



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:34 AM UTC

PDB ID : 2AWD / pdb_00002awd
Title : Crystal structure of LacC from *Enterococcus faecalis*
Authors : Gorman, J.; Shapiro, L.; Burley, S.K.; New York SGX Research Center for Structural Genomics (NYSGXRC)
Deposited on : 2005-08-31
Resolution : 2.00 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

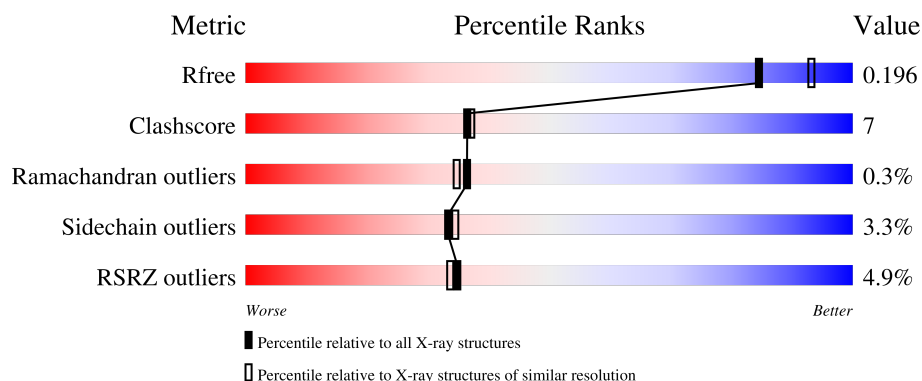
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	10052 (2.00-2.00)
Clashscore	190562	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	323	4% 85% 12% .
1	B	323	5% 80% 15% ..

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	BR	B	405	-	-	X	-
2	BR	B	409	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5147 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 tagatose-6-phosphate kinase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	316	Total	C	N	O	Se	0	0	0
			2399	1524	407	462	6			
1	B	313	Total	C	N	O	Se	0	0	0
			2377	1511	403	457	6			

There are 34 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MSE	-	cloning artifact	UNP Q833W9
A	0	SER	-	cloning artifact	UNP Q833W9
A	1	LEU	-	cloning artifact	UNP Q833W9
A	7	MSE	MET	modified residue	UNP Q833W9
A	213	MSE	MET	modified residue	UNP Q833W9
A	279	MSE	MET	modified residue	UNP Q833W9
A	283	MSE	MET	modified residue	UNP Q833W9
A	290	MSE	MET	modified residue	UNP Q833W9
A	304	MSE	MET	modified residue	UNP Q833W9
A	314	GLU	-	cloning artifact	UNP Q833W9
A	315	GLY	-	cloning artifact	UNP Q833W9
A	316	HIS	-	expression tag	UNP Q833W9
A	317	HIS	-	expression tag	UNP Q833W9
A	318	HIS	-	expression tag	UNP Q833W9
A	319	HIS	-	expression tag	UNP Q833W9
A	320	HIS	-	expression tag	UNP Q833W9
A	321	HIS	-	expression tag	UNP Q833W9
B	-1	MSE	-	cloning artifact	UNP Q833W9
B	0	SER	-	cloning artifact	UNP Q833W9
B	1	LEU	-	cloning artifact	UNP Q833W9
B	7	MSE	MET	modified residue	UNP Q833W9
B	213	MSE	MET	modified residue	UNP Q833W9
B	279	MSE	MET	modified residue	UNP Q833W9
B	283	MSE	MET	modified residue	UNP Q833W9
B	290	MSE	MET	modified residue	UNP Q833W9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	304	MSE	MET	modified residue	UNP Q833W9
B	314	GLU	-	cloning artifact	UNP Q833W9
B	315	GLY	-	cloning artifact	UNP Q833W9
B	316	HIS	-	expression tag	UNP Q833W9
B	317	HIS	-	expression tag	UNP Q833W9
B	318	HIS	-	expression tag	UNP Q833W9
B	319	HIS	-	expression tag	UNP Q833W9
B	320	HIS	-	expression tag	UNP Q833W9
B	321	HIS	-	expression tag	UNP Q833W9

- Molecule 2 is BROMIDE ION (CCD ID: BR) (formula: Br).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	7	Total Br 7 7	0	0
2	B	5	Total Br 5 5	0	0

