



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 04:53 AM UTC

PDB ID : 5VVI / pdb_00005vvi
Title : Crystal Structure of the Ligand Binding Domain of LysR-type Transcriptional Regulator, OccR from Agrobacterium tumefaciens in the Complex with Octopine
Authors : Kim, Y.; Chhor, G.; Jedrzejczak, R.; Winans, S.C.; Joachimiak, A.; Midwest Center for Structural Genomics (MCSG)
Deposited on : 2017-05-19
Resolution : 2.28 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

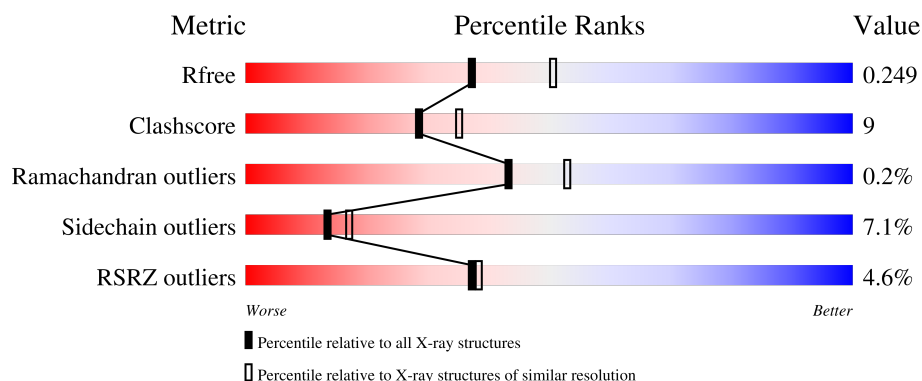
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.28 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	9078 (2.30-2.26)
Clashscore	190562	9802 (2.30-2.26)
Ramachandran outliers	187476	9690 (2.30-2.26)
Sidechain outliers	187428	9691 (2.30-2.26)
RSRZ outliers	180081	9085 (2.30-2.26)

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	210	6% 80% 17% ..
1	B	210	6% 73% 21% ..
1	C	210	6% 74% 20% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 4933 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.

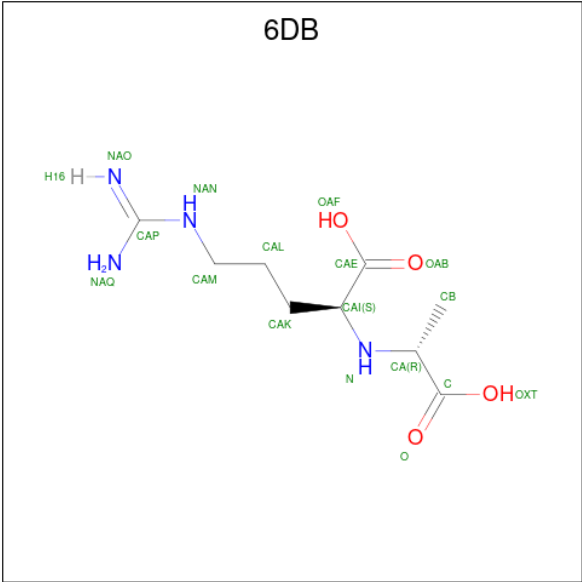
- Molecule 1 is a protein called Octopine catabolism/uptake operon regulatory protein OccR.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	208	Total	C	N	O	Se	0	4	0
			1634	1034	297	294	9			
1	B	203	Total	C	N	O	Se	0	2	0
			1569	995	280	286	8			
1	C	204	Total	C	N	O	Se	0	1	0
			1568	995	281	284	8			

There are 12 discrepancies between the modelled and reference sequences:

