2.80-2.80)
RSRZ outliers	101464	2610 (2.80-2.80)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	<div> <div>5%</div> <div>87%</div> <div>11%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	OLA	A	604	-	-	-	X
5	OLC	A	605	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	OLC	A	606	-	-	-	X
7	CLR	A	608	-	-	-	X

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 3461 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.

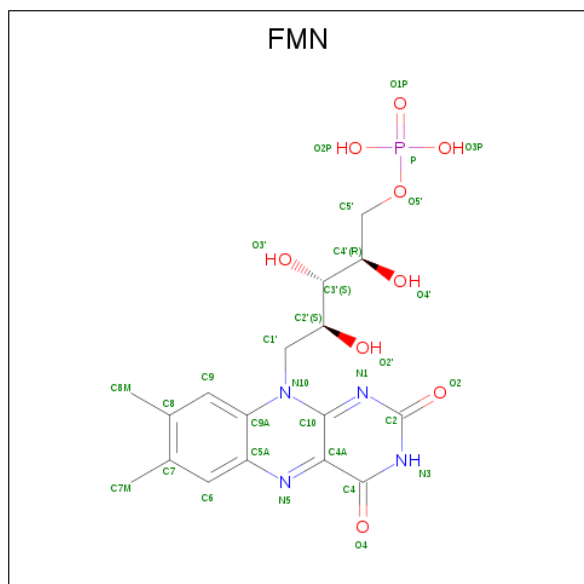
- Molecule 1 is a protein called Cannabinoid receptor 1,Flavodoxin,Cannabinoid receptor 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	428	Total	C	N	O	S	0	0	0
			3311	2162	535	593	21			

There are 6 discrepancies between the modelled and reference sequences:

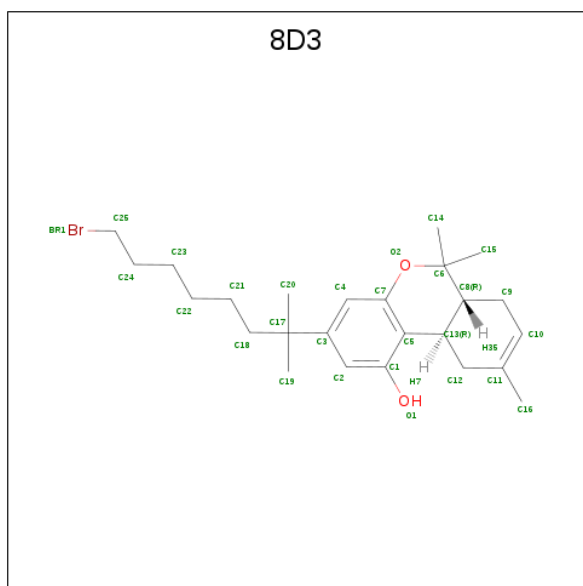
Chain	Residue	Modelled	Actual	Comment	Reference
A	210	ALA	THR	engineered mutation	UNP P21554
A	273	LYS	GLU	engineered mutation	UNP P21554
A	283	VAL	THR	engineered mutation	UNP P21554
A	1002	ALA	-	linker	UNP P21554
A	1098	TRP	TYR	engineered mutation	UNP P00323
A	340	GLU	ARG	engineered mutation	UNP P21554

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



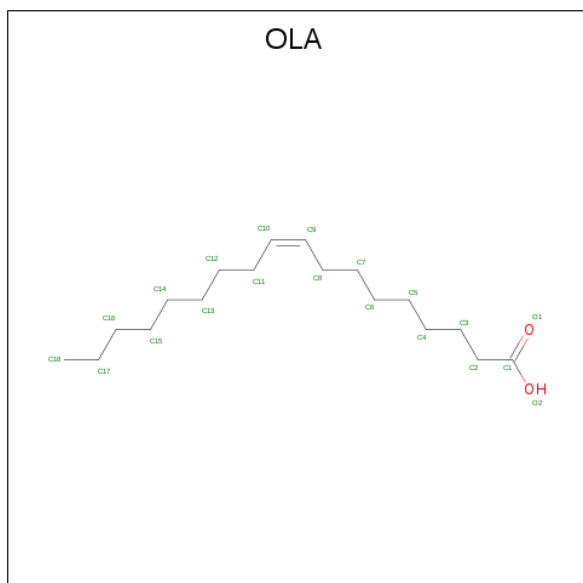
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	17	4	9	1		

- Molecule 3 is (6aR,10aR)-3-(8-bromanyl-2-methyl-octan-2-yl)-6,6,9-trimethyl-6a,7,10,10a-tetrahydrobenzo[c]chromen-1-ol (three-letter code: 8D3) (formula: C₂₅H₃₇BrO₂).