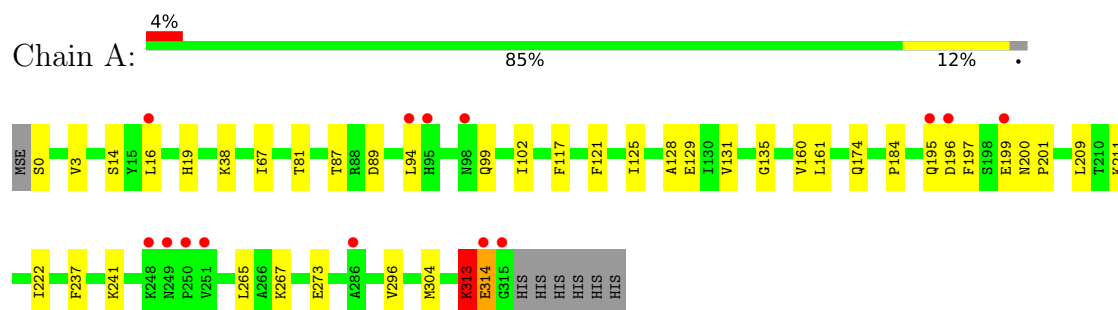
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	185	Total O 185 185	0	0
3	B	174	Total O 174 174	0	0

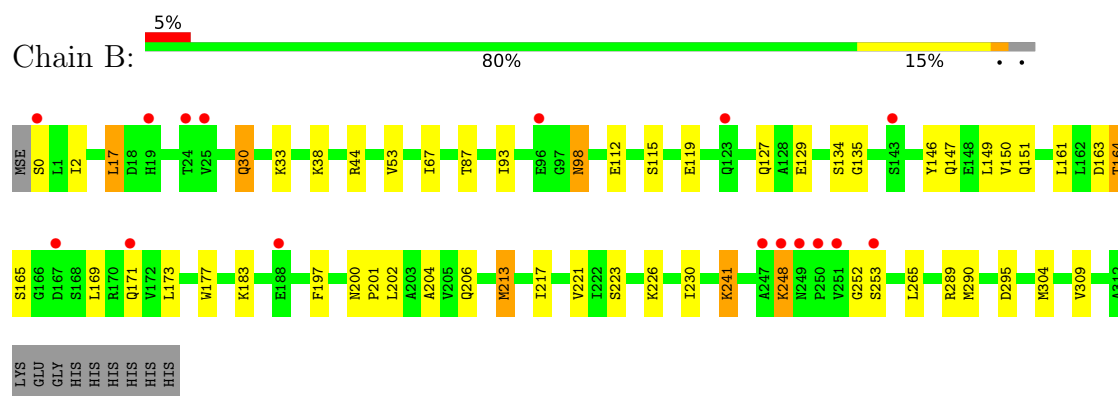
3 Residue-property plots

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: tagatose-6-phosphate kinase



- Molecule 1: tagatose-6-phosphate kinase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	65.21Å 62.24Å 91.97Å 90.00° 99.28° 90.00°	Depositor
Resolution (Å)	20.00 – 2.00 20.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (20.00-2.00) 99.3 (20.00-2.00)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.70 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.193 , 0.246 0.197 , 0.196	Depositor DCC
R_{free} test set	2441 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å ²)	32.7	Xtriage
Anisotropy	0.389	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.43 , 50.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5147	wwPDB-VP
Average B, all atoms (Å ²)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.71% 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: BR

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	0.89	1/2435 (0.0%)	0.95	2/3293 (0.1%)
1	B	0.87	2/2413 (0.1%)	0.92	1/3265 (0.0%)
All	All	0.88	3/4848 (0.1%)	0.93	3/6558 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	253	SER	C-O	-7.39	1.15	1.24
1	B	241	LYS	CE-NZ	5.15	1.64	1.49
1	A	200	ASN	CA-C	5.12	1.59	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	165	SER	N-CA-C	5.33	116.91	108.96
1	A	314	GLU	N-CA-C	5.25	121.99	110.80
1	A	199	GLU	N-CA-C	-5.21	103.27	110.35

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	313	LYS	Peptide

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	2399	0	2437	28	0
1	B	2377	0	2415	43	0
2	A	7	0	0	1	0
2	B	5	0	0	5	0
3	A	185	0	0	9	0
3	B	174	0	0	12	0
All	All	5147	0	4852	69	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 7.