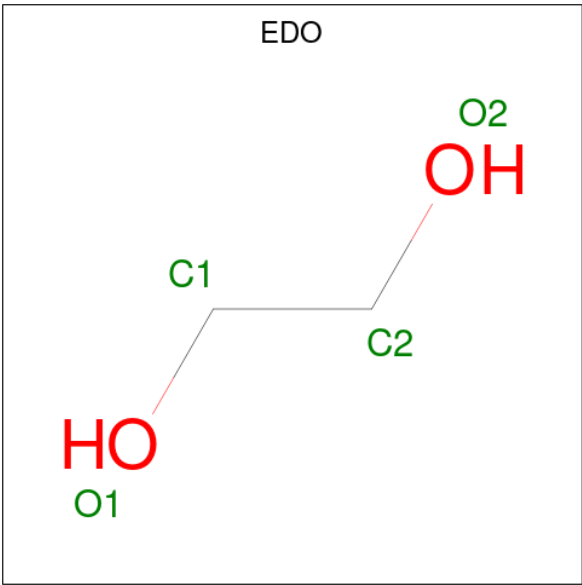
Chain	Residue	Modelled	Actual	Comment	Reference
A	89	SER	-	expression tag	UNP P0A4T4
A	90	ASN	-	expression tag	UNP P0A4T4
A	91	ALA	-	expression tag	UNP P0A4T4
A	261	GLU	GLY	conflict	UNP P0A4T4
B	89	SER	-	expression tag	UNP P0A4T4
B	90	ASN	-	expression tag	UNP P0A4T4
B	91	ALA	-	expression tag	UNP P0A4T4
B	261	GLU	GLY	conflict	UNP P0A4T4
C	89	SER	-	expression tag	UNP P0A4T4
C	90	ASN	-	expression tag	UNP P0A4T4
C	91	ALA	-	expression tag	UNP P0A4T4
C	261	GLU	GLY	conflict	UNP P0A4T4

- Molecule 2 is octopine (CCD ID: 6DB) (formula: $C_9H_{18}N_4O_4$).



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

- Molecule 3 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



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

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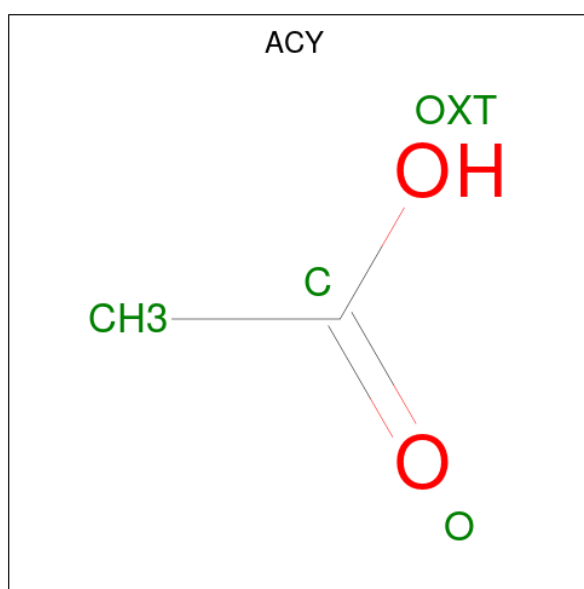
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Cl	0	0
			1	1		

- Molecule 5 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	C	1	Total	C	O	0	0
			4	2	2		

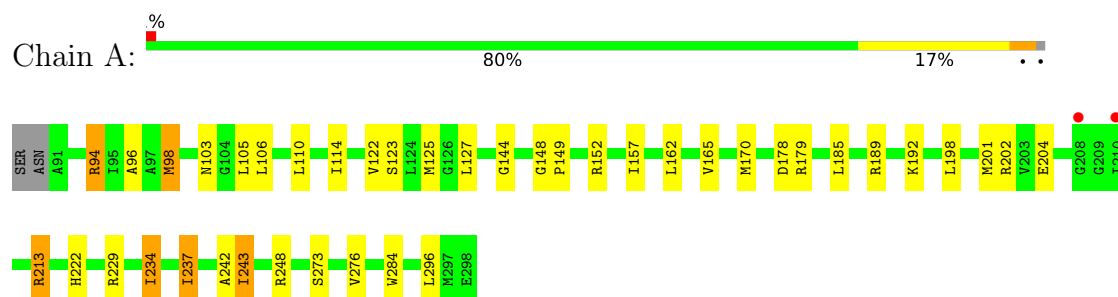
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	42	Total	O	0	0
			42	42		
6	B	36	Total	O	0	0
			36	36		
6	C	20	Total	O	0	0
			20	20		

