Full wwPDB X-ray Structure Validation Report (i)

Sep 24, 2023 – 12:43 PM EDT

PDB ID	:	5UEN
Title	:	Crystal structure of the human adenosine A1 receptor A1AR-bRIL in complex with the covalent antagonist DU172 at 3.2A resolution
Authors	:	Glukhova, A.; Thal, D.M.; Nguyen, A.T.; Vecchio, E.A.; Jorg, M.; Scammells, P.J.; May, L.T.; Sexton, P.M.; Christopoulos, A.
Deposited on	:	2017-01-03
Resolution	:	3.20 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 (i) 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 (i)) were used in the production of this report:

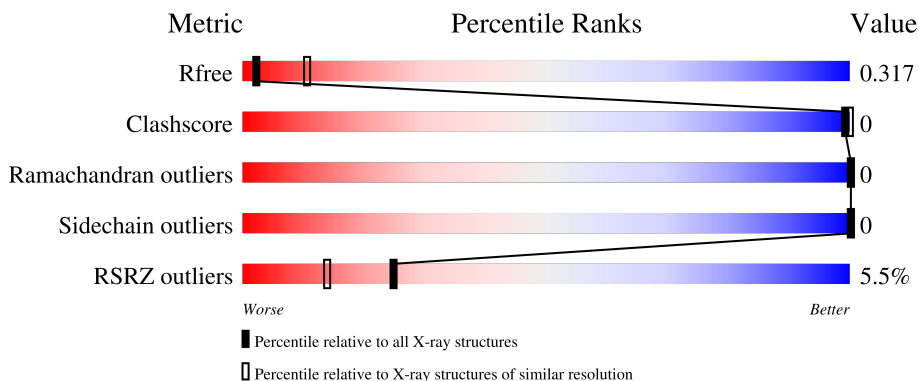|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35.1
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35.1

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 3.20 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	Percentile Ranks	Value
Rfree		0.317
Clashscore		0
Ramachandran outliers		0
Sidechain outliers		0
RSRZ outliers		5.5%

Worse .... *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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 <=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	416	7% / 92% / 8%
1	B	416	3% / 92% / 8%

2 Entry composition ⓘ

There are 3 unique types of molecules in this entry. The entry contains 6250 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 Adenosine receptor A1,Soluble cytochrome b562,Adenosine receptor A1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	384	Total 3039	C 2009	N 499	O 512	S 19	0	0	0
1	B	383	Total 3022	C 1992	N 502	O 510	S 18	0	0	0

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P30542
A	1	PRO	-	expression tag	UNP P30542
A	159	ALA	ASN	engineered mutation	UNP P30542
A	1007	TRP	MET	conflict	UNP P0ABE7
A	1102	ILE	HIS	conflict	UNP P0ABE7
A	1106	LEU	-	linker	UNP P0ABE7
A	220	GLU	-	linker	UNP P0ABE7
A	221	ARG	-	linker	UNP P0ABE7
A	222	ALA	-	linker	UNP P0ABE7
A	223	ARG	-	linker	UNP P0ABE7
A	224	SER	-	linker	UNP P0ABE7
A	225	THR	-	linker	UNP P0ABE7
A	226	LEU	-	linker	UNP P0ABE7
A	227	GLN	-	linker	UNP P0ABE7
A	312	LEU	-	expression tag	UNP P30542
A	313	GLU	-	expression tag	UNP P30542
A	314	VAL	-	expression tag	UNP P30542
A	315	LEU	-	expression tag	UNP P30542
A	316	PHE	-	expression tag	UNP P30542
A	317	GLN	-	expression tag	UNP P30542
B	0	GLY	-	expression tag	UNP P30542
B	1	PRO	-	expression tag	UNP P30542
B	159	ALA	ASN	engineered mutation	UNP P30542
B	1007	TRP	MET	conflict	UNP P0ABE7

