



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 05:30 PM UTC

PDB ID : 3QUJ / pdb_00003quj
Title : Crystal structure of the phosphonate binding protein, PhnD, from Escherichia coli
Authors : Alicea, I.; Schreiter, E.R.
Deposited on : 2011-02-24
Resolution : 2.20 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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

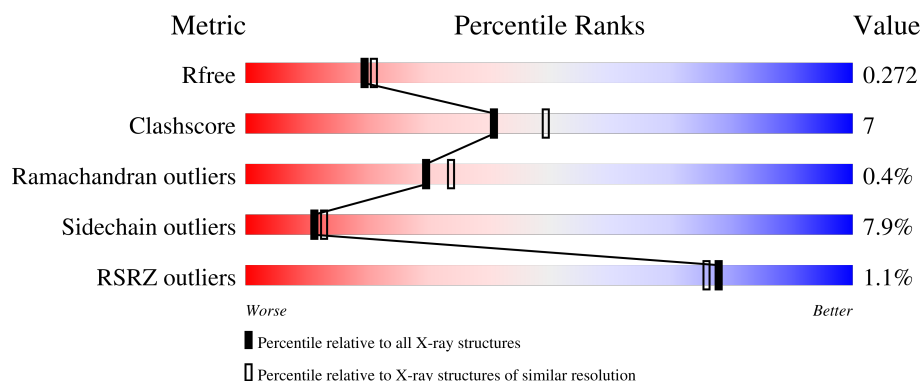
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	321	 76% 16% • 6%
1	B	321	 78% 14% • 5%
1	C	321	 69% 17% • 12%
1	D	321	 70% 17% • 11%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9467 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 PhnD, subunit of alkylphosphonate ABC transporter.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	301	Total	C	N	O	Se	0	1	0
			2359	1501	403	449	6			
1	B	304	Total	C	N	O	Se	0	1	0
			2386	1516	407	457	6			
1	C	284	Total	C	N	O	Se	0	2	0
			2241	1430	381	424	6			
1	D	287	Total	C	N	O	Se	0	2	0
			2260	1441	384	428	7			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-8	MSE	-	expression tag	UNP Q1R3F7
A	-7	HIS	-	expression tag	UNP Q1R3F7
A	-6	HIS	-	expression tag	UNP Q1R3F7
A	-5	HIS	-	expression tag	UNP Q1R3F7
A	-4	HIS	-	expression tag	UNP Q1R3F7
A	-3	HIS	-	expression tag	UNP Q1R3F7
A	-2	HIS	-	expression tag	UNP Q1R3F7
A	-1	GLY	-	expression tag	UNP Q1R3F7
A	0	SER	-	expression tag	UNP Q1R3F7
B	-8	MSE	-	expression tag	UNP Q1R3F7
B	-7	HIS	-	expression tag	UNP Q1R3F7
B	-6	HIS	-	expression tag	UNP Q1R3F7
B	-5	HIS	-	expression tag	UNP Q1R3F7
B	-4	HIS	-	expression tag	UNP Q1R3F7
B	-3	HIS	-	expression tag	UNP Q1R3F7
B	-2	HIS	-	expression tag	UNP Q1R3F7
B	-1	GLY	-	expression tag	UNP Q1R3F7
B	0	SER	-	expression tag	UNP Q1R3F7
C	-8	MSE	-	expression tag	UNP Q1R3F7
C	-7	HIS	-	expression tag	UNP Q1R3F7
C	-6	HIS	-	expression tag	UNP Q1R3F7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	-5	HIS	-	expression tag	UNP Q1R3F7
C	-4	HIS	-	expression tag	UNP Q1R3F7
C	-3	HIS	-	expression tag	UNP Q1R3F7
C	-2	HIS	-	expression tag	UNP Q1R3F7
C	-1	GLY	-	expression tag	UNP Q1R3F7
C	0	SER	-	expression tag	UNP Q1R3F7
D	-8	MSE	-	expression tag	UNP Q1R3F7
D	-7	HIS	-	expression tag	UNP Q1R3F7
D	-6	HIS	-	expression tag	UNP Q1R3F7
D	-5	HIS	-	expression tag	UNP Q1R3F7
D	-4	HIS	-	expression tag	UNP Q1R3F7
D	-3	HIS	-	expression tag	UNP Q1R3F7
D	-2	HIS	-	expression tag	UNP Q1R3F7
D	-1	GLY	-	expression tag	UNP Q1R3F7
D	0	SER	-	expression tag	UNP Q1R3F7