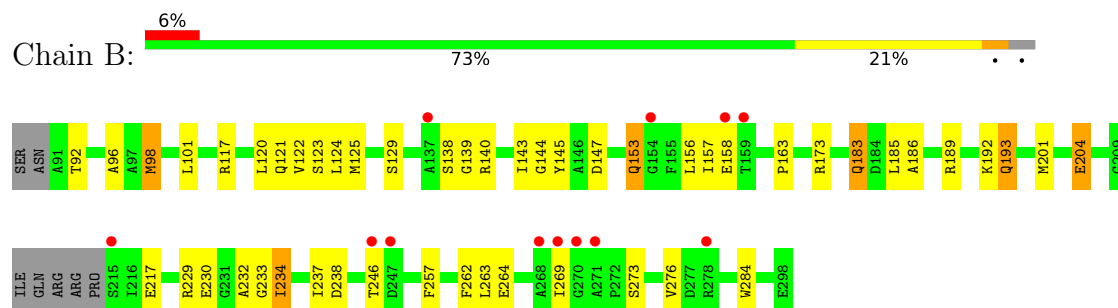
3 Residue-property plots

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.

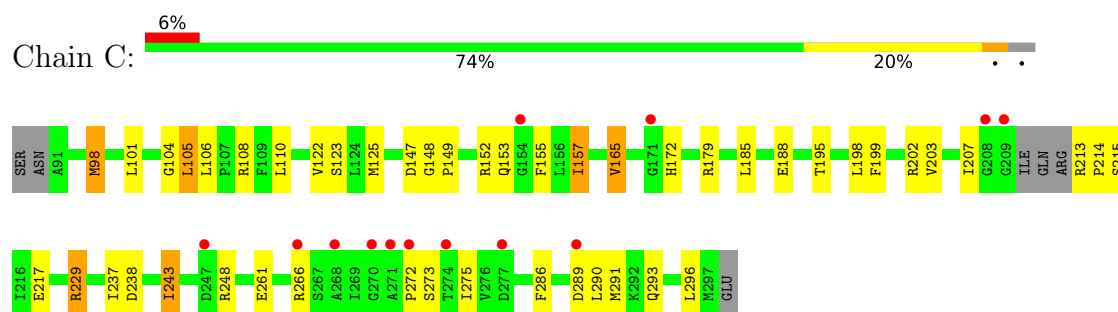
- Molecule 1: Octopine catabolism/uptake operon regulatory protein OccR



- Molecule 1: Octopine catabolism/uptake operon regulatory protein OccR



- Molecule 1: Octopine catabolism/uptake operon regulatory protein OccR



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	58.42Å 101.98Å 112.71Å 90.00° 98.14° 90.00°	Depositor
Resolution (Å)	31.84 – 2.28 31.84 – 2.28	Depositor EDS
% Data completeness (in resolution range)	89.0 (31.84-2.28) 89.1 (31.84-2.28)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.76 (at 2.27Å)	Xtriage
Refinement program	PHENIX DEV_1839	Depositor
R, R_{free}	0.192 , 0.249 0.193 , 0.249	Depositor DCC
R_{free} test set	1414 reflections (4.72%)	wwPDB-VP
Wilson B-factor (Å ²)	29.6	Xtriage
Anisotropy	0.081	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 40.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4933	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.77% 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: 6DB, ACY, EDO, CL

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	0.65	0/1655	0.88	2/2226 (0.1%)
1	B	0.64	0/1588	0.98	4/2136 (0.2%)
1	C	0.55	0/1587	0.86	4/2135 (0.2%)
All	All	0.62	0/4830	0.91	10/6497 (0.2%)

There are no bond length outliers.