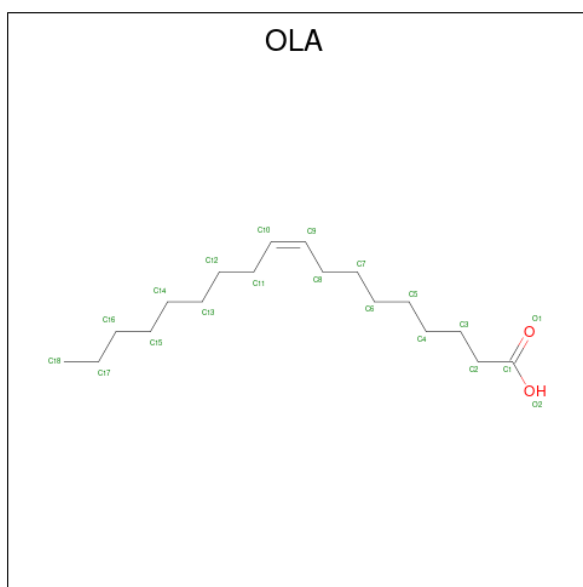*Continued on next page...*

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Chain	Residue	Modelled	Actual	Comment	Reference
B	1102	ILE	HIS	conflict	UNP P0ABE7
B	1106	LEU	-	linker	UNP P0ABE7
B	220	GLU	-	linker	UNP P0ABE7
B	221	ARG	-	linker	UNP P0ABE7
B	222	ALA	-	linker	UNP P0ABE7
B	223	ARG	-	linker	UNP P0ABE7
B	224	SER	-	linker	UNP P0ABE7
B	225	THR	-	linker	UNP P0ABE7
B	226	LEU	-	linker	UNP P0ABE7
B	227	GLN	-	linker	UNP P0ABE7
B	312	LEU	-	expression tag	UNP P30542
B	313	GLU	-	expression tag	UNP P30542
B	314	VAL	-	expression tag	UNP P30542
B	315	LEU	-	expression tag	UNP P30542
B	316	PHE	-	expression tag	UNP P30542
B	317	GLN	-	expression tag	UNP P30542

- Molecule 2 is 4-{[3-(8-cyclohexyl-2,6-dioxo-1-propyl-1,2,6,7-tetrahydro-3H-purin-3-yl)propyl]carbamoyl}benzene-1-sulfonyl fluoride (three-letter code: DU1) (formula: $C_{24}H_{30}FN_5O_5S$).
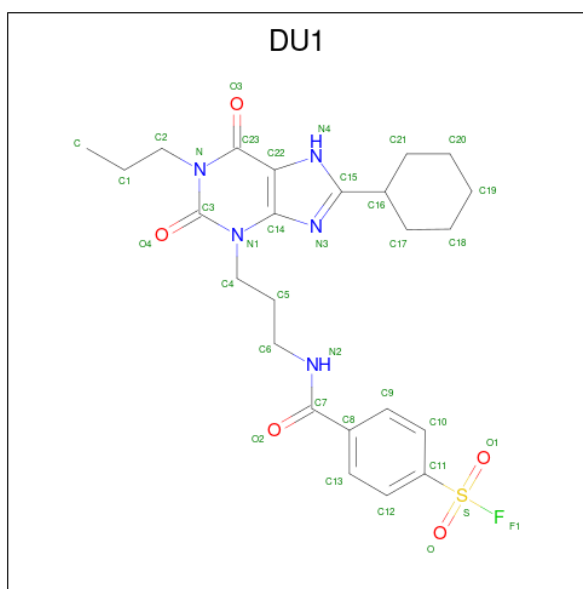
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			35	24	5	5	1		
2	B	1	Total	C	N	O	S	0	0
			35	24	5	5	1		

- Molecule 3 is OLEIC ACID (three-letter code: OLA) (formula: $C_{18}H_{34}O_2$).

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total 20	C 18	O 2	0	0
3	A	1	Total 20	C 18	O 2	0	0
3	A	1	Total 14	C 12	O 2	0	0
3	A	1	Total 12	C 10	O 2	0	0
3	B	1	Total 20	C 18	O 2	0	0
3	B	1	Total 20	C 18	O 2	0	0
3	B	1	Total 13	C 11	O 2	0	0

3 Residue-property plots ⓘ

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: Adenosine receptor A1,Soluble cytochrome b562,Adenosine receptor A1
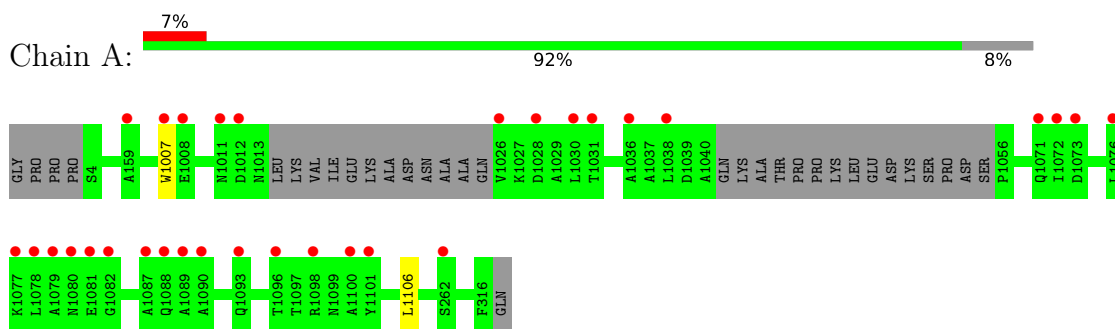
Chain A:

• Molecule 1: Adenosine receptor A1,Soluble cytochrome b562,Adenosine receptor A1

Chain B:
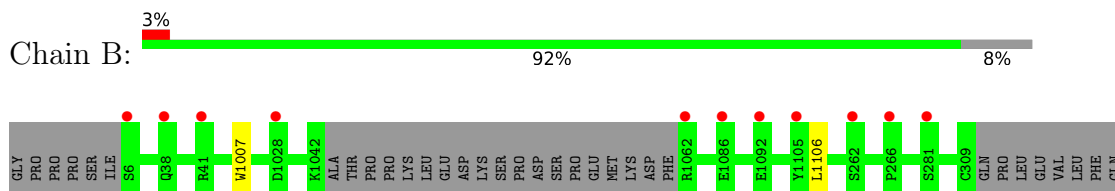
4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, α, β, γ	96.49Å 112.96Å 124.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.20 29.68 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.2 (30.00-3.20) 99.4 (29.68-3.20)	Depositor EDS
R_{merge}	0.33	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.44 (at 3.18Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.286 , 0.316 0.286 , 0.317	Depositor DCC
R_{free} test set	1105 reflections (4.83%)	wwPDB-VP
Wilson B-factor (Å^2)	83.8	Xtriage
Anisotropy	0.300	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.30 , 52.8	EDS
L-test for twinning[2]	$< |L| > = 0.49, < L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.89	EDS
Total number of atoms	6250	wwPDB-VP
Average B, all atoms (Å^2)	93.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% of the height of the origin peak. No significant pseudotranslation is detected.*

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[1]Intensities estimated from amplitudes.
[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: DU1, OLA

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	0/3108	0.53	0/4227
1	B	0.42	0/3088	0.50	0/4200
All	All	0.43	0/6196	0.51	0/8427

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	3039	0	3169	1	0
1	B	3022	0	3161	1	0
2	A	35	0	0	0	0
2	B	35	0	0	0	0
3	A	66	0	99	0	0
3	B	53	0	82	0	0
All	All	6250	0	6511	2	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 0.

All (2) 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:1007:TRP:CD2	1:A:1106:LEU:HD22	2.56	0.41
1:B:1007:TRP:CD2	1:B:1106:LEU:HD22	2.55	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	378/416 (91%)	369 (98%)	9 (2%)	0	100	100
1	B	379/416 (91%)	369 (97%)	10 (3%)	0	100	100
All	All	757/832 (91%)	738 (98%)	19 (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	326/353 (92%)	326 (100%)	0	100	100
1	B	322/353 (91%)	322 (100%)	0	100	100
All	All	648/706 (92%)	648 (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 monosaccharides in this entry.

5.6   Ligand geometry ⓘ

9 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	#$|Z| > 2$
3	OLA	B	1202	-	19,19,19	0.50	0	19,19,19	0.75	0
3	OLA	A	1204	-	13,13,19	0.58	0	12,13,19	0.92	0
3	OLA	B	1203	-	19,19,19	0.52	0	19,19,19	0.67	0
3	OLA	A	1202	-	19,19,19	0.49	0	19,19,19	0.76	0
3	OLA	A	1203	-	19,19,19	0.48	0	19,19,19	0.75	0
2	DU1	A	1201	1	30,38,39	0.69	1 (3%)	40,53,56	0.66	1 (2%)
2	DU1	B	1201	1	30,38,39	0.71	1 (3%)	40,53,56	0.66	1 (2%)
3	OLA	A	1205	-	11,11,19	0.70	0	11,11,19	0.72	0
3	OLA	B	1204	-	12,12,19	0.64	0	12,12,19	0.88	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
3	OLA	B	1202	-	-	8/17/17/17	-
3	OLA	A	1204	-	-	5/11/11/17	-
3	OLA	B	1203	-	-	6/17/17/17	-
3	OLA	A	1202	-	-	7/17/17/17	-
3	OLA	A	1203	-	-	4/17/17/17	-
2	DU1	A	1201	1	-	0/18/30/32	0/4/4/4
2	DU1	B	1201	1	-	1/18/30/32	0/4/4/4
3	OLA	A	1205	-	-	0/9/9/17	-
3	OLA	B	1204	-	-	4/10/10/17	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1201	DU1	C22-C14	-2.32	1.37	1.43
2	A	1201	DU1	C22-C14	-2.26	1.37	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1201	DU1	C14-N1-C3	-2.82	119.56	122.22
2	A	1201	DU1	C14-N1-C3	-2.72	119.66	122.22

There are no chirality outliers.

