



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 21, 2017 – 06:01 PM EST

PDB ID : 5UEN
Title : Crystal structure of the human adenosine A1 receptor A1AR-bRIL in complex with the covalent antagonist DU172 at 3.2Å resolution
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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

<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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20028442
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
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-20028442

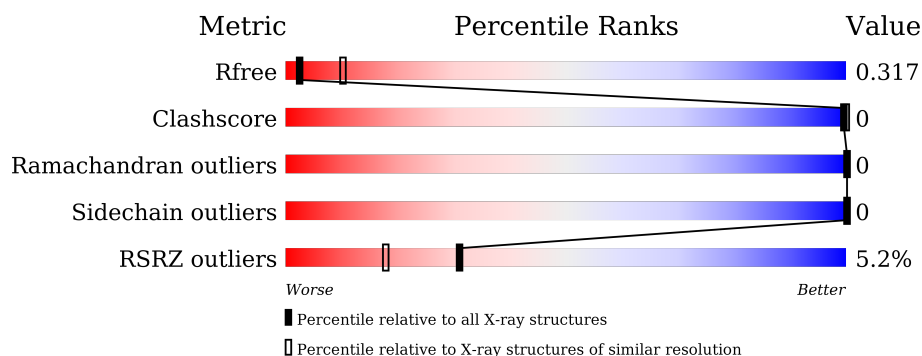
1 Overall quality at a glance

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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	91344	1124 (3.24-3.16)
Clashscore	102246	1024 (3.22-3.18)
Ramachandran outliers	100387	1004 (3.22-3.18)
Sidechain outliers	100360	1003 (3.22-3.18)
RSRZ outliers	91569	1129 (3.24-3.16)

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	416	
1	B	416	

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
3	OLA	A	1202	-	-	-	X
3	OLA	A	1203	-	-	-	X
3	OLA	A	1204	-	-	-	X
3	OLA	B	1202	-	-	-	X
3	OLA	B	1203	-	-	-	X
3	OLA	B	1204	-	-	-	X

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	C	N	O	S	0	0	0
			3039	2009	499	512	19			
1	B	383	Total	C	N	O	S	0	0	0
			3022	1992	502	510	18			

There are 40 discrepancies between the modelled and reference sequences:

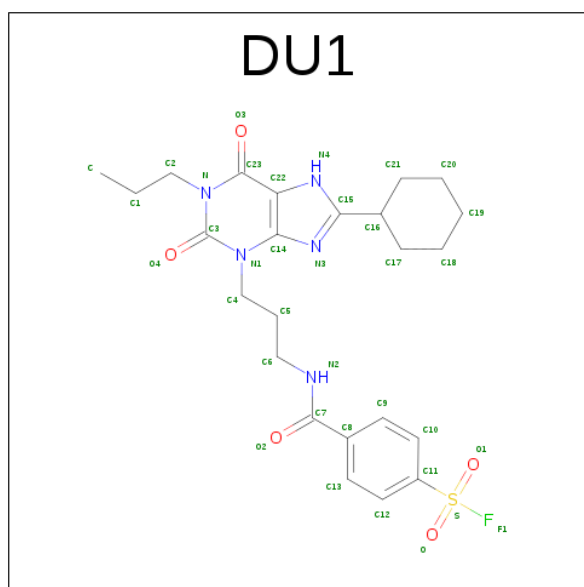
Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP P30542
A	1	PRO	-	expression tag	UNP P30542
A	159	ALA	ASN	engineered mutation	UNP P30542
A	1007	TRP	MET	conflict	UNP P0ABE7
A	1102	ILE	HIS	conflict	UNP P0ABE7
A	1106	LEU	-	linker	UNP P0ABE7
A	220	GLU	-	linker	UNP P0ABE7
A	221	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