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	106	LEU	CA-C-N	-7.53	111.95	119.56
1	A	106	LEU	C-N-CA	-7.53	111.95	119.56
1	B	139	GLY	N-CA-C	-6.78	107.01	115.08
1	B	117	ARG	CA-C-N	5.77	125.45	119.56
1	B	117	ARG	C-N-CA	5.77	125.45	119.56
1	B	269	ILE	N-CA-C	-5.52	107.11	112.29
1	C	155	PHE	N-CA-C	5.17	117.67	109.50
1	C	106	LEU	CA-C-N	-5.03	113.86	119.19
1	C	106	LEU	C-N-CA	-5.03	113.86	119.19
1	C	157	ILE	N-CA-C	5.01	115.13	108.11

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	1634	0	1667	31	0
1	B	1569	0	1594	35	0
1	C	1568	0	1602	26	0
2	A	17	0	0	0	0
2	B	17	0	0	0	0
2	C	17	0	0	1	0
3	A	4	0	6	0	0
3	B	4	0	6	1	0
4	B	1	0	0	0	0
5	C	4	0	3	0	0
6	A	42	0	0	3	0
6	B	36	0	0	5	0
6	C	20	0	0	0	0
All	All	4933	0	4878	86	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 9.

All (86) 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:B:233:GLY:HA2	3:B:302:EDO:H11	1.64	0.78
1:A:229:ARG:HH11	1:A:248:ARG:NH1	1.89	0.70
1:B:156:LEU:HD12	1:B:157:ILE:H	1.59	0.67
1:A:103:ASN:HD22	1:A:222[B]:HIS:CD2	2.12	0.66
1:A:152:ARG:HG2	1:A:157:ILE:HD12	1.80	0.64
1:C:152:ARG:HD3	1:C:157:ILE:HD12	1.78	0.64
1:C:266[A]:ARG:HH22	1:C:272:PRO:HA	1.64	0.62
1:A:123:SER:HB2	1:A:125:MSE:HE3	1.83	0.59
1:A:94[A]:ARG:HG3	6:A:402:HOH:O	2.03	0.58
1:A:94[A]:ARG:NH2	6:A:402:HOH:O	2.37	0.57
1:C:98:MSE:SE	1:C:101:LEU:HG	2.55	0.57
1:C:290:LEU:HD22	1:C:291:MSE:HE2	1.88	0.56
1:A:222[B]:HIS:HD2	6:A:410:HOH:O	1.90	0.55
1:B:192:LYS:HG2	1:B:193:GLN:O	2.07	0.54
1:A:201:MSE:SE	1:B:204:GLU:HG2	2.58	0.54
1:A:149:PRO:HD3	1:A:198:LEU:HD23	1.91	0.53
1:B:125:MSE:HE1	1:C:217:GLU:HG2	1.90	0.53
1:B:186:ALA:O	6:B:401:HOH:O	2.19	0.53
1:A:110:LEU:HD11	1:A:122:VAL:HG11	1.92	0.52
1:B:129:SER:OG	1:B:147:ASP:N	2.35	0.51
1:A:229:ARG:HH11	1:A:248:ARG:HH12	1.56	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:237:ILE:HD13	1:A:242:ALA:HB2	1.94	0.50
1:C:213:ARG:HD3	1:C:214:PRO:HD2	1.94	0.50
1:B:183:GLN:HG3	6:B:432:HOH:O	2.12	0.50
1:C:105:LEU:HD23	1:C:286:PHE:HE2	1.76	0.50
1:C:273:SER:OG	1:C:275:ILE:HG22	2.12	0.49
1:A:94[A]:ARG:NH2	1:A:123:SER:OG	2.41	0.49
1:C:148:GLY:HA3	1:C:261:GLU:HG2	1.93	0.49
1:B:138:SER:HB3	1:B:140:ARG:HG3	1.95	0.49
1:B:173:ARG:NH1	6:B:405:HOH:O	2.31	0.49
1:A:189:ARG:HB2	1:A:213:ARG:HH11	1.77	0.48
1:C:238:ASP:OD1	1:C:238:ASP:N	2.42	0.48
1:C:203:VAL:O	1:C:207:ILE:HG12	2.14	0.48
1:A:165:VAL:HG11	1:A:296:LEU:HD22	1.95	0.48
1:B:238:ASP:HB2	6:B:417:HOH:O	2.15	0.47
1:C:198:LEU:HD21	1:C:202:ARG:HE	1.79	0.47
