



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 01:42 PM UTC

PDB ID : 3AQT / pdb_00003aqt
Title : CRYSTAL STRUCTURE OF RoIR (NCGL1110) complex WITH ligand RE-SORCINOL
Authors : Li, D.F.; Zhang, N.; Hou, Y.J.; Liu, S.J.; Wang, D.C.
Deposited on : 2010-11-18
Resolution : 2.50 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
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

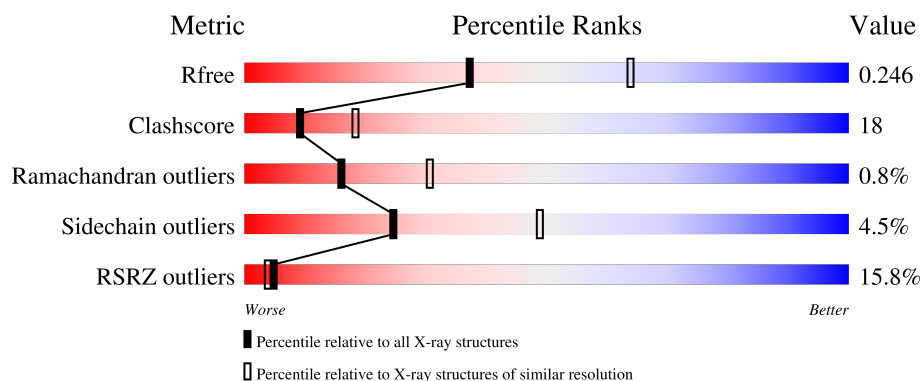
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	245	11% 57% 21% • 20%
1	B	245	14% 53% 24% • 20%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 3190 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 Bacterial regulatory proteins, tetR family.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	195	Total	C	N	O	S	Se	8	0	0
			1505	942	273	283	1	6			
1	B	196	Total	C	N	O	S	Se	8	0	0
			1510	945	274	284	1	6			

There are 32 discrepancies between the modelled and reference sequences:

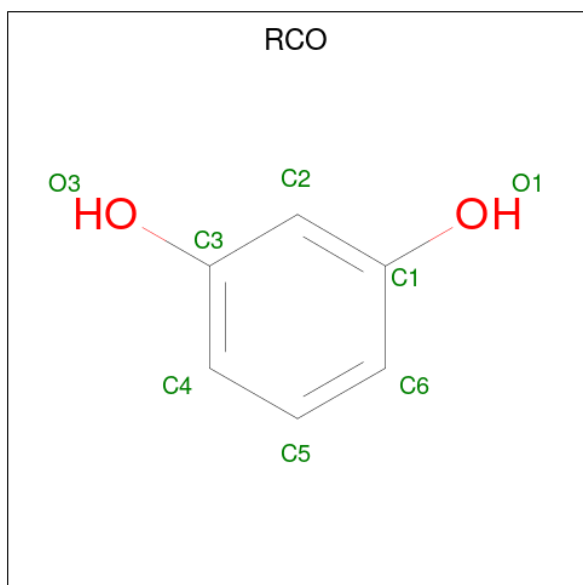
Chain	Residue	Modelled	Actual	Comment	Reference
A	-15	HIS	-	expression tag	UNP Q8NR95
A	-14	HIS	-	expression tag	UNP Q8NR95
A	-13	HIS	-	expression tag	UNP Q8NR95
A	-12	HIS	-	expression tag	UNP Q8NR95
A	-11	HIS	-	expression tag	UNP Q8NR95
A	-10	HIS	-	expression tag	UNP Q8NR95
A	-9	SER	-	expression tag	UNP Q8NR95
A	-8	SER	-	expression tag	UNP Q8NR95
A	-7	GLY	-	expression tag	UNP Q8NR95
A	-6	LEU	-	expression tag	UNP Q8NR95
A	-5	VAL	-	expression tag	UNP Q8NR95
A	-4	PRO	-	expression tag	UNP Q8NR95
A	-3	ARG	-	expression tag	UNP Q8NR95
A	-2	GLY	-	expression tag	UNP Q8NR95
A	-1	SER	-	expression tag	UNP Q8NR95
A	0	HIS	-	expression tag	UNP Q8NR95
B	-15	HIS	-	expression tag	UNP Q8NR95
B	-14	HIS	-	expression tag	UNP Q8NR95
B	-13	HIS	-	expression tag	UNP Q8NR95
B	-12	HIS	-	expression tag	UNP Q8NR95
B	-11	HIS	-	expression tag	UNP Q8NR95
B	-10	HIS	-	expression tag	UNP Q8NR95
B	-9	SER	-	expression tag	UNP Q8NR95
B	-8	SER	-	expression tag	UNP Q8NR95
B	-7	GLY	-	expression tag	UNP Q8NR95

