



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 01:14 pm GMT

PDB ID : 4RAK
Title : Crystal structure of nuclear receptor subfamily 1, group h, member 2 (lxrb) complexed with partial agonist
Authors : Nanao, M.
Deposited on : 2014-09-10
Resolution : 2.04 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 : trunk28620
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) : recalc28949

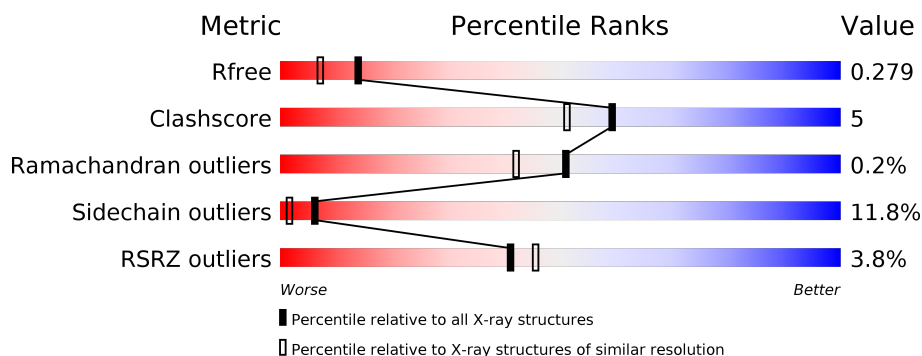
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.04 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	1316 (2.04-2.04)
Clashscore	112137	1394 (2.04-2.04)
Ramachandran outliers	110173	1383 (2.04-2.04)
Sidechain outliers	110143	1383 (2.04-2.04)
RSRZ outliers	101464	1319 (2.04-2.04)

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	264	 4% 72% 15% • 11%
1	B	264	 3% 74% 12% • 12%

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
2	BU1	A	501	-	-	-	X
2	BU1	A	502	-	-	-	X
2	BU1	B	501	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 4115 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 Oxysterols receptor LXR-beta.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	236	Total	C	N	O	S	0	1	0
			1922	1228	339	348	7			
1	B	232	Total	C	N	O	S	0	4	0
			1922	1229	340	346	7			

There are 32 discrepancies between the modelled and reference sequences:

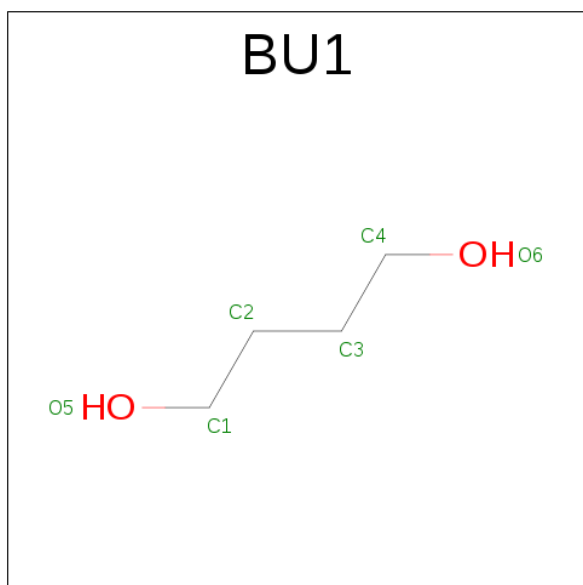
Chain	Residue	Modelled	Actual	Comment	Reference
A	198	MET	-	EXPRESSION TAG	UNP P55055
A	199	HIS	-	EXPRESSION TAG	UNP P55055
A	200	HIS	-	EXPRESSION TAG	UNP P55055
A	201	HIS	-	EXPRESSION TAG	UNP P55055
A	202	HIS	-	EXPRESSION TAG	UNP P55055
A	203	HIS	-	EXPRESSION TAG	UNP P55055
A	204	HIS	-	EXPRESSION TAG	UNP P55055
A	205	GLY	-	EXPRESSION TAG	UNP P55055
A	206	GLU	-	EXPRESSION TAG	UNP P55055
A	207	ASN	-	EXPRESSION TAG	UNP P55055
A	208	LEU	-	EXPRESSION TAG	UNP P55055
A	209	TYR	-	EXPRESSION TAG	UNP P55055
A	210	PHE	-	EXPRESSION TAG	UNP P55055
A	211	GLN	-	EXPRESSION TAG	UNP P55055
A	212	GLY	-	EXPRESSION TAG	UNP P55055
A	213	SER	-	EXPRESSION TAG	UNP P55055
B	198	MET	-	EXPRESSION TAG	UNP P55055
B	199	HIS	-	EXPRESSION TAG	UNP P55055
B	200	HIS	-	EXPRESSION TAG	UNP P55055
B	201	HIS	-	EXPRESSION TAG	UNP P55055
B	202	HIS	-	EXPRESSION TAG	UNP P55055
B	203	HIS	-	EXPRESSION TAG	UNP P55055
B	204	HIS	-	EXPRESSION TAG	UNP P55055
B	205	GLY	-	EXPRESSION TAG	UNP P55055
B	206	GLU	-	EXPRESSION TAG	UNP P55055