All (69) 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:44:ARG:HD3	2:B:409:BR:BR	2.25	0.92
1:A:237:PHE:HD1	3:A:417:HOH:O	1.57	0.87
1:A:237:PHE:CD1	3:A:417:HOH:O	2.28	0.82
1:B:164:THR:HG21	2:B:405:BR:BR	2.33	0.82
1:A:241:LYS:HE2	3:A:547:HOH:O	1.85	0.77
1:B:252:GLY:HA3	3:B:412:HOH:O	1.85	0.76
1:B:98:ASN:HD22	1:B:98:ASN:N	1.85	0.74
1:B:171:GLN:NE2	3:B:563:HOH:O	2.25	0.69
1:B:241:LYS:HE3	1:B:309:VAL:HG21	1.76	0.67
1:B:0:SER:HB2	1:B:129:GLU:HG3	1.76	0.66
1:B:151:GLN:HG2	1:B:177:TRP:CD2	2.30	0.66
1:B:164:THR:CG2	2:B:405:BR:BR	2.99	0.66
1:B:304:MSE:HE2	3:B:489:HOH:O	1.97	0.64
1:B:151:GLN:HG2	1:B:177:TRP:CE3	2.35	0.62
1:A:313:LYS:HG2	2:A:411:BR:BR	2.56	0.60
1:B:241:LYS:CE	3:B:512:HOH:O	2.51	0.58
1:B:38:LYS:NZ	3:B:565:HOH:O	2.38	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:202:LEU:HD23	1:B:230:ILE:HD11	1.87	0.56
1:B:241:LYS:CE	1:B:309:VAL:HG21	2.36	0.55
1:B:241:LYS:HE2	3:B:483:HOH:O	2.08	0.53
1:B:304:MSE:CE	3:B:489:HOH:O	2.55	0.52
1:A:304:MSE:HE3	3:A:507:HOH:O	2.09	0.51
1:A:121:PHE:CZ	1:A:125:ILE:HD12	2.46	0.51
1:A:313:LYS:HD3	3:A:421:HOH:O	2.11	0.51
1:B:164:THR:HG23	1:B:169:LEU:HB2	1.93	0.50
1:B:248:LYS:HB3	3:B:496:HOH:O	2.12	0.49
1:A:131:VAL:CG1	1:A:160:VAL:HG22	2.42	0.49
1:A:67:ILE:HD12	1:A:87:THR:HG21	1.93	0.49
1:A:195:GLN:HE22	1:A:211:LYS:NZ	2.10	0.49
1:A:16:LEU:CD2	1:A:94:LEU:HD12	2.43	0.48
1:B:38:LYS:HD3	1:B:135:GLY:HA2	1.95	0.48
1:A:197:PHE:HB3	1:A:201:PRO:HB3	1.95	0.48
1:A:38:LYS:HD3	1:A:135:GLY:HA2	1.96	0.47
1:B:213:MSE:CG	2:B:406:BR:BR	3.18	0.47
1:B:183:LYS:HA	1:B:221:VAL:O	2.15	0.47
1:A:296:VAL:CG2	3:A:490:HOH:O	2.63	0.46
1:B:147:GLN:HG2	1:B:151:GLN:HE21	1.79	0.46
1:B:173:LEU:HD22	1:B:217:ILE:HD11	1.97	0.46
1:A:94:LEU:HD22	1:A:99:GLN:HG2	1.96	0.46
1:B:202:LEU:CD2	1:B:230:ILE:HD11	2.45	0.46
1:A:184:PRO:HG2	1:A:222:ILE:CD1	2.47	0.45
1:B:241:LYS:HE2	3:B:512:HOH:O	2.14	0.44
1:B:161:LEU:HD11	1:B:265:LEU:HD12	2.00	0.44
1:B:30:GLN:HE21	1:B:30:GLN:HA	1.81	0.44
1:A:241:LYS:CE	3:A:547:HOH:O	2.54	0.44
1:B:197:PHE:CD1	1:B:204:ALA:HB1	2.52	0.44
1:B:98:ASN:N	1:B:98:ASN:ND2	2.57	0.44
1:A:161:LEU:HD11	1:A:265:LEU:HD12	1.98	0.44
1:A:296:VAL:HG21	3:A:490:HOH:O	2.17	0.43
1:B:206:GLN:NE2	3:B:504:HOH:O	2.51	0.43
1:B:241:LYS:CD	3:B:512:HOH:O	2.66	0.43
1:A:267:LYS:NZ	1:A:273:GLU:OE1	2.48	0.43
1:B:200:ASN:N	1:B:201:PRO:CD	2.81	0.43
1:B:146:TYR:O	1:B:150:VAL:HG23	2.19	0.43
1:A:3:VAL:HG23	1:A:128:ALA:HB2	2.01	0.42
1:B:17:LEU:HD22	1:B:93:ILE:CG2	2.49	0.42
1:B:115:SER:O	1:B:119:GLU:HG3	2.20	0.42
1:B:44:ARG:CD	2:B:409:BR:BR	3.11	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:102:ILE:HD11	1:B:93:ILE:HD13	2.02	0.41
1:A:161:LEU:HD11	1:A:265:LEU:CD1	2.50	0.41
1:B:67:ILE:HD12	1:B:87:THR:HG21	2.02	0.41
1:A:81:THR:HG21	1:A:117:PHE:HA	2.03	0.41
1:A:89:ASP:OD2	1:B:33:LYS:NZ	2.54	0.41
1:B:2:ILE:O	1:B:53:VAL:HA	2.21	0.41
1:B:134:SER:HB3	1:B:163:ASP:HB3	2.01	0.41
1:A:209:LEU:HD12	1:A:237:PHE:HE2	1.86	0.41
1:A:174:GLN:OE1	3:A:584:HOH:O	2.22	0.40
1:B:304:MSE:HE3	3:B:482:HOH:O	2.21	0.40
1:A:0:SER:HB2	1:A:129:GLU:CG	2.51	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	314/323 (97%)	309 (98%)	4 (1%)	1 (0%)	36	35
1	B	311/323 (96%)	303 (97%)	7 (2%)	1 (0%)	36	35
All	All	625/646 (97%)	612 (98%)	11 (2%)	2 (0%)	36	35