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-6	LEU	-	expression tag	UNP Q8NR95
B	-5	VAL	-	expression tag	UNP Q8NR95
B	-4	PRO	-	expression tag	UNP Q8NR95
B	-3	ARG	-	expression tag	UNP Q8NR95
B	-2	GLY	-	expression tag	UNP Q8NR95
B	-1	SER	-	expression tag	UNP Q8NR95
B	0	HIS	-	expression tag	UNP Q8NR95

- Molecule 2 is RESORCINOL (CCD ID: RCO) (formula: $C_6H_6O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		
2	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	71	Total	O	0	0
			71	71		
3	B	88	Total	O	0	0
			88	88		

4 Data and refinement statistics

Property	Value	Source
Space group	I 2 3	Depositor
Cell constants a, b, c, α , β , γ	167.12Å 167.12Å 167.12Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 2.50 50.00 – 2.50	Depositor EDS
% Data completeness (in resolution range)	94.7 (50.00-2.50) 96.1 (50.00-2.50)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.26 (at 2.51Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.212 , 0.245 (Not available) , 0.246	Depositor DCC
R_{free} test set	1256 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	41.5	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 29.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.023 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	3190	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% 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: RCO

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	0/1520	0.81	2/2042 (0.1%)
1	B	0.43	0/1525	0.82	4/2049 (0.2%)
All	All	0.43	0/3045	0.81	6/4091 (0.1%)

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	141	ILE	N-CA-C	6.24	117.25	111.45
1	A	173	GLY	N-CA-C	-6.17	105.35	112.50
1	B	69	ASN	N-CA-C	-5.29	106.87	113.38
1	B	100	LEU	N-CA-C	-5.27	101.69	110.17
1	A	69	ASN	N-CA-C	-5.24	106.66	113.16
1	B	46	ARG	N-CA-C	5.03	120.26	113.72

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	1505	0	1509	42	0
1	B	1510	0	1514	69	0
2	A	8	0	6	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	8	0	6	0	0
3	A	71	0	0	0	0
3	B	88	0	0	0	0
All	All	3190	0	3035	110	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 18.