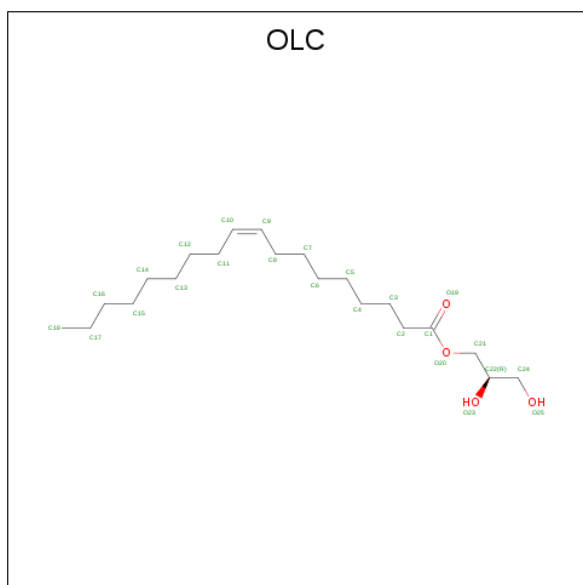
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	Br	C	O	0	0
			28	1	25	2		

- Molecule 4 is OLEIC ACID (three-letter code: OLA) (formula: C₁₈H₃₄O₂).



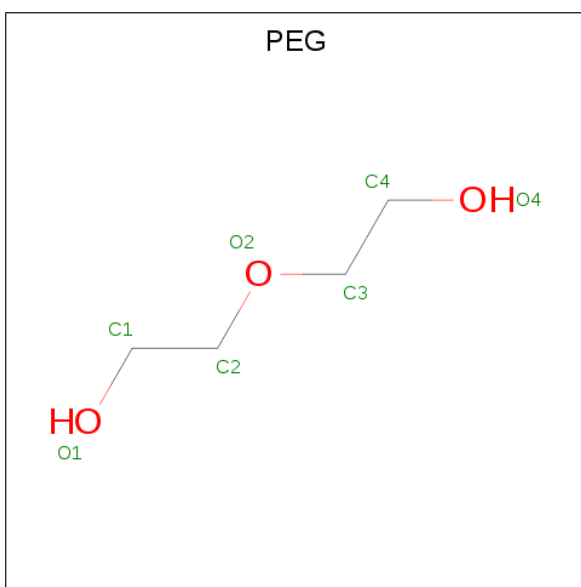
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			13	11	2		
4	A	1	Total	C	O	0	0
			13	11	2		

- Molecule 5 is (2R)-2,3-dihydroxypropyl (9Z)-octadec-9-enoate (three-letter code: OLC) (formula: C₂₁H₄₀O₄).



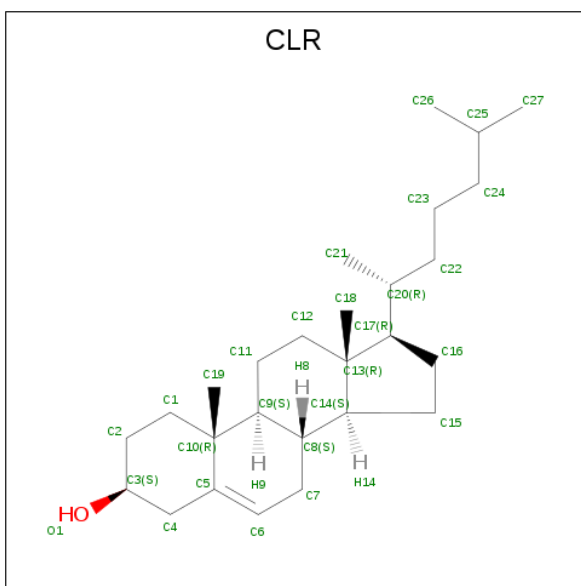
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			17	13	4		
5	A	1	Total	C	O	0	0
			13	9	4		

- Molecule 6 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



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

- Molecule 7 is CHOLESTEROL (three-letter code: CLR) (formula: $C_{27}H_{46}O$).