1:C:199:PHE:O	1:C:203:VAL:HG23	2.14	0.47
1:B:157:ILE:HD13	1:B:263:LEU:HD13	1.96	0.47
1:B:217:GLU:HG2	1:C:125:MSE:HE1	1.97	0.47
1:B:121:GLN:NE2	1:C:215:SER:O	2.47	0.47
1:C:172:HIS:NE2	1:C:188:GLU:OE2	2.48	0.46
1:A:185:LEU:HD22	1:A:234:ILE:HD11	1.97	0.46
1:A:148:GLY:HA2	1:A:149:PRO:HA	1.64	0.46
1:B:145:TYR:HA	1:B:263:LEU:O	2.15	0.46
1:C:243:ILE:HA	1:C:243:ILE:HD12	1.59	0.46
1:C:266[A]:ARG:HE	1:C:266[A]:ARG:HB3	1.52	0.46
1:A:170:MSE:HE2	1:A:248:ARG:O	2.15	0.46
1:A:96:ALA:O	1:A:144:GLY:HA2	2.16	0.45
1:B:229:ARG:NH2	1:B:230:GLU:OE2	2.50	0.45
1:B:98:MSE:HG3	1:B:147:ASP:OD1	2.16	0.45
1:A:98:MSE:HA	1:A:127:LEU:O	2.16	0.45
1:B:96:ALA:O	1:B:144:GLY:HA2	2.16	0.45
1:B:273:SER:HB3	1:B:276:VAL:HB	1.99	0.45
1:C:110:LEU:HD11	1:C:122:VAL:HG11	1.99	0.45
1:B:153:GLN:HE21	1:B:153:GLN:HB3	1.57	0.45
1:A:198:LEU:O	1:A:202:ARG:HG3	2.17	0.44
1:B:98:MSE:HE1	1:B:262:PHE:HB2	2.00	0.44
1:B:230:GLU:HG3	1:C:108:ARG:HA	1.99	0.44
1:B:124:LEU:C	1:B:125:MSE:HE2	2.43	0.44
1:A:229:ARG:NH1	1:A:248:ARG:HH12	2.15	0.44
1:A:201:MSE:HE1	1:B:204:GLU:HG2	1.98	0.44
1:B:138:SER:OG	1:B:140:ARG:NH2	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:189:ARG:HD2	1:B:232:ALA:O	2.18	0.43
1:C:98:MSE:HG2	1:C:147:ASP:OD2	2.19	0.43
1:A:94[B]:ARG:HE	1:A:94[B]:ARG:HB2	1.60	0.42
1:C:148:GLY:HA2	1:C:149:PRO:HA	1.79	0.42
1:A:105:LEU:HD23	1:A:105:LEU:HA	1.86	0.42
1:A:162:LEU:HD23	1:A:162:LEU:HA	1.87	0.42
1:A:284:TRP:HA	1:A:284:TRP:CE3	2.54	0.42
1:C:98:MSE:HB3	2:C:301:6DB:OXT	2.20	0.42
1:B:185:LEU:HD22	1:B:234:ILE:HD11	2.02	0.41
1:C:229:ARG:HD2	1:C:248:ARG:CZ	2.51	0.41
1:B:193:GLN:HG2	6:B:418:HOH:O	2.21	0.41
1:A:192:LYS:NZ	1:A:204:GLU:OE1	2.52	0.41
1:C:165:VAL:HG11	1:C:296:LEU:HD22	2.03	0.41
1:A:273:SER:HB3	1:A:276:VAL:HB	2.02	0.41
1:B:120:LEU:O	1:B:122:VAL:HG23	2.21	0.41
1:B:138:SER:C	1:B:140:ARG:H	2.28	0.41
1:B:163:PRO:HB3	1:B:257:PHE:CD1	2.56	0.41
1:B:237:ILE:HD12	1:B:237:ILE:HA	1.81	0.41
1:A:213:ARG:HB3	1:A:213:ARG:CZ	2.51	0.40
1:A:243:ILE:HD12	1:A:243:ILE:HA	1.54	0.40
1:B:156:LEU:HD12	1:B:157:ILE:N	2.29	0.40
1:B:183:GLN:HG3	1:B:183:GLN:H	1.69	0.40
1:B:284:TRP:CE3	1:B:284:TRP:HA	2.57	0.40
1:C:237:ILE:HD12	1:C:237:ILE:HA	1.92	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	210/210 (100%)	204 (97%)	6 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	201/210 (96%)	197 (98%)	4 (2%)	0	100	100
1	C	201/210 (96%)	194 (96%)	6 (3%)	1 (0%)	24	29
All	All	612/630 (97%)	595 (97%)	16 (3%)	1 (0%)	43	53