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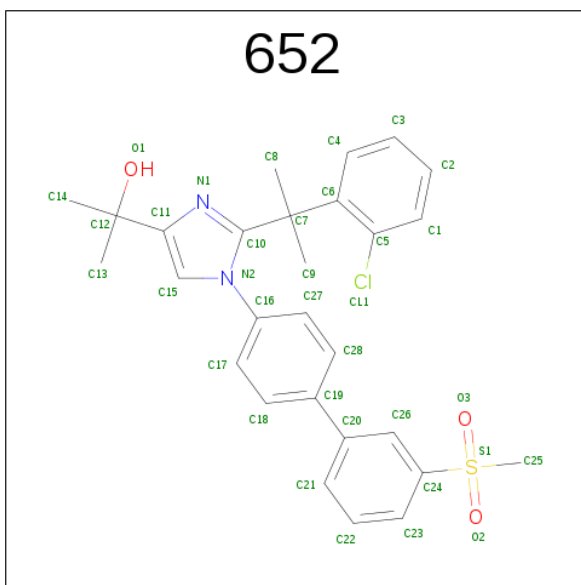
Chain	Residue	Modelled	Actual	Comment	Reference
B	207	ASN	-	EXPRESSION TAG	UNP P55055
B	208	LEU	-	EXPRESSION TAG	UNP P55055
B	209	TYR	-	EXPRESSION TAG	UNP P55055
B	210	PHE	-	EXPRESSION TAG	UNP P55055
B	211	GLN	-	EXPRESSION TAG	UNP P55055
B	212	GLY	-	EXPRESSION TAG	UNP P55055
B	213	SER	-	EXPRESSION TAG	UNP P55055

- Molecule 2 is 1,4-BUTANEDIOL (three-letter code: BU1) (formula: C₄H₁₀O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			6	4	2		
2	A	1	Total	C	O	0	0
			6	4	2		
2	B	1	Total	C	O	0	0
			6	4	2		

- Molecule 3 is 2-{2-[2-(2-CHLOROPHENYL)PROPAN-2-YL]-1-[3'-(METHYLSULFONYL)BIPHENYL-4-YL]-1H-IMIDAZOL-4-YL}PROPAN-2-OL (three-letter code: 652) (formula: C₂₈H₂₉ClN₂O₃S).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	Cl	N	O	S	0	0
			35	28	1	2	3	1		
3	B	1	Total	C	Cl	N	O	S	0	0
			35	28	1	2	3	1		

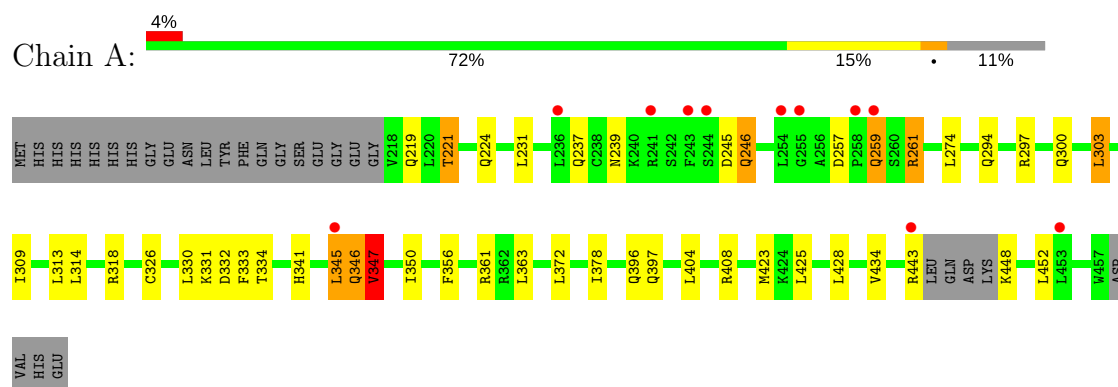
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	90	Total	O	0	0
			90	90		
4	B	93	Total	O	0	0
			93	93		