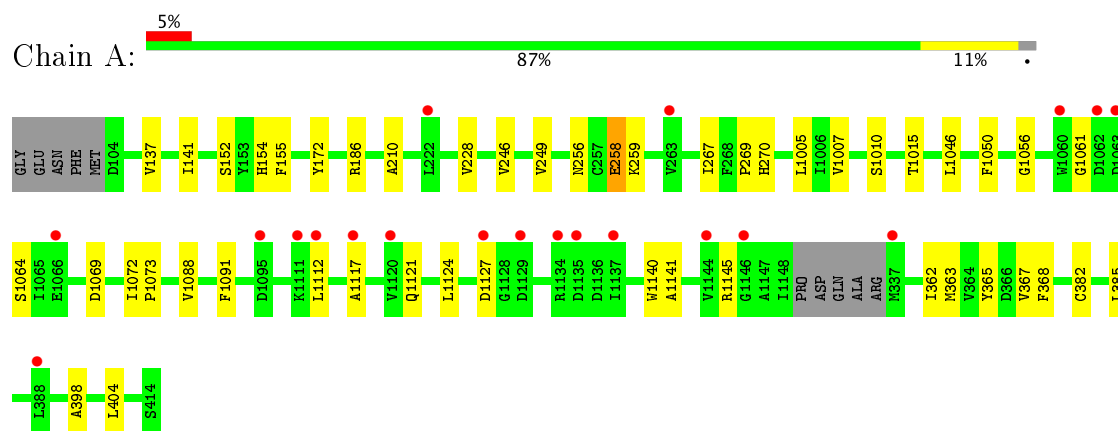


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			28	27	1		

3 Residue-property plots

These plots are drawn for all protein, RNA and DNA 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	66.05Å 75.87Å 138.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	37.91 – 2.80 37.94 – 2.80	Depositor EDS
% Data completeness (in resolution range)	93.6 (37.91-2.80) 92.4 (37.94-2.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.55 (at 2.81Å)	Xtriage
Refinement program	PHENIX 1.10.1 _2155	Depositor
R, R_{free}	0.234 , 0.252 0.239 , 0.259	Depositor DCC
R_{free} test set	789 reflections (4.79%)	DCC
Wilson B-factor (Å ²)	68.9	Xtriage
Anisotropy	0.232	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 57.8	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	0.89	EDS
Total number of atoms	3461	wwPDB-VP
Average B, all atoms (Å ²)	89.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.59% 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: OLA, OLC, FMN, 8D3, PEG, CLR

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	0/3386	0.41	0/4607

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	3311	0	3311	41	0
2	A	31	0	19	0	0
3	A	28	0	0	0	0
4	A	26	0	32	0	0
5	A	30	0	37	2	0
6	A	7	0	10	0	0
7	A	28	0	46	1	0
All	All	3461	0	3455	42	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 6.

All (42) 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:1112:LEU:HD11	1:A:1117:ALA:CB	1.74	1.18
1:A:1112:LEU:CD1	1:A:1117:ALA:HB3	1.81	1.10
1:A:1088:VAL:HB	1:A:1112:LEU:HD21	1.38	1.03
1:A:1112:LEU:CD1	1:A:1117:ALA:CB	2.42	0.92
1:A:1112:LEU:HD11	1:A:1117:ALA:HB3	1.44	0.92
1:A:1088:VAL:CB	1:A:1112:LEU:HD21	2.14	0.78
1:A:186:ARG:HG3	1:A:270:HIS:ND1	2.02	0.74
1:A:1088:VAL:HB	1:A:1112:LEU:CD2	2.17	0.73
1:A:1069:ASP:O	1:A:1072:ILE:HG12	1.94	0.68
1:A:1112:LEU:CG	1:A:1117:ALA:HB3	2.24	0.67
1:A:1010:SER:HB3	1:A:1015:THR:HB	1.82	0.62
1:A:269:PRO:HB2	1:A:270:HIS:HD2	1.64	0.62
1:A:1112:LEU:HD11	1:A:1117:ALA:HB2	1.78	0.61
1:A:137:VAL:O	1:A:141:ILE:HG12	2.02	0.60
1:A:1112:LEU:HD12	1:A:1117:ALA:HB3	1.85	0.56
1:A:269:PRO:CB	1:A:270:HIS:HD2	2.19	0.56
1:A:1112:LEU:HG	1:A:1117:ALA:HB3	1.88	0.56
1:A:1072:ILE:HG12	1:A:1073:PRO:HD3	1.88	0.55
1:A:256:ASN:OD1	1:A:259:LYS:HB2	2.08	0.52
1:A:1005:LEU:HB2	1:A:1050:PHE:CD1	2.45	0.51
1:A:186:ARG:HH21	1:A:258:GLU:HB2	1.77	0.48
1:A:363:MET:O	1:A:367:VAL:HG23	2.13	0.48
1:A:228:VAL:HG13	5:A:606:OLC:H2	1.96	0.47
1:A:1112:LEU:CD1	1:A:1117:ALA:HB2	2.41	0.47
1:A:1112:LEU:HD11	1:A:1117:ALA:HB1	1.84	0.47
1:A:246:VAL:O	1:A:249:VAL:HG12	2.15	0.46
1:A:1061:GLY:HA3	1:A:1064:SER:O	2.16	0.45
1:A:152:SER:HB3	1:A:154:HIS:CD2	2.52	0.45
1:A:1141:ALA:O	1:A:1145:ARG:HB2	2.17	0.45
1:A:1124:LEU:HD13	1:A:1140:TRP:HB2	2.00	0.44
1:A:1072:ILE:CG1	1:A:1073:PRO:HD3	2.48	0.44
1:A:382:CYS:O	1:A:385:LEU:HB2	2.17	0.43
1:A:1056:GLY:HA3	1:A:1091:PHE:CZ	2.54	0.43
1:A:155:PHE:CD1	1:A:210:ALA:HB2	2.54	0.43
1:A:1127:ASP:N	1:A:1127:ASP:OD1	2.44	0.42
1:A:172:TYR:HD2	5:A:605:OLC:H5A	1.85	0.41
1:A:398:ALA:O	1:A:404:LEU:HD23	2.21	0.41
1:A:267:ILE:HD11	1:A:362:ILE:HG22	2.02	0.41
7:A:608:CLR:H231	7:A:608:CLR:H213	1.80	0.41
1:A:362:ILE:O	1:A:365:TYR:HB2	2.21	0.41
1:A:368:PHE:N	1:A:368:PHE:CD2	2.89	0.41
1:A:1007:VAL:HG21	1:A:1046:LEU:HD21	2.03	0.41