All (110) 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:24:ARG:HG2	1:A:25:ALA:H	1.24	1.01
1:A:161:ILE:HD11	1:A:205:VAL:HG12	1.42	0.98
1:B:175:LEU:O	1:B:179:ILE:HD13	1.70	0.92
1:B:139:MSE:HA	1:B:139:MSE:HE2	1.55	0.88
1:B:36:ILE:HD13	1:B:77:LEU:HD12	1.59	0.84
1:A:164:LEU:O	1:A:168:THR:HG22	1.78	0.84
1:B:129:ILE:HG13	1:B:130:GLN:H	1.47	0.79
1:A:139:MSE:HE1	1:A:172:PHE:HB2	1.66	0.77
1:B:215:ILE:HD13	1:B:218:ARG:NH2	2.01	0.75
1:B:215:ILE:HD13	1:B:218:ARG:CZ	2.21	0.71
1:A:161:ILE:HD11	1:A:205:VAL:CG1	2.20	0.71
1:B:139:MSE:HE3	1:B:172:PHE:CD2	2.27	0.69
1:B:129:ILE:HG13	1:B:130:GLN:N	2.09	0.67
1:B:139:MSE:HA	1:B:139:MSE:CE	2.23	0.67
1:A:195:GLN:NE2	1:A:213:ARG:HH21	1.92	0.66
1:A:195:GLN:HE21	1:A:213:ARG:HH21	1.42	0.65
1:B:133:ALA:C	1:B:136:PRO:HD2	2.22	0.64
1:B:135:HIS:HB3	1:B:136:PRO:HD3	1.79	0.64
1:B:124:TRP:HA	1:B:127:PHE:CD2	2.33	0.64
1:A:24:ARG:HG2	1:A:25:ALA:N	2.04	0.63
1:A:151:LEU:O	1:A:155:GLU:HG2	1.99	0.63
1:B:36:ILE:HD13	1:B:77:LEU:CD1	2.27	0.63
1:B:43:MSE:HB3	1:B:123:ILE:CD1	2.30	0.62
1:A:135:HIS:CE1	1:A:139:MSE:HE3	2.34	0.62
1:A:133:ALA:C	1:A:136:PRO:HD2	2.27	0.59
1:B:24:ARG:HG2	1:B:25:ALA:N	2.17	0.59
1:B:133:ALA:O	1:B:136:PRO:HD2	2.03	0.59
1:B:36:ILE:CD1	1:B:77:LEU:HD12	2.32	0.58
1:A:100:LEU:HD13	1:A:105:GLU:HG2	1.85	0.57
1:A:28:ARG:HH12	1:A:32:ARG:HD2	1.68	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:53:ILE:HD11	1:A:74:ARG:HB2	1.87	0.56
1:B:36:ILE:HD12	1:B:80:ALA:HB3	1.87	0.56
1:B:171:THR:HA	1:B:201:MSE:CE	2.36	0.55
1:A:135:HIS:NE2	1:A:139:MSE:HE3	2.21	0.55
1:B:46:ARG:NH2	1:B:55:GLU:CD	2.64	0.55
1:B:99:LYS:CD	1:B:99:LYS:N	2.70	0.55
1:A:161:ILE:CD1	1:A:205:VAL:HG12	2.25	0.54
1:B:139:MSE:HE1	1:B:168:THR:HG22	1.89	0.54
1:B:203:ARG:HD3	1:B:209:ALA:HA	1.89	0.54
1:B:112:ARG:O	1:B:116:ARG:HG3	2.09	0.53
1:B:131:MSE:HE3	1:B:134:ALA:HA	1.91	0.53
1:B:195:GLN:HG2	1:B:216:ALA:O	2.09	0.52
1:B:43:MSE:CB	1:B:123:ILE:CD1	2.87	0.52
1:B:139:MSE:CE	1:B:172:PHE:CD2	2.92	0.52
1:B:115:VAL:HG22	1:B:179:ILE:HD11	1.91	0.52
1:B:28:ARG:NH1	1:B:70:TYR:HA	2.24	0.52
1:B:127:PHE:O	1:B:131:MSE:HB3	2.10	0.52
1:A:160:THR:HG21	1:B:209:ALA:HB1	1.92	0.52
1:B:91:ILE:O	1:B:95:GLN:HG2	2.11	0.51
1:A:117:HIS:HD2	1:A:121:ASP:OD2	1.94	0.51
1:B:124:TRP:HA	1:B:127:PHE:HD2	1.75	0.50
1:A:133:ALA:O	1:A:136:PRO:HD2	2.11	0.50
1:B:125:GLY:O	1:B:129:ILE:HG12	2.12	0.50
1:A:147:ARG:NH1	1:A:164:LEU:HD23	2.27	0.49
1:A:153:GLY:HA3	1:A:159:PHE:CE2	2.47	0.49
1:B:43:MSE:HG2	1:B:48:VAL:HA	1.94	0.49