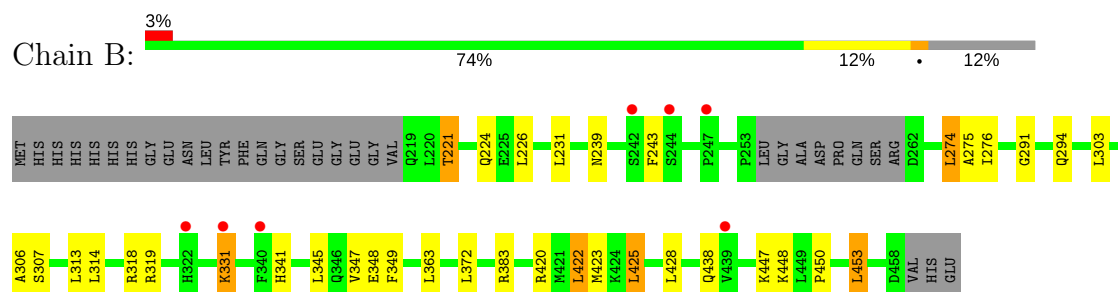
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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: Oxysterols receptor LXR-beta



• Molecule 1: Oxysterols receptor LXR-beta



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.82Å 120.63Å 176.25Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	53.21 – 2.04 88.12 – 2.04	Depositor EDS
% Data completeness (in resolution range)	99.7 (53.21-2.04) 99.6 (88.12-2.04)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.38 (at 2.03Å)	Xtriage
Refinement program	REFMAC 5.8.0049	Depositor
R, R_{free}	0.229 , 0.271 0.233 , 0.279	Depositor DCC
R_{free} test set	1921 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	40.8	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 72.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4115	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.06% 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: BU1, 652

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	0.51	0/1963	0.66	1/2655 (0.0%)
1	B	0.51	0/1968	0.66	0/2661
All	All	0.51	0/3931	0.66	1/5316 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	257	ASP	C-N-CD	5.13	139.18	128.40

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	1922	0	1945	24	1
1	B	1922	0	1954	19	0
2	A	12	0	20	3	0
2	B	6	0	10	0	0
3	A	35	0	29	0	0
3	B	35	0	29	2	0
4	A	90	0	0	2	0
4	B	93	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	4115	0	3987	43	1

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 5.