All (35) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	B	1204	OLA	C1-C2-C3-C4
3	B	1202	OLA	C12-C13-C14-C15
3	B	1202	OLA	C2-C3-C4-C5
3	B	1203	OLA	C12-C13-C14-C15
3	A	1202	OLA	C6-C7-C8-C9
3	B	1203	OLA	C5-C6-C7-C8
3	A	1204	OLA	C3-C4-C5-C6
3	B	1202	OLA	C4-C5-C6-C7
3	A	1204	OLA	C9-C10-C11-C12
3	A	1202	OLA	C4-C5-C6-C7
3	A	1203	OLA	C11-C12-C13-C14
3	B	1202	OLA	C9-C10-C11-C12
3	A	1204	OLA	C7-C8-C9-C10

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Mol	Chain	Res	Type	Atoms
3	B	1203	OLA	C9-C10-C11-C12
3	B	1203	OLA	C10-C11-C12-C13
3	B	1204	OLA	O2-C1-C2-C3
3	B	1202	OLA	O1-C1-C2-C3
3	A	1202	OLA	C9-C10-C11-C12
3	B	1204	OLA	O1-C1-C2-C3
3	A	1202	OLA	C15-C16-C17-C18
3	B	1202	OLA	O2-C1-C2-C3
3	B	1202	OLA	C7-C8-C9-C10
3	B	1204	OLA	C7-C8-C9-C10
3	A	1204	OLA	O2-C1-C2-C3
2	B	1201	DU1	C12-C11-S-O
3	B	1202	OLA	C15-C16-C17-C18
3	B	1203	OLA	O2-C1-C2-C3
3	A	1204	OLA	O1-C1-C2-C3
3	A	1202	OLA	O2-C1-C2-C3
3	A	1203	OLA	O2-C1-C2-C3
3	B	1203	OLA	O1-C1-C2-C3
3	A	1202	OLA	O1-C1-C2-C3
3	A	1203	OLA	O1-C1-C2-C3
3	A	1203	OLA	C12-C13-C14-C15
3	A	1202	OLA	C11-C12-C13-C14

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 then 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.

Ligand OLA B 1202

Bond lengths

Bond angles

Torsions

Rings

Ligand OLA A 1204

Bond lengths

Bond angles

Torsions

Rings

Ligand OLA B 1203

Bond lengths

Bond angles

Torsions

Rings

Ligand OLA A 1202

Bond lengths

Bond angles

Torsions

Rings

Ligand OLA A 1203

Bond lengths

Bond angles

Torsions

Rings

Ligand DU1 A 1201

Bond lengths

Bond angles

Torsions

Rings

Ligand DU1 B 1201

Bond lengths

Bond angles

Torsions

Rings

Ligand OLA B 1204

Bond lengths

Bond angles

Torsions

Rings

5.7 Other polymers ⓘ

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	384/416 (92%)	0.34	31 (8%)	12	6	50, 77, 191, 231	0
1	B	383/416 (92%)	0.16	11 (2%)	51	36	59, 86, 150, 162	0
All	All	767/832 (92%)	0.25	42 (5%)	25	14	50, 82, 172, 231	0

All (42) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1080	ASN	6.4
1	B	1062	ARG	4.8
1	A	1077	LYS	4.8
1	A	1079	ALA	4.5
1	A	1081	GLU	4.0
1	A	1088	GLN	3.9
1	B	262	SER	3.6
1	A	1026	VAL	3.6
1	A	1082	GLY	3.5
1	A	1072	ILE	3.2
1	A	1007	TRP	3.2
1	A	262	SER	3.1
1	B	1092	GLU	3.1
1	A	1087	ALA	3.1
1	B	38	GLN	3.0
1	A	1073	ASP	3.0
1	A	1011	ASN	2.9
1	A	1076	LEU	2.9
1	A	1100	ALA	2.8
1	A	1078	LEU	2.8
1	B	1105	TYR	2.8
1	B	1028	ASP	2.7
1	A	1090	ALA	2.5
1	B	6	SER	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1089	ALA	2.4
1	A	1030	LEU	2.4
1	B	1086	GLU	2.4
1	A	1101	TYR	2.4
1	A	1038	LEU	2.4
1	A	1098	ARG	2.4
1	A	1008	GLU	2.3
1	B	266	PRO	2.2
1	A	159	ALA	2.2
1	A	1093	GLN	2.2
1	A	1071	GLN	2.1
1	A	1031	THR	2.1
1	A	1028	ASP	2.1
1	B	281	SER	2.1
1	A	1012	ASP	2.0
1	A	1036	ALA	2.0
1	B	41	ARG	2.0
1	A	1096	THR	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 ⓘ

There are no monosaccharides in this entry.