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	424/438 (97%)	415 (98%)	9 (2%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains [i](#)

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	353/369 (96%)	351 (99%)	2 (1%)	89	97

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	258	GLU
1	A	1121	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	270	HIS

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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

8 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	601	-	31,33,33	1.30	4 (12%)	38,50,50	2.15	8 (21%)
3	8D3	A	602	-	30,30,30	2.75	6 (20%)	42,45,45	2.26	14 (33%)
4	OLA	A	603	-	9,12,19	0.41	0	8,12,19	0.96	0
4	OLA	A	604	-	9,12,19	0.43	0	8,12,19	0.89	0
5	OLC	A	605	-	16,16,24	0.99	2 (12%)	17,17,25	1.04	1 (5%)
5	OLC	A	606	-	12,12,24	1.10	2 (16%)	13,13,25	1.06	1 (7%)
6	PEG	A	607	-	6,6,6	0.50	0	5,5,5	0.30	0
7	CLR	A	608	-	31,31,31	0.66	1 (3%)	48,48,48	1.38	9 (18%)

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	601	-	-	0/16/18/18	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	8D3	A	602	-	-	0/14/42/42	0/3/3/3
4	OLA	A	603	-	-	0/8/10/17	0/0/0/0
4	OLA	A	604	-	-	0/8/10/17	0/0/0/0
5	OLC	A	605	-	-	0/16/16/24	0/0/0/0
5	OLC	A	606	-	-	0/12/12/24	0/0/0/0
6	PEG	A	607	-	-	0/4/4/4	0/0/0/0
7	CLR	A	608	-	-	0/10/68/68	0/4/4/4

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	602	8D3	C17-C3	-8.16	1.40	1.53
3	A	602	8D3	C5-C13	-7.57	1.40	1.51
3	A	602	8D3	C6-C8	-6.06	1.44	1.53
3	A	602	8D3	C9-C10	-5.25	1.39	1.50
3	A	602	8D3	C16-C11	-4.32	1.39	1.50
3	A	602	8D3	C12-C11	-3.08	1.41	1.50
2	A	601	FMN	C4A-C10	-2.75	1.36	1.41
2	A	601	FMN	C9A-N10	-2.66	1.35	1.38
2	A	601	FMN	C9A-C5A	-2.50	1.37	1.42
7	A	608	CLR	C10-C9	-2.31	1.52	1.56
2	A	601	FMN	O4-C4	-2.21	1.19	1.24
5	A	606	OLC	O20-C21	-2.10	1.40	1.45
5	A	605	OLC	O20-C21	-2.05	1.40	1.45
5	A	606	OLC	O20-C1	2.44	1.40	1.33
5	A	605	OLC	O20-C1	2.50	1.40	1.33