- Molecule 2 is UNKNOWN LIGAND (CCD ID: UNL) (formula:).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total O P 5 4 1	0	0
2	B	1	Total O P 5 4 1	0	0
2	C	1	Total O P 5 4 1	0	0
2	D	1	Total O P 5 4 1	0	0

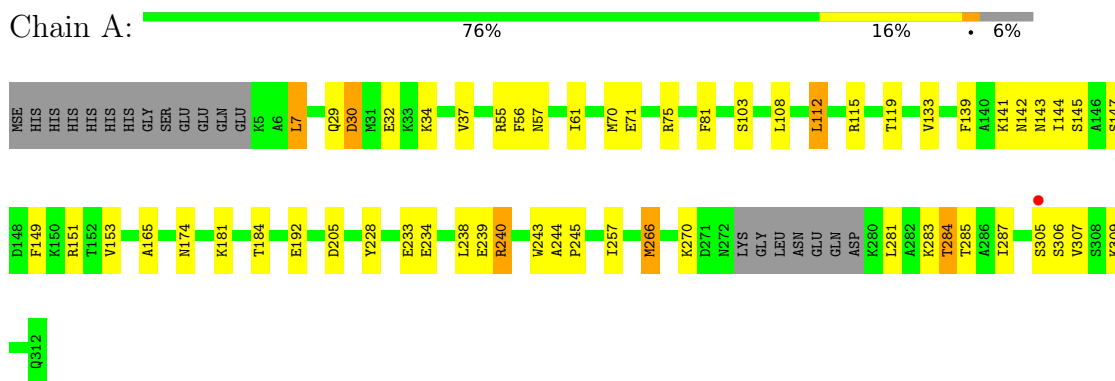
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	68	Total O 68 68	0	0
3	B	66	Total O 66 66	0	0
3	C	40	Total O 40 40	0	0
3	D	27	Total O 27 27	0	0

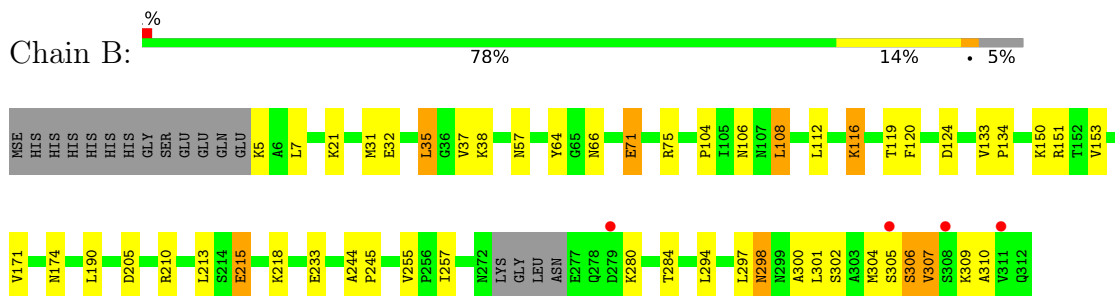
3 Residue-property plots

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.

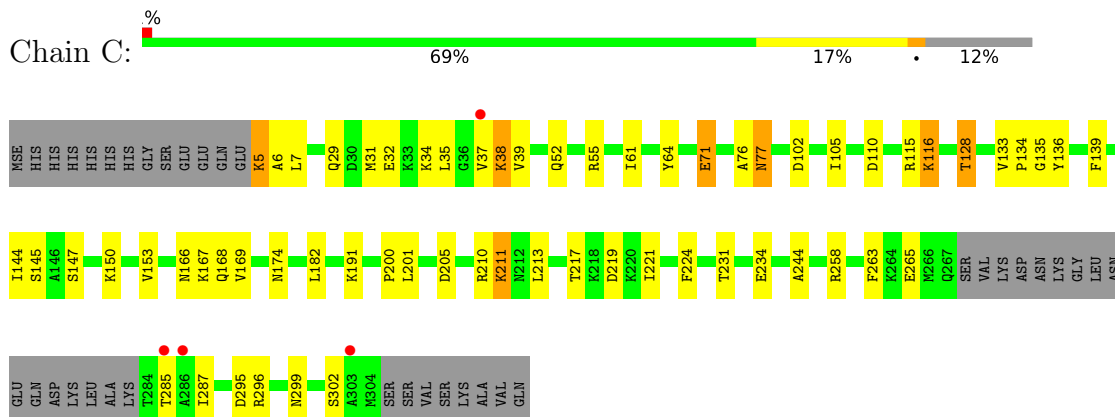
- Molecule 1: PhnD, subunit of alkylphosphonate ABC transporter