6.4 Ligands ⓘ

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
3	OLA	A	1204	14/20	0.80	0.37	65,66,71,72	0
3	OLA	B	1204	13/20	0.80	0.51	81,82,84,84	0
2	DU1	A	1201	35/36	0.82	0.29	54,58,79,82	0
3	OLA	A	1203	20/20	0.82	0.36	57,61,64,64	0
3	OLA	A	1202	20/20	0.83	0.52	80,84,88,88	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	OLA	B	1203	20/20	0.83	0.41	70,72,74,74	0
2	DU1	B	1201	35/36	0.83	0.31	76,82,90,91	0
3	OLA	B	1202	20/20	0.86	0.39	84,87,92,92	0
3	OLA	A	1205	12/20	0.89	0.33	59,61,66,66	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.
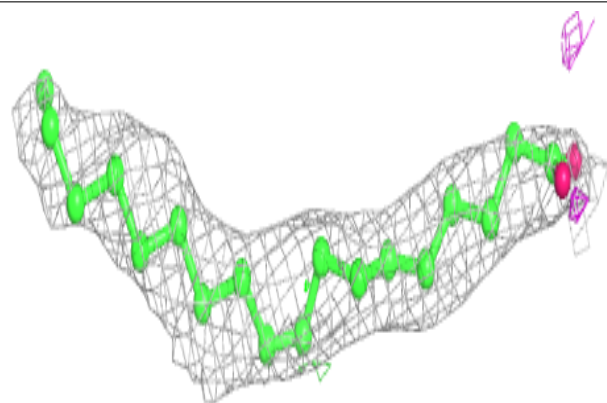