All (33) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	602	8D3	C12-C13-C8	-7.74	92.20	109.84
3	A	602	8D3	O2-C7-C5	-4.79	114.25	121.98
3	A	602	8D3	C12-C13-C5	-4.59	104.73	113.26
2	A	601	FMN	C1'-N10-C10	-4.11	114.29	118.50
3	A	602	8D3	C4-C7-C5	-3.43	116.47	121.89
3	A	602	8D3	C7-C5-C13	-3.23	115.94	121.07
3	A	602	8D3	C21-C18-C17	-2.94	111.11	117.29
7	A	608	CLR	C19-C10-C9	-2.85	108.16	111.68
3	A	602	8D3	C6-C8-C13	-2.75	103.19	109.77
7	A	608	CLR	C14-C8-C9	-2.55	105.62	109.09
2	A	601	FMN	C4A-C4-N3	-2.55	119.85	123.48
7	A	608	CLR	C13-C14-C8	-2.52	110.54	114.39

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	A	608	CLR	C11-C9-C10	-2.33	109.88	113.10
7	A	608	CLR	C21-C20-C22	-2.31	106.71	110.35
2	A	601	FMN	C7M-C7-C6	-2.29	114.59	120.34
3	A	602	8D3	O2-C6-C8	-2.23	103.88	109.01
3	A	602	8D3	C9-C10-C11	-2.14	116.58	123.72
7	A	608	CLR	C13-C17-C20	-2.14	116.03	119.47
7	A	608	CLR	C3-C4-C5	-2.14	108.19	111.98
7	A	608	CLR	C18-C13-C14	-2.04	107.87	111.73
7	A	608	CLR	C23-C22-C20	-2.01	108.94	115.00
3	A	602	8D3	C16-C11-C12	2.00	119.81	116.14
3	A	602	8D3	C1-C5-C7	2.24	118.37	116.37
2	A	601	FMN	C7M-C7-C8	2.33	125.61	120.72
5	A	605	OLC	O20-C1-C2	2.78	120.00	111.90
5	A	606	OLC	O20-C1-C2	2.82	120.11	111.90
3	A	602	8D3	C5-C13-C8	2.85	118.29	106.06
2	A	601	FMN	C4A-N5-C5A	3.02	119.95	116.76
3	A	602	8D3	C6-O2-C7	3.46	124.22	117.47
2	A	601	FMN	C5A-C9A-N10	3.52	120.28	117.66
3	A	602	8D3	O2-C7-C4	3.61	122.19	116.45
2	A	601	FMN	C4-N3-C2	5.54	120.00	115.16
2	A	601	FMN	C1'-N10-C9A	8.68	126.30	118.35

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	605	OLC	1	0
5	A	606	OLC	1	0
7	A	608	CLR	1	0

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	428/438 (97%)	-0.07	20 (4%) 32 22	52, 86, 132, 161	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1060	TRP	5.2
1	A	1112	LEU	4.9
1	A	1062	ASP	3.9
1	A	1066	GLU	3.7
1	A	1134	ARG	3.2
1	A	263	VAL	3.1
1	A	1127	ASP	3.1
1	A	1111	LYS	3.0
1	A	1095	ASP	3.0
1	A	1120	VAL	2.9
1	A	1137	ILE	2.9
1	A	1144	VAL	2.6
1	A	1129	ASP	2.5
1	A	1063	ASP	2.5
1	A	1117	ALA	2.5
1	A	1146	GLY	2.5
1	A	337	MET	2.4
1	A	388	LEU	2.2
1	A	222	LEU	2.2
1	A	1135	ASP	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 carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
4	OLA	A	604	13/20	0.82	0.32	6.63	81,84,96,96	0
5	OLC	A	605	17/25	0.77	0.33	5.85	85,100,107,108	0
5	OLC	A	606	13/25	0.78	0.29	3.68	86,102,105,106	0
7	CLR	A	608	28/28	0.96	0.22	2.63	58,62,72,73	0
3	8D3	A	602	28/28	0.95	0.22	1.22	52,59,80,87	0
4	OLA	A	603	13/20	0.88	0.16	0.11	80,81,86,89	0
2	FMN	A	601	31/31	0.94	0.25	0.08	64,72,79,80	0
6	PEG	A	607	7/7	0.73	0.33	-	104,106,106,106	0

6.5 Other polymers [i](#)

There are no such residues in this entry.