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	314	GLU
1	B	248	LYS

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	258/258 (100%)	254 (98%)	4 (2%)	55	62
1	B	256/258 (99%)	243 (95%)	13 (5%)	21	19
All	All	514/516 (100%)	497 (97%)	17 (3%)	33	34

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	SER
1	A	19	HIS
1	A	196	ASP
1	A	313	LYS
1	B	17	LEU
1	B	30	GLN
1	B	98	ASN
1	B	112	GLU
1	B	127	GLN
1	B	149	LEU
1	B	164	THR
1	B	213	MSE
1	B	223	SER
1	B	226	LYS
1	B	289	ARG
1	B	290	MSE
1	B	295	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	41	ASN
1	A	47	HIS
1	A	69	ASN
1	A	120	ASN
1	A	195	GLN

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Mol	Chain	Res	Type
1	A	234	HIS
1	A	307	GLN
1	B	30	GLN
1	B	78	GLN
1	B	98	ASN
1	B	127	GLN
1	B	151	GLN
1	B	249	ASN
1	B	285	ASN
1	B	305	ASN

5.3.3 RNA [i](#)

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 12 ligands modelled in this entry, 12 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

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 ⓘ

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	310/323 (95%)	0.22	14 (4%) 38 37	20, 32, 57, 64	0
1	B	307/323 (95%)	0.31	16 (5%) 33 31	22, 34, 55, 61	0
All	All	617/646 (95%)	0.27	30 (4%) 35 34	20, 33, 56, 64	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	315	GLY	4.8
1	B	250	PRO	4.3
1	B	167	ASP	4.0
1	B	248	LYS	3.8
1	A	314	GLU	3.2
1	B	249	ASN	3.2
1	A	199	GLU	2.9
1	A	98	ASN	2.8
1	B	247	ALA	2.8
1	B	188	GLU	2.7
1	B	19	HIS	2.7
1	A	251	VAL	2.6
1	B	24	THR	2.6
1	B	25	VAL	2.4
1	A	286	ALA	2.4
1	A	195	GLN	2.4
1	B	123	GLN	2.4
1	A	249	ASN	2.4
1	B	253	SER	2.3
1	B	143	SER	2.3
1	B	96	GLU	2.2
1	A	94	LEU	2.2
1	B	171	GLN	2.2
1	B	251	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	248	LYS	2.2
1	A	196	ASP	2.1
1	A	250	PRO	2.1
1	A	16	LEU	2.1
1	B	0	SER	2.1
1	A	95	HIS	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(Å ²)	Q<0.9
2	BR	A	411	1/1	0.95	0.07	35,35,35,35	1
2	BR	A	412	1/1	0.96	0.05	46,46,46,46	1
2	BR	B	407	1/1	0.97	0.05	38,38,38,38	1
2	BR	A	410	1/1	0.98	0.03	35,35,35,35	1
2	BR	B	406	1/1	0.98	0.10	49,49,49,49	0
2	BR	A	404	1/1	0.98	0.10	50,50,50,50	0
2	BR	B	409	1/1	0.98	0.09	36,36,36,36	1
2	BR	A	408	1/1	0.99	0.09	35,35,35,35	1
2	BR	A	403	1/1	0.99	0.11	37,37,37,37	0
2	BR	B	405	1/1	0.99	0.10	48,48,48,48	0
2	BR	A	401	1/1	1.00	0.05	31,31,31,31	0
2	BR	B	402	1/1	1.00	0.04	32,32,32,32	0

6.5 Other polymers [i](#)

There are no such residues in this entry.