Electron density around OLA A 1204:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
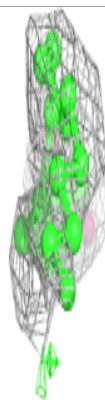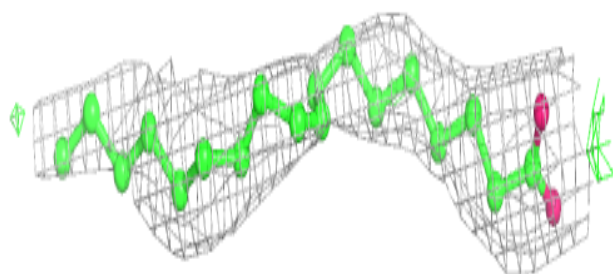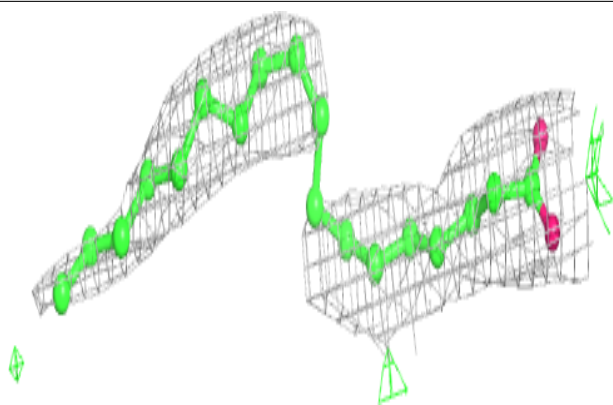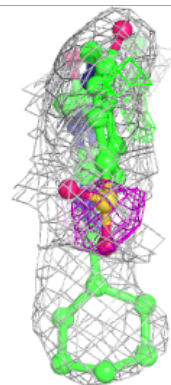$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative) and green (positive)
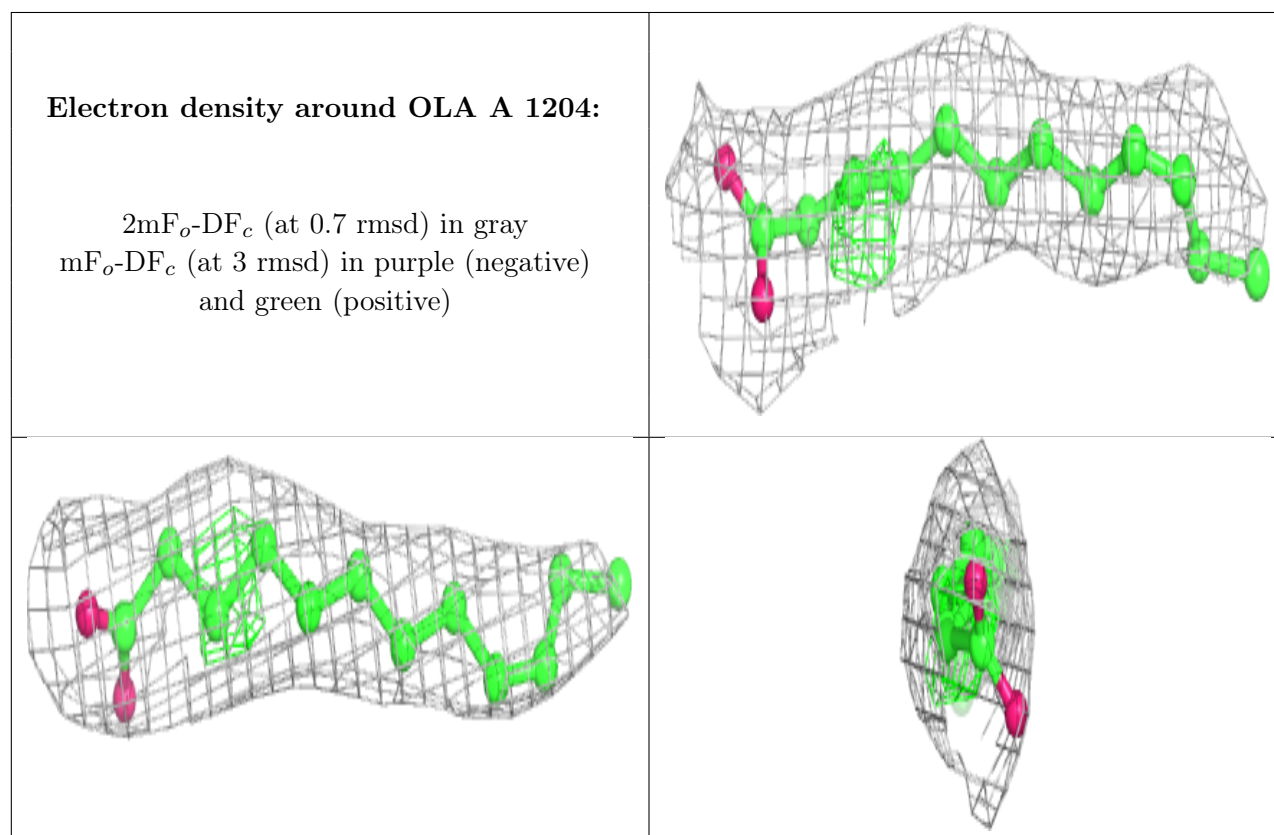
Electron density around OLA B 1204:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
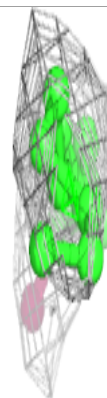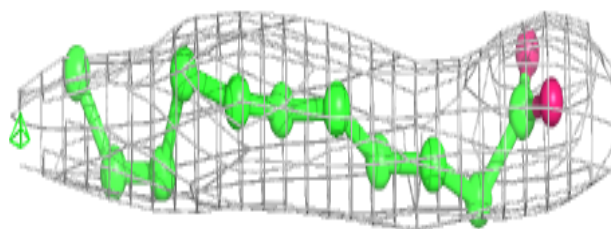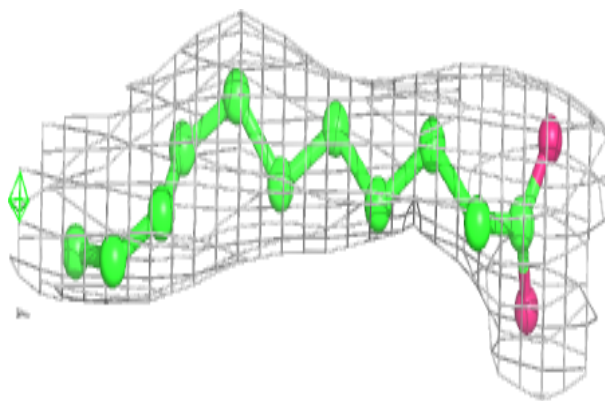
Electron density around DU1 A 1201:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
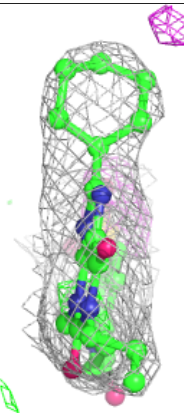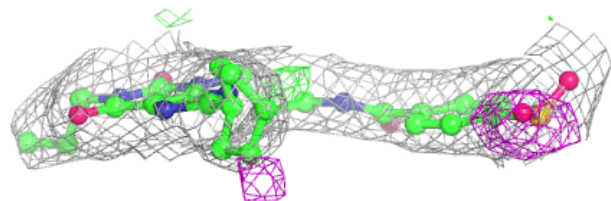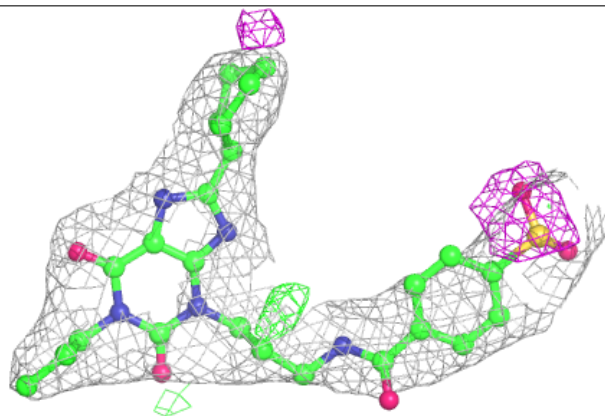
Electron density around OLA A 1203:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)
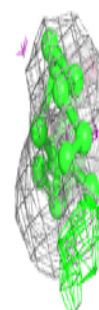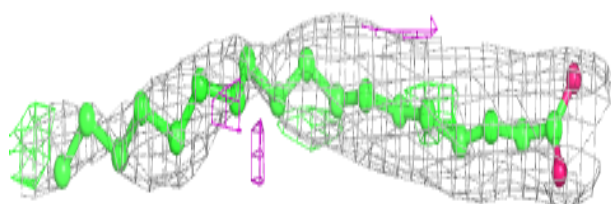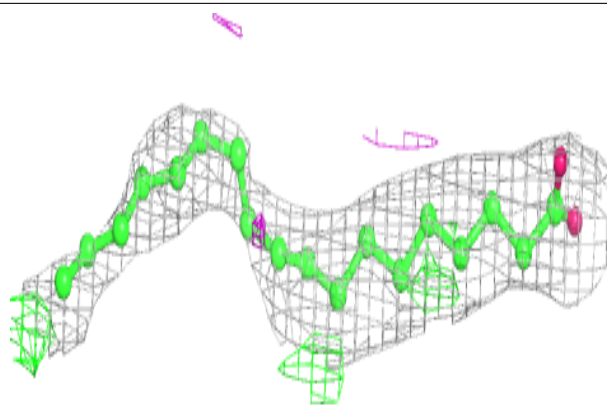
Electron density around OLA A 1202:

$2mF_o\text{-}DF_c$ (at 0.7 rmsd) in gray
$mF_o\text{-}DF_c$ (at 3 rmsd) in purple (negative)
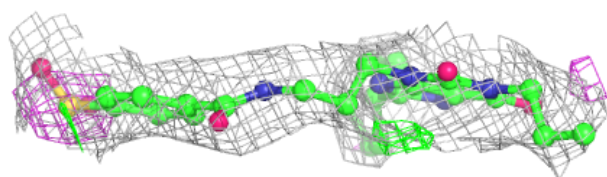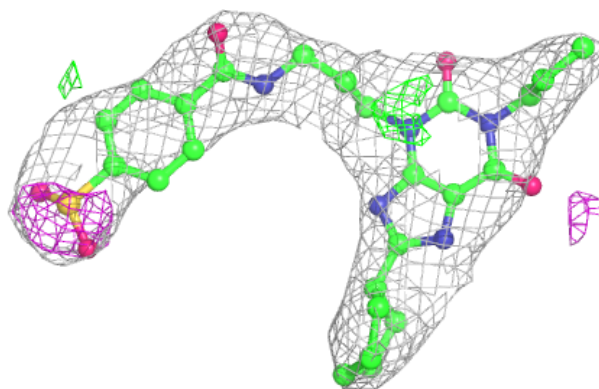and green (positive)
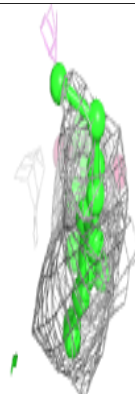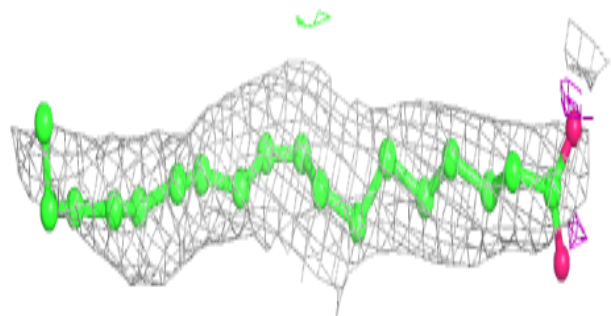
Electron density around OLA B 1203:

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

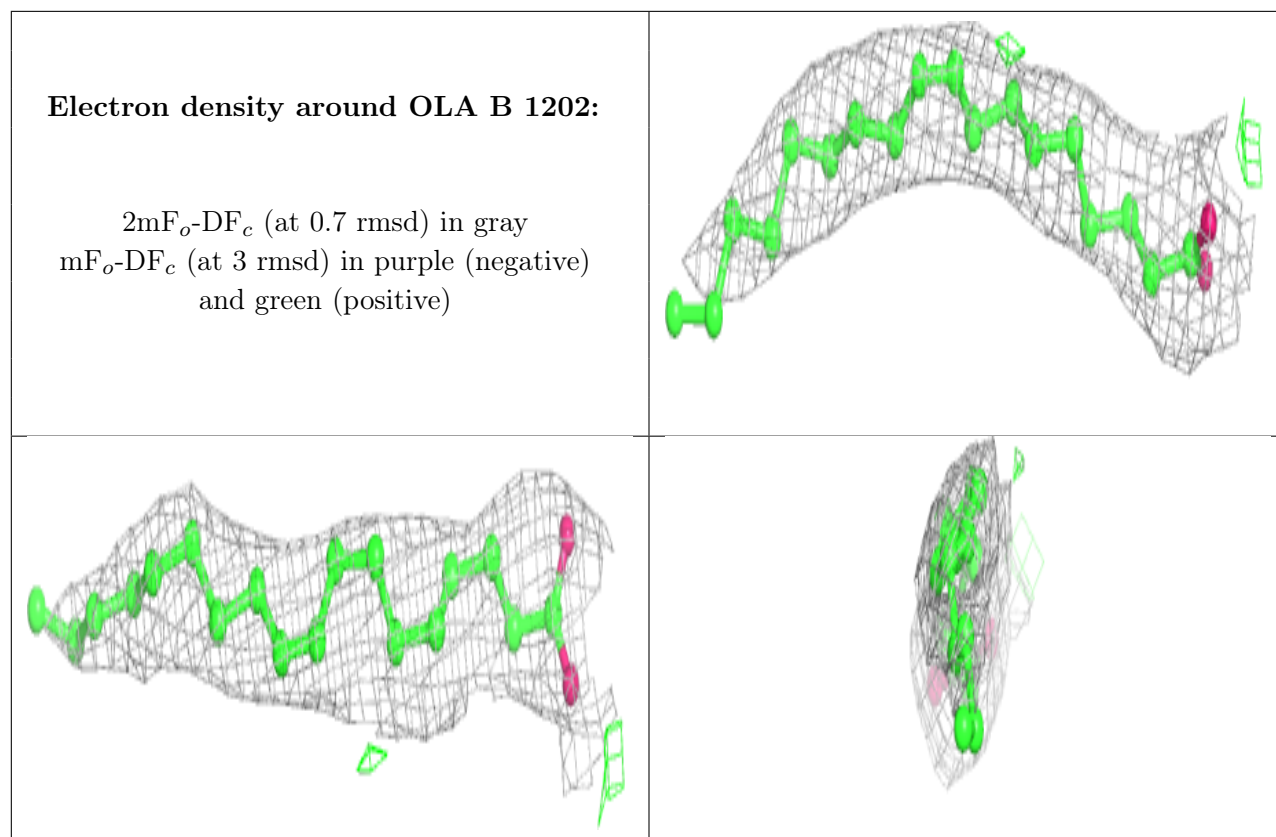**Electron density around DU1 B 1201:**

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

Electron density around OLA B 1202:

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

6.5 Other polymers ⓘ

There are no such residues in this entry.