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	104	GLY

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	171/161 (106%)	160 (94%)	11 (6%)	16	20
1	B	164/161 (102%)	150 (92%)	14 (8%)	10	12
1	C	164/161 (102%)	152 (93%)	12 (7%)	13	16
All	All	499/483 (103%)	462 (93%)	37 (7%)	13	15

All (37) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94[A]	ARG
1	A	94[B]	ARG
1	A	98	MSE
1	A	114	ILE
1	A	178	ASP
1	A	179[A]	ARG
1	A	179[B]	ARG
1	A	213	ARG
1	A	234	ILE
1	A	237	ILE
1	A	243	ILE
1	B	92	THR
1	B	98	MSE

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Mol	Chain	Res	Type
1	B	101	LEU
1	B	123	SER
1	B	143	ILE
1	B	153	GLN
1	B	158	GLU
1	B	183	GLN
1	B	193	GLN
1	B	201	MSE
1	B	204	GLU
1	B	234	ILE
1	B	246	THR
1	B	264	GLU
1	C	98	MSE
1	C	105	LEU
1	C	123	SER
1	C	153	GLN
1	C	165	VAL
1	C	179	ARG
1	C	185	LEU
1	C	195	THR
1	C	229	ARG
1	C	243	ILE
1	C	289	ASP
1	C	293	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	A	121	GLN
1	B	153	GLN
1	C	153	GLN
1	C	183	GLN
1	C	293	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 1 is monoatomic - leaving 6 for Mogul analysis.

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	6DB	C	301	-	16,16,16	1.06	1 (6%)	17,20,20	1.97	5 (29%)
5	ACY	C	302	-	3,3,3	0.73	0	3,3,3	1.12	0
2	6DB	A	301	-	16,16,16	1.05	1 (6%)	17,20,20	1.93	5 (29%)
3	EDO	A	302	-	3,3,3	0.41	0	2,2,2	0.43	0
2	6DB	B	301	-	16,16,16	1.15	1 (6%)	17,20,20	2.18	6 (35%)
3	EDO	B	302	-	3,3,3	0.37	0	2,2,2	0.46	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	6DB	C	301	-	-	5/19/19/19	-
2	6DB	A	301	-	-	6/19/19/19	-
3	EDO	A	302	-	-	0/1/1/1	-
2	6DB	B	301	-	-	5/19/19/19	-
3	EDO	B	302	-	-	1/1/1/1	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	301	6DB	CAP-NAN	2.59	1.38	1.33
2	A	301	6DB	CAP-NAN	2.58	1.38	1.33
2	B	301	6DB	CAP-NAN	2.42	1.38	1.33