1:B:66:THR:O	1:B:69:ASN:HB2	2.12	0.49
1:B:24:ARG:HG2	1:B:25:ALA:H	1.75	0.48
1:B:53:ILE:HD13	1:B:67:PHE:CB	2.43	0.48
1:B:129:ILE:HD12	1:B:130:GLN:NE2	2.28	0.48
1:B:46:ARG:NH2	1:B:55:GLU:OE1	2.46	0.48
1:A:124:TRP:HA	1:A:127:PHE:CD2	2.48	0.48
1:B:171:THR:HA	1:B:201:MSE:HE2	1.95	0.48
1:A:54:ALA:HB3	1:A:55:GLU:OE1	2.13	0.47
1:A:139:MSE:HE1	1:A:172:PHE:CB	2.42	0.47
1:B:136:PRO:O	1:B:140:ARG:HG3	2.13	0.47
1:B:171:THR:HG23	1:B:201:MSE:HE2	1.97	0.47
1:B:67:PHE:C	1:B:69:ASN:H	2.22	0.47
1:B:36:ILE:CD1	1:B:80:ALA:HB3	2.45	0.47
1:A:91:ILE:HD13	1:A:145:ARG:HH21	1.79	0.46
1:A:123:ILE:HG12	1:A:127:PHE:CZ	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:ARG:NH1	1:A:32:ARG:HD2	2.31	0.46
1:A:92:ALA:HB1	1:A:223:ILE:HG12	1.97	0.46
1:A:223:ILE:O	1:A:224:SER:HB2	2.16	0.46
1:B:151:LEU:O	1:B:155:GLU:HG2	2.16	0.46
1:A:208:GLN:HB3	1:A:211:GLU:HG2	1.98	0.45
1:B:153:GLY:HA3	1:B:159:PHE:CD2	2.51	0.45
1:A:220:LEU:HD12	1:A:221:PRO:HD2	1.97	0.45
1:A:24:ARG:C	1:A:26:GLN:H	2.23	0.45
1:A:45:GLU:HG3	1:A:46:ARG:HG3	1.98	0.45
1:B:53:ILE:HD12	1:B:53:ILE:O	2.16	0.45
1:B:116:ARG:NH2	1:B:220:LEU:HD23	2.32	0.45
1:B:24:ARG:HG2	1:B:26:GLN:H	1.81	0.45
1:B:129:ILE:CG1	1:B:130:GLN:H	2.25	0.44
1:B:41:THR:O	1:B:45:GLU:HG3	2.18	0.44
1:A:215:ILE:O	1:A:218:ARG:HG3	2.18	0.43
1:B:129:ILE:HD12	1:B:130:GLN:HE22	1.82	0.43
1:A:93:LEU:CD2	1:A:223:ILE:HD12	2.48	0.43
1:A:116:ARG:NH1	1:A:220:LEU:HD23	2.33	0.43
1:B:220:LEU:HA	1:B:221:PRO:HD3	1.85	0.43
1:A:97:LEU:O	1:A:106:VAL:HG22	2.18	0.43
1:A:161:ILE:HD11	1:A:205:VAL:CB	2.48	0.42
1:B:43:MSE:HB3	1:B:123:ILE:HD12	2.01	0.42
1:B:179:ILE:CD1	1:B:179:ILE:N	2.82	0.42
1:A:135:HIS:HB3	1:A:136:PRO:HD3	2.00	0.41
1:B:97:LEU:O	1:B:99:LYS:N	2.53	0.41
1:B:215:ILE:CD1	1:B:218:ARG:NH2	2.79	0.41
1:B:179:ILE:N	1:B:179:ILE:HD12	2.35	0.41
1:B:31:THR:HG21	1:B:70:TYR:CE2	2.55	0.41
1:B:69:ASN:HD22	1:B:69:ASN:HA	1.60	0.41
1:B:113:HIS:CE1	1:B:223:ILE:HB	2.54	0.41
1:B:48:VAL:HG12	1:B:123:ILE:CD1	2.50	0.41
1:A:25:ALA:O	1:A:28:ARG:HB3	2.20	0.41
1:A:53:ILE:HD12	1:A:74:ARG:HD2	2.02	0.41
1:B:99:LYS:N	1:B:99:LYS:HD2	2.35	0.41
1:A:164:LEU:HD12	1:A:164:LEU:HA	1.95	0.41
1:B:129:ILE:CG1	1:B:130:GLN:N	2.81	0.41
1:B:139:MSE:HE2	1:B:143:GLY:HA3	2.02	0.41
1:B:31:THR:HG21	1:B:70:TYR:CZ	2.56	0.40
1:B:46:ARG:NH2	1:B:55:GLU:OE2	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	191/245 (78%)	184 (96%)	6 (3%)	1 (0%)	24	43
1	B	192/245 (78%)	183 (95%)	7 (4%)	2 (1%)	12	24
All	All	383/490 (78%)	367 (96%)	13 (3%)	3 (1%)	16	31