All (43) 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:341:HIS:HE1	1:A:347:VAL:HG21	1.05	1.15
1:A:341:HIS:HE1	1:A:347:VAL:CG2	1.58	1.14
1:A:341:HIS:CE1	1:A:347:VAL:CG2	2.32	1.12
1:A:346:GLN:NE2	4:A:609:HOH:O	1.80	1.10
1:A:341:HIS:CE1	1:A:347:VAL:HG23	1.90	1.06
1:A:341:HIS:CE1	1:A:347:VAL:HG21	1.97	0.95
1:B:306:ALA:HB3	1:B:383[B]:ARG:HD3	1.50	0.93
2:A:502:BU1:H21	1:B:420:ARG:HG2	1.50	0.93
1:A:331:LYS:HE3	4:A:615:HOH:O	1.89	0.73
1:A:345:LEU:CB	1:A:350:ILE:HD11	2.27	0.64
1:A:346:GLN:O	1:A:347:VAL:HG12	2.05	0.57
1:A:261:ARG:CG	1:A:261:ARG:HH11	2.18	0.56
1:A:345:LEU:HB3	1:A:350:ILE:HD11	1.86	0.56
1:A:239:ASN:HD21	1:A:318:ARG:HH22	1.53	0.55
1:B:274:LEU:HG	3:B:502:652:H1	1.88	0.54
1:A:396:GLN:OE1	2:A:502:BU1:H11	2.08	0.53
1:A:221:THR:HG22	1:A:224:GLN:H	1.75	0.52
1:A:347:VAL:HA	1:A:350:ILE:HB	1.93	0.51
1:B:221:THR:HG22	1:B:224:GLN:H	1.75	0.51
1:B:349:PHE:HB2	1:B:438:GLN:HG2	1.91	0.51
1:B:307:SER:HB3	1:B:383[B]:ARG:CZ	2.40	0.50
1:A:246:GLN:HG3	1:A:333:PHE:CZ	2.47	0.49
1:B:221:THR:H	1:B:224:GLN:HE21	1.58	0.49
1:B:274:LEU:HG	3:B:502:652:C25	2.42	0.49
1:B:275:ALA:HB3	1:B:453:LEU:HD21	1.96	0.48
1:A:297:ARG:HH11	1:A:300:GLN:HE22	1.63	0.46
1:B:348:GLU:HB2	4:B:648:HOH:O	2.16	0.46
1:B:341:HIS:CE1	1:B:347:VAL:HG12	2.51	0.45
1:A:345:LEU:HB2	1:A:350:ILE:HD11	1.98	0.45
1:B:243:PHE:CE1	1:B:331:LYS:HB2	2.52	0.44
1:B:422:LEU:O	1:B:425:LEU:HB2	2.18	0.44
1:A:259:GLN:HG3	1:A:259:GLN:O	2.18	0.43
1:B:306:ALA:CB	1:B:383[B]:ARG:HD3	2.35	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:276:ILE:HD11	1:B:450:PRO:HG3	1.99	0.43
1:A:261:ARG:HH11	1:A:261:ARG:HG3	1.83	0.42
1:A:326:CYS:HB3	1:A:334:THR:HG22	2.01	0.42
1:B:291:GLY:O	1:B:294:GLN:HG2	2.20	0.42
1:A:356:PHE:CZ	1:A:428:LEU:HD13	2.55	0.41
1:B:243:PHE:CZ	1:B:331:LYS:HD2	2.56	0.41
1:A:303:LEU:HG	1:A:378:ILE:O	2.21	0.41
1:A:397:GLN:HE22	2:A:502:BU1:H12	1.87	0.40
1:B:307:SER:HB3	1:B:383[B]:ARG:NH2	2.36	0.40
1:B:239:ASN:ND2	1:B:318:ARG:HH22	2.20	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:346:GLN:OE1	1:A:346:GLN:OE1[8_554]	1.97	0.23

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	233/264 (88%)	229 (98%)	3 (1%)	1 (0%)	38	27
1	B	232/264 (88%)	227 (98%)	5 (2%)	0	100	100
All	All	465/528 (88%)	456 (98%)	8 (2%)	1 (0%)	51	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	347	VAL

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	209/233 (90%)	179 (86%)	30 (14%)	4	1
1	B	210/233 (90%)	191 (91%)	19 (9%)	11	5
All	All	419/466 (90%)	370 (88%)	49 (12%)	6	2

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	219	GLN
1	A	221	THR
1	A	231	LEU
1	A	237	GLN
1	A	245	ASP
1	A	246	GLN
1	A	259	GLN
1	A	261	ARG
1	A	274	LEU
1	A	294	GLN
1	A	303	LEU
1	A	309	ILE
1	A	313	LEU
1	A	314	LEU
1	A	330	LEU
1	A	332	ASP
1	A	345	LEU
1	A	346	GLN
1	A	347	VAL
1	A	361	ARG
1	A	363	LEU
1	A	372	LEU
1	A	404	LEU
1	A	408	ARG
1	A	423	MET
1	A	425	LEU
1	A	434	VAL

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Mol	Chain	Res	Type
1	A	443	ARG
1	A	448	LYS
1	A	452	LEU
1	B	221	THR
1	B	226	LEU
1	B	231	LEU
1	B	274	LEU
1	B	303	LEU
1	B	313	LEU
1	B	314	LEU
1	B	319	ARG
1	B	331	LYS
1	B	345	LEU
1	B	363	LEU
1	B	372	LEU
1	B	422	LEU
1	B	423	MET
1	B	425	LEU
1	B	428	LEU
1	B	447	LYS
1	B	448	LYS
1	B	453	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	224	GLN
1	A	239	ASN
1	A	300	GLN
1	A	341	HIS
1	A	397	GLN
1	B	224	GLN
1	B	239	ASN
1	B	280	GLN
1	B	300	GLN
1	B	351	ASN
1	B	435	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