- Molecule 1: PhnD, subunit of alkylphosphonate ABC transporter



- Molecule 1: PhnD, subunit of alkylphosphonate ABC transporter



- Chain D:
-
- | Amino Acid | Percentage |
|------------|------------|
| VAL | 70% |
| LYS | 70% |
| ASP | 70% |
| ASN | 70% |
| LYS | 70% |
| GLY | 70% |
| LEU | 70% |
| ASN | 70% |
| GLU | 70% |
| GLN | 70% |
| ASP | 70% |
| LYS | 70% |
| LEU | 70% |
| ALA | 70% |
| LYS | 70% |
| THR | 70% |
| ALA | 70% |
| ILE | 70% |
| Q288 | 70% |
| S305 | 70% |
| S306 | 70% |
| S307 | 70% |
| S308 | 70% |
| K309 | 70% |
| A310 | 70% |
| V311 | 70% |
| Q312 | 70% |
| MSE | 17% |
| HIS | 17% |
| HIS | 17% |
| HIS | 17% |
| HIS | 17% |
| HIS | 17% |
| GLY | 17% |
| SER | 17% |
| GLU | 17% |
| GLU | 17% |
| GLN | 17% |
| GLU | 17% |
| K5 | 17% |
| A6 | 17% |
| L7 | 17% |
| N8 | 17% |
| F9 | 17% |
| E15 | 17% |
| Q23 | 17% |
| K31 | 17% |
| L35 | 17% |
| G36 | 17% |
| V37 | 17% |
| K38 | 17% |
| V39 | 17% |
| Q52 | 17% |
| D60 | 17% |
| I61 | 17% |
| M70 | 17% |
| E71 | 17% |
| R75 | 17% |
| D102 | 17% |
| I105 | 17% |
| N109 | 17% |
| K116 | 17% |
| D117 | 17% |
| L118 | 17% |
| T119 | 17% |
| F120 | 17% |
| D124 | 17% |
| S127 | 17% |
| Y137 | 17% |
| F138 | 17% |
| A140 | 11% |
| K141 | 11% |
| H142 | 11% |
| N143 | 11% |
| I144 | 11% |
| V153 | 11% |
| H157 | 11% |
| E158 | 11% |
| V171 | 11% |
| N174 | 11% |
| K181 | 11% |
| A186 | 11% |
| E192 | 11% |
| N212 | 11% |
| E215 | 11% |
| T216 | 11% |
| T217 | 11% |
| K220 | 11% |
| D223 | 11% |
| F224 | 11% |
| Y228 | 11% |
| G229 | 11% |
| G230 | 11% |
| T231 | 11% |
| K235 | 11% |
| L241 | 11% |
| A244 | 11% |
| P245 | 11% |
| F246 | 11% |
| R247 | 11% |
| A248 | 11% |
| V255 | 11% |
| P256 | 11% |
| I257 | 11% |
| R258 | 11% |
| Q259 | 11% |
| L260 | 11% |
| F263 | 11% |
| K264 | 11% |
| E265 | 11% |
| M266 | 11% |
| GLN | 11% |
| SER | 11% |

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	79.77Å 64.40Å 107.69Å 90.00° 93.52° 90.00°	Depositor
Resolution (Å)	28.90 – 2.20 28.90 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.8 (28.90-2.20) 98.7 (28.90-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.56 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.5.0072	Depositor
R, R_{free}	0.202 , 0.276 0.201 , 0.272	Depositor DCC
R_{free} test set	2798 reflections (5.09%)	wwPDB-VP
Wilson B-factor (Å ²)	22.6	Xtriage
Anisotropy	0.626	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 35.0	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	0.94	EDS
Total number of atoms	9467	wwPDB-VP
Average B, all atoms (Å ²)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 38.77 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 3.5096e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: UNL