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	68	TYR
1	B	98	THR
1	A	96	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	154/191 (81%)	149 (97%)	5 (3%)	34	62
1	B	154/191 (81%)	145 (94%)	9 (6%)	18	38
All	All	308/382 (81%)	294 (96%)	14 (4%)	24	49

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	78	LEU
1	A	117	HIS

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Mol	Chain	Res	Type
1	A	168	THR
1	A	218	ARG
1	B	53	ILE
1	B	69	ASN
1	B	76	GLN
1	B	78	LEU
1	B	99	LYS
1	B	117	HIS
1	B	139	MSE
1	B	179	ILE
1	B	215	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	30	GLN
1	A	79	GLN
1	A	117	HIS
1	A	180	GLN
1	A	195	GLN
1	A	208	GLN
1	B	69	ASN
1	B	130	GLN
1	B	180	GLN

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

2 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	RCO	A	230	-	8,8,8	1.80	3 (37%)	10,10,10	0.59	0
2	RCO	B	230	-	8,8,8	1.74	3 (37%)	10,10,10	0.50	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	RCO	A	230	-	-	-	0/1/1/1
2	RCO	B	230	-	-	-	0/1/1/1

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	230	RCO	C2-C1	2.88	1.43	1.39
2	A	230	RCO	C2-C1	2.46	1.42	1.39
2	A	230	RCO	C2-C3	2.40	1.42	1.39
2	B	230	RCO	C2-C3	2.34	1.42	1.39
2	A	230	RCO	C5-C6	2.13	1.42	1.38
2	B	230	RCO	C5-C6	2.11	1.42	1.38

There are no bond angle outliers.

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 [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	189/245 (77%)	0.91	26 (13%) 6 5	27, 42, 72, 99	2 (1%)
1	B	190/245 (77%)	0.97	34 (17%) 3 3	29, 42, 68, 102	2 (1%)
All	All	379/490 (77%)	0.94	60 (15%) 5 4	27, 42, 71, 102	4 (1%)

All (60) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	191	ASP	6.6
1	B	222	GLU	5.2
1	B	98	THR	5.0
1	B	24	ARG	5.0
1	A	223	ILE	4.9
1	A	192	ASP	4.8
1	B	26	GLN	4.8
1	A	25	ALA	4.8
1	B	130	GLN	4.8
1	B	223	ILE	4.7
1	A	26	GLN	4.6
1	B	123	ILE	4.5
1	A	224	SER	4.5
1	B	191	ASP	4.4
1	A	24	ARG	4.4
1	A	161	ILE	4.0
1	A	99	LYS	3.7
1	B	28	ARG	3.7
1	B	129	ILE	3.7
1	B	65	GLY	3.6
1	B	121	ASP	3.3
1	B	27	LYS	3.3
1	B	224	SER	3.2
1	B	192	ASP	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	97	LEU	3.1
1	B	29	GLU	3.1
1	B	64	THR	3.0
1	B	185	ALA	3.0
1	A	130	GLN	3.0
1	B	25	ALA	3.0
1	B	208	GLN	2.9
1	A	184	SER	2.8
1	A	129	ILE	2.7
1	A	27	LYS	2.6
1	B	53	ILE	2.6
1	B	221	PRO	2.6
1	A	160	THR	2.6
1	B	76	GLN	2.6
1	B	120	GLU	2.5
1	A	28	ARG	2.5
1	A	206	GLY	2.4
1	B	36	ILE	2.4
1	A	97	LEU	2.4
1	B	96	VAL	2.3
1	A	221	PRO	2.3
1	A	49	ASP	2.3
1	B	210	ALA	2.3
1	A	133	ALA	2.3
1	A	98	THR	2.3
1	A	95	GLN	2.2
1	B	99	LYS	2.2
1	A	125	GLY	2.2
1	B	63	GLY	2.2
1	B	49	ASP	2.1
1	B	100	LEU	2.1
1	A	46	ARG	2.1
1	A	72	PRO	2.1
1	B	127	PHE	2.1
1	A	208	GLN	2.1
1	B	119	LEU	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
2	RCO	A	230	8/8	0.92	0.13	43,44,45,45	0
2	RCO	B	230	8/8	0.96	0.08	36,36,37,40	0

6.5 Other polymers [i](#)

There are no such residues in this entry.