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	301	6DB	CAK-CAI-CAE	-5.52	97.26	110.35
2	A	301	6DB	CB-CA-N	4.94	119.28	108.89
2	B	301	6DB	NAN-CAP-NAO	-4.48	112.98	120.67
2	B	301	6DB	CAK-CAI-CAE	-3.89	101.12	110.35
2	B	301	6DB	CB-CA-N	2.90	115.00	108.89
2	C	301	6DB	CB-CA-C	-2.77	104.15	110.23
2	B	301	6DB	OXT-C-O	2.64	130.07	124.08
2	B	301	6DB	O-C-CA	-2.62	114.19	122.14
2	C	301	6DB	OXT-C-O	2.61	130.00	124.08
2	A	301	6DB	NAQ-CAP-NAN	-2.49	113.62	119.27
2	A	301	6DB	CAK-CAI-CAE	-2.32	104.85	110.35
2	A	301	6DB	OAB-CAE-CAI	-2.30	114.82	122.26
2	B	301	6DB	CB-CA-C	-2.22	105.36	110.23
2	C	301	6DB	OAB-CAE-CAI	-2.18	115.21	122.26
2	A	301	6DB	CAL-CAK-CAI	-2.11	107.30	113.80
2	C	301	6DB	O-C-CA	-2.05	115.92	122.14

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	6DB	O-C-CA-N
2	A	301	6DB	C-CA-N-CAI
2	B	301	6DB	O-C-CA-N
2	B	301	6DB	OXT-C-CA-N
2	B	301	6DB	C-CA-N-CAI
2	C	301	6DB	C-CA-N-CAI
2	C	301	6DB	O-C-CA-CB
2	A	301	6DB	OXT-C-CA-N
3	B	302	EDO	O1-C1-C2-O2
2	A	301	6DB	O-C-CA-CB
2	A	301	6DB	OXT-C-CA-CB
2	B	301	6DB	O-C-CA-CB
2	B	301	6DB	OXT-C-CA-CB
2	C	301	6DB	OXT-C-CA-CB

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Mol	Chain	Res	Type	Atoms
2	C	301	6DB	O-C-CA-N
2	C	301	6DB	OXT-C-CA-N
2	A	301	6DB	CB-CA-N-CAI

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	301	6DB	1	0
3	B	302	EDO	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

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	200/210 (95%)	-0.02	2 (1%) 79 81	7, 29, 68, 91	3 (1%)
1	B	195/210 (92%)	0.36	12 (6%) 26 27	8, 39, 73, 90	2 (1%)
1	C	196/210 (93%)	0.58	13 (6%) 24 25	20, 47, 84, 99	1 (0%)
All	All	591/630 (93%)	0.30	27 (4%) 37 38	7, 39, 76, 99	6 (1%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	209	GLY	4.9
1	C	271	ALA	4.5
1	C	289	ASP	3.3
1	C	208	GLY	3.2
1	B	278	ARG	2.8
1	B	271	ALA	2.8
1	C	268	ALA	2.8
1	C	247	ASP	2.7
1	C	274	THR	2.7
1	C	277	ASP	2.6
1	B	215	SER	2.6
1	A	210	ILE	2.5
1	B	158	GLU	2.5
1	C	272	PRO	2.5
1	B	154	GLY	2.3
1	C	154	GLY	2.3
1	B	247	ASP	2.2
1	B	268	ALA	2.2
1	C	266[A]	ARG	2.2
1	B	270	GLY	2.1
1	C	270	GLY	2.1
1	A	208	GLY	2.1
1	C	171	GLY	2.1

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Mol	Chain	Res	Type	RSRZ
1	B	246	THR	2.0
1	B	269	ILE	2.0
1	B	159	THR	2.0
1	B	137	ALA	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 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
5	ACY	C	302	4/4	0.84	0.18	47,47,47,47	0
2	6DB	B	301	17/17	0.89	0.09	20,24,27,27	0
4	CL	B	303	1/1	0.90	0.13	73,73,73,73	0
3	EDO	A	302	4/4	0.92	0.11	28,28,28,28	4
2	6DB	C	301	17/17	0.93	0.07	28,31,32,32	0
3	EDO	B	302	4/4	0.93	0.07	39,39,39,39	0
2	6DB	A	301	17/17	0.95	0.06	16,18,19,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.