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	1.02	3/2402 (0.1%)	1.10	4/3242 (0.1%)
1	B	1.05	1/2429 (0.0%)	1.11	2/3278 (0.1%)
1	C	0.98	1/2287 (0.0%)	1.07	3/3090 (0.1%)
1	D	0.97	1/2306 (0.0%)	1.06	6/3112 (0.2%)
All	All	1.01	6/9424 (0.1%)	1.09	15/12722 (0.1%)

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	D	0	1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	255	VAL	CA-CB	11.40	1.59	1.54
1	A	133	VAL	CA-CB	7.09	1.58	1.54
1	C	128	THR	CA-CB	5.72	1.62	1.53
1	B	21	LYS	C-O	-5.42	1.19	1.24
1	A	81	PHE	C-O	-5.24	1.18	1.24

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	124	ASP	N-CA-C	-6.17	100.59	109.48
1	B	124	ASP	CA-C-N	6.16	125.85	119.82
1	B	124	ASP	C-N-CA	6.16	125.85	119.82
1	D	157	HIS	N-CA-C	5.94	117.42	111.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	205	ASP	CA-C-N	5.86	126.35	120.14

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	212	ASN	Peptide

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	2359	0	2370	23	0
1	B	2386	0	2390	27	0
1	C	2241	0	2242	31	0
1	D	2260	0	2264	43	0
2	A	5	0	0	0	0
2	B	5	0	0	1	0
2	C	5	0	0	0	0
2	D	5	0	0	1	0
3	A	68	0	0	0	0
3	B	66	0	0	1	0
3	C	40	0	0	0	0
3	D	27	0	0	1	0
All	All	9467	0	9266	121	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.

The worst 5 of 121 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:D:306:SER:O	1:D:307:VAL:HB	1.58	0.98
1:D:307:VAL:HG13	1:D:308:SER:HB2	1.49	0.94
1:B:32:GLU:OE2	1:B:38:LYS:HD2	1.84	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:70[A]:MSE:SE	1:D:258:ARG:HG3	2.35	0.76
1:D:105:ILE:HD11	1:D:118:LEU:HD11	1.66	0.76

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	298/321 (93%)	283 (95%)	14 (5%)	1 (0%)	36	42
1	B	301/321 (94%)	293 (97%)	7 (2%)	1 (0%)	36	42
1	C	282/321 (88%)	277 (98%)	5 (2%)	0	100	100
1	D	285/321 (89%)	264 (93%)	18 (6%)	3 (1%)	11	10
All	All	1166/1284 (91%)	1117 (96%)	44 (4%)	5 (0%)	30	34

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	D	307	VAL
1	D	265	GLU
1	D	309	LYS
1	A	305	SER
1	B	306	SER

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	256/266 (96%)	234 (91%)	22 (9%)	10	10
1	B	259/266 (97%)	245 (95%)	14 (5%)	20	25
1	C	242/266 (91%)	220 (91%)	22 (9%)	9	9
1	D	245/266 (92%)	221 (90%)	24 (10%)	7	8
All	All	1002/1064 (94%)	920 (92%)	82 (8%)	11	12

5 of 82 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	296	ARG
1	D	215	GLU
1	D	52	GLN
1	D	116	LYS
1	D	231	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 14 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	52	GLN
1	C	154	ASN
1	D	154	ASN
1	D	23	GLN
1	D	52	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

Of 4 ligands modelled in this entry, 4 are unknown - 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

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	295/321 (91%)	-0.42	1 (0%) 90 88	9, 20, 39, 63	1 (0%)
1	B	298/321 (92%)	-0.45	4 (1%) 75 73	7, 18, 42, 75	1 (0%)
1	C	278/321 (86%)	-0.26	4 (1%) 73 71	10, 24, 44, 50	2 (0%)
1	D	281/321 (87%)	-0.10	4 (1%) 73 71	9, 27, 51, 64	1 (0%)
All	All	1152/1284 (89%)	-0.31	13 (1%) 78 76	7, 22, 46, 75	5 (0%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	308	SER	3.2
1	B	308	SER	3.1
1	D	307	VAL	3.0
1	C	286	ALA	3.0
1	C	285	THR	2.9

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
2	UNL	A	313	5/-	0.99	0.03	8,10,11,11	0
2	UNL	B	313	5/-	0.99	0.03	7,9,13,13	0
2	UNL	C	313	5/-	0.99	0.03	3,4,8,9	0
2	UNL	D	313	5/-	0.99	0.03	10,13,15,16	0

6.5 Other polymers [i](#)

There are no such residues in this entry.