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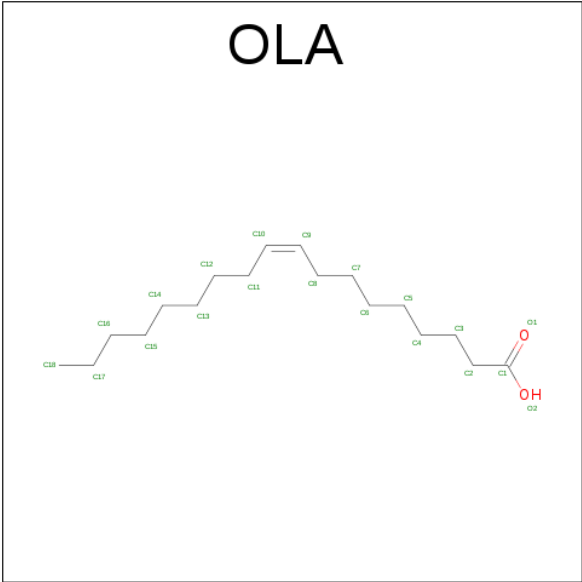
Chain	Residue	Modelled	Actual	Comment	Reference
B	1102	ILE	HIS	conflict	UNP P0ABE7
B	1106	LEU	-	linker	UNP P0ABE7
B	220	GLU	-	linker	UNP P0ABE7
B	221	ARG	-	linker	UNP P0ABE7
B	222	ALA	-	linker	UNP P0ABE7
B	223	ARG	-	linker	UNP P0ABE7
B	224	SER	-	linker	UNP P0ABE7
B	225	THR	-	linker	UNP P0ABE7
B	226	LEU	-	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: C₂₄H₃₀FN₅O₅S).



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: C₁₈H₃₄O₂).

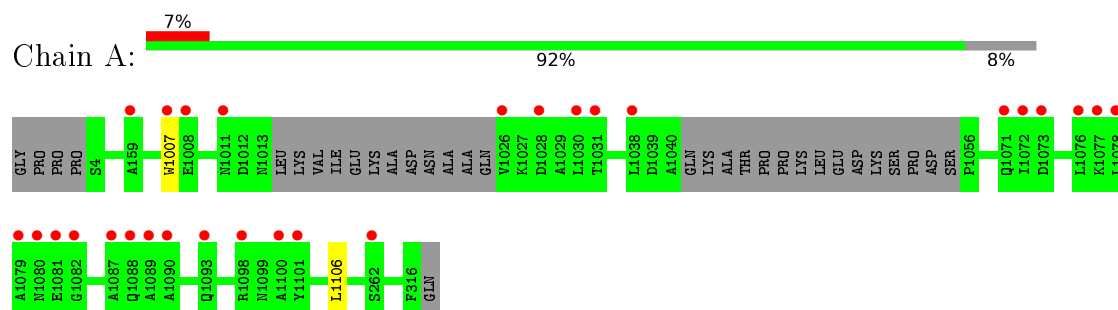


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			20	18	2		
3	A	1	Total	C	O	0	0
			20	18	2		
3	A	1	Total	C	O	0	0
			14	12	2		
3	A	1	Total	C	O	0	0
			12	10	2		
3	B	1	Total	C	O	0	0
			20	18	2		
3	B	1	Total	C	O	0	0
			20	18	2		
3	B	1	Total	C	O	0	0
			13	11	2		

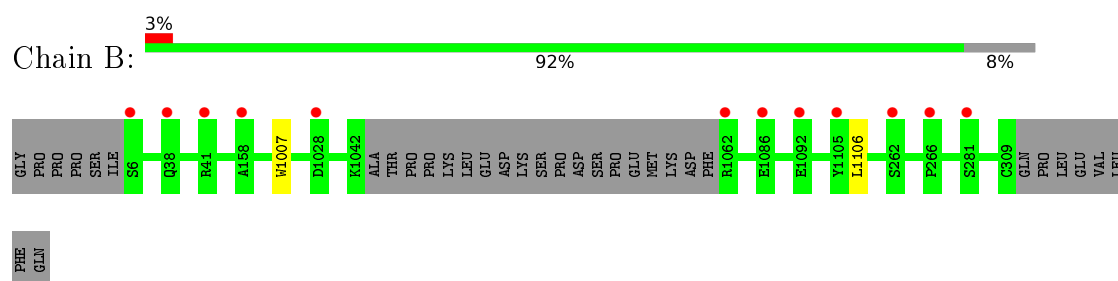
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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



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



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	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
$\langle I/\sigma(I) \rangle$ ¹	2.44 (at 3.18Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.286 , 0.316 0.286 , 0.317	Depositor DCC
R_{free} test set	1105 reflections (5.08%)	DCC
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 , 52.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	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.*

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, DU1

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

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 [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	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 [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	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.