5 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	BU1	A	501	-	5,5,5	0.35	0	4,4,4	0.43	0
2	BU1	A	502	-	5,5,5	0.38	0	4,4,4	0.26	0
3	652	A	503	-	35,38,38	2.18	5 (14%)	48,59,59	1.76	4 (8%)
2	BU1	B	501	-	5,5,5	0.30	0	4,4,4	0.58	0
3	652	B	502	-	35,38,38	2.16	6 (17%)	48,59,59	1.71	7 (14%)

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	BU1	A	501	-	-	0/3/3/3	0/0/0/0
2	BU1	A	502	-	-	0/3/3/3	0/0/0/0
3	652	A	503	-	-	0/26/32/32	0/4/4/4
2	BU1	B	501	-	-	0/3/3/3	0/0/0/0
3	652	B	502	-	-	0/26/32/32	0/4/4/4

All (11) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	502	652	O1-C12	-3.41	1.39	1.44
3	A	503	652	O1-C12	-2.63	1.40	1.44
3	B	502	652	C5-CL1	2.09	1.78	1.73
3	B	502	652	C16-N2	2.54	1.47	1.44
3	A	503	652	C5-CL1	2.63	1.79	1.73
3	A	503	652	C24-S1	4.28	1.81	1.77
3	B	502	652	C24-S1	4.88	1.82	1.77
3	B	502	652	O3-S1	6.97	1.64	1.43
3	B	502	652	O2-S1	6.99	1.64	1.43
3	A	503	652	O2-S1	7.41	1.65	1.43
3	A	503	652	O3-S1	7.46	1.66	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	503	652	O2-S1-O3	-5.11	108.44	117.84
3	B	502	652	O2-S1-O3	-4.00	110.48	117.84
3	B	502	652	C8-C7-C10	-2.63	106.08	110.57
3	B	502	652	C9-C7-C8	-2.22	105.02	107.57
3	A	503	652	C8-C7-C10	-2.00	107.15	110.57
3	B	502	652	C6-C7-C10	2.08	114.54	108.81
3	B	502	652	C4-C6-C5	2.13	119.15	116.66
3	A	503	652	C25-S1-C24	5.88	111.58	104.58
3	B	502	652	C10-N1-C11	6.00	109.33	101.33
3	A	503	652	C10-N1-C11	6.11	109.48	101.33
3	B	502	652	C25-S1-C24	6.41	112.22	104.58

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	502	BU1	3	0
3	B	502	652	2	0

5.7 Other polymers [i](#)

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 [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	236/264 (89%)	0.43	11 (4%) 32 35	30, 55, 96, 118	0
1	B	232/264 (87%)	0.29	7 (3%) 51 56	31, 52, 84, 99	0
All	All	468/528 (88%)	0.36	18 (3%) 41 45	30, 53, 91, 118	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	439	VAL	8.3
1	A	255	GLY	3.9
1	A	453	LEU	3.8
1	A	241	ARG	3.3
1	A	243	PHE	3.2
1	A	443	ARG	3.1
1	B	244	SER	3.1
1	A	259	GLN	3.1
1	A	244	SER	2.9
1	A	258	PRO	2.8
1	A	345	LEU	2.7
1	A	236	LEU	2.4
1	B	247	PRO	2.4
1	B	340	PHE	2.3
1	A	254	LEU	2.1
1	B	242	SER	2.1
1	B	322	HIS	2.1
1	B	331	LYS	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(\AA^2)	Q<0.9
2	BU1	A	502	6/6	0.66	0.89	39.24	88,91,95,99	0
2	BU1	B	501	6/6	0.86	0.22	7.15	61,63,66,69	0
2	BU1	A	501	6/6	0.85	0.18	2.47	60,62,66,67	0
3	652	B	502	35/35	0.96	0.14	-0.24	41,46,57,58	0
3	652	A	503	35/35	0.95	0.13	-0.68	46,62,65,68	0

6.5 Other polymers [i](#)

There are no such residues in this entry.