Some 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 carbohydrates 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	$\# Z > 2$
2	DU1	A	1201	1	29,38,39	0.97	2 (6%)	34,53,56	1.98	4 (11%)
3	OLA	A	1202	-	16,19,19	0.24	0	16,19,19	0.56	0
3	OLA	A	1203	-	16,19,19	0.25	0	16,19,19	0.57	0
3	OLA	A	1204	-	10,13,19	0.30	0	10,13,19	0.64	0
3	OLA	A	1205	-	8,11,19	0.38	0	8,11,19	0.59	0
2	DU1	B	1201	1	29,38,39	0.98	2 (6%)	34,53,56	1.96	4 (11%)
3	OLA	B	1202	-	16,19,19	0.26	0	16,19,19	0.48	0
3	OLA	B	1203	-	16,19,19	0.30	0	16,19,19	0.45	0
3	OLA	B	1204	-	9,12,19	0.35	0	9,12,19	0.62	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	DU1	A	1201	1	-	0/18/30/32	0/4/4/4
3	OLA	A	1202	-	-	0/15/17/17	0/0/0/0
3	OLA	A	1203	-	-	0/15/17/17	0/0/0/0
3	OLA	A	1204	-	-	0/9/11/17	0/0/0/0
3	OLA	A	1205	-	-	0/7/9/17	0/0/0/0
2	DU1	B	1201	1	-	0/18/30/32	0/4/4/4
3	OLA	B	1202	-	-	0/15/17/17	0/0/0/0
3	OLA	B	1203	-	-	0/15/17/17	0/0/0/0
3	OLA	B	1204	-	-	0/8/10/17	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1201	DU1	C23-N	2.36	1.41	1.38
2	A	1201	DU1	C23-N	2.56	1.42	1.38
2	A	1201	DU1	C14-N3	3.82	1.36	1.33
2	B	1201	DU1	C14-N3	3.92	1.37	1.33

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1201	DU1	C22-C23-N	-9.88	113.34	120.52
2	B	1201	DU1	C22-C23-N	-9.66	113.50	120.52
2	B	1201	DU1	C2-N-C23	-2.08	117.06	119.10
2	A	1201	DU1	C2-N-C23	-2.07	117.06	119.10
2	A	1201	DU1	C4-N1-C14	3.15	122.25	119.15
2	B	1201	DU1	C4-N1-C14	3.41	122.50	119.15
2	A	1201	DU1	C23-C22-C14	3.94	122.74	119.93
2	B	1201	DU1	C23-C22-C14	3.99	122.77	119.93

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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%)	0.35	28 (7%) 18 10	50, 77, 191, 231	0
1	B	383/416 (92%)	0.16	12 (3%) 52 38	59, 86, 150, 162	0
All	All	767/832 (92%)	0.25	40 (5%) 31 18	50, 82, 172, 231	0

All (40) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1080	ASN	6.4
1	A	1077	LYS	5.0
1	B	1062	ARG	4.8
1	A	1079	ALA	4.5
1	A	1081	GLU	4.0
1	A	1088	GLN	3.9
1	B	262	SER	3.8
1	A	1082	GLY	3.6
1	A	1026	VAL	3.5
1	A	1072	ILE	3.3
1	A	1087	ALA	3.2
1	B	1092	GLU	3.2
1	A	1007	TRP	3.2
1	A	262	SER	3.2
1	A	1073	ASP	3.1
1	B	38	GLN	3.0
1	A	1011	ASN	3.0
1	A	1076	LEU	2.9
1	A	1078	LEU	2.8
1	B	1105	TYR	2.7
1	A	1100	ALA	2.7
1	A	1090	ALA	2.7
1	B	1028	ASP	2.7
1	B	1086	GLU	2.5

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Mol	Chain	Res	Type	RSRZ
1	A	1038	LEU	2.5
1	B	6	SER	2.5
1	A	1101	TYR	2.4
1	A	1089	ALA	2.4
1	A	1098	ARG	2.3
1	A	1030	LEU	2.3
1	A	1008	GLU	2.3
1	B	266	PRO	2.3
1	A	159	ALA	2.2
1	A	1093	GLN	2.2
1	A	1031	THR	2.2
1	A	1028	ASP	2.1
1	B	281	SER	2.1
1	A	1071	GLN	2.0
1	B	158	ALA	2.0
1	B	41	ARG	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
3	OLA	A	1202	20/20	0.82	0.53	5.88	80,84,88,88	0
3	OLA	A	1203	20/20	0.82	0.36	5.74	57,61,64,64	0
3	OLA	B	1203	20/20	0.83	0.40	5.07	70,72,74,74	0
3	OLA	A	1204	14/20	0.81	0.36	3.87	65,66,71,72	0
3	OLA	B	1202	20/20	0.86	0.39	3.34	84,87,92,92	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
3	OLA	B	1204	13/20	0.81	0.52	2.79	81,82,84,84	0
3	OLA	A	1205	12/20	0.89	0.33	1.75	59,61,66,66	0
2	DU1	B	1201	35/36	0.83	0.31	1.65	76,82,90,91	0
2	DU1	A	1201	35/36	0.83	0.29	1.05	54,58,79,82	0

6.5 Other polymers ⓘ

There are no such residues in this entry.