



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 04:19 AM UTC

PDB ID : 7UPS / pdb_00007ups
Title : Structural study of Legionella pneumophila effector DotY (Lpg0294)
Authors : Chung, I.Y.W.; Cygler, M.
Deposited on : 2022-04-16
Resolution : 2.43 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)
Xtrriage (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

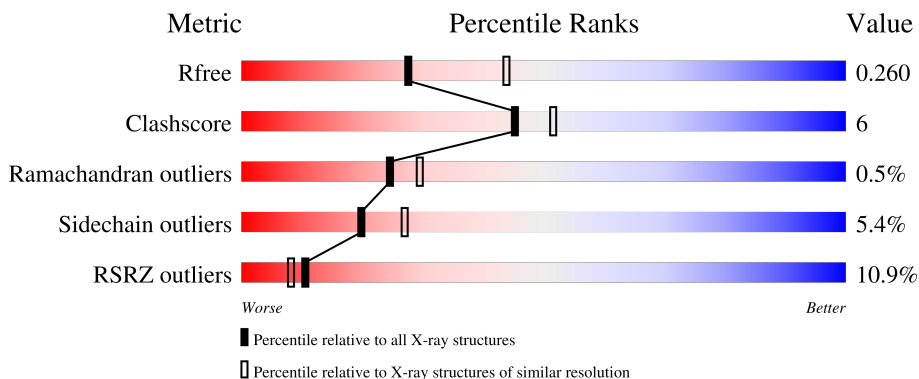
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

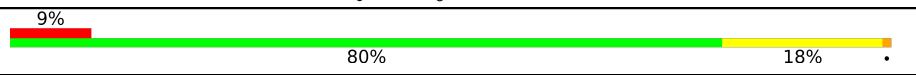
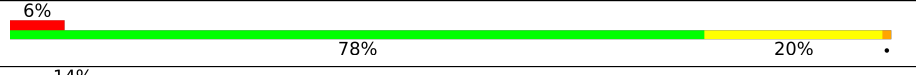

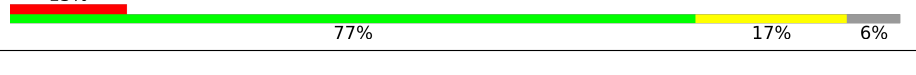
The reported resolution of this entry is 2.43 Å.

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	2340 (2.46-2.42)
Clashscore	190562	2400 (2.46-2.42)
Ramachandran outliers	187476	2379 (2.46-2.42)
Sidechain outliers	187428	2379 (2.46-2.42)
RSRZ outliers	180081	2340 (2.46-2.42)

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	215	
1	B	215	
1	C	215	
1	D	215	

2 Entry composition i

There are 3 unique types of molecules in this entry. The entry contains 6495 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 DotY (Lpg0294).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	215	Total 1635	C 1025	N 278	O 325	S 7	0	0	0
1	B	215	Total 1648	C 1031	N 279	O 331	S 7	0	2	0
1	C	202	Total 1494	C 932	N 252	O 303	S 7	0	0	0
1	D	202	Total 1508	C 947	N 259	O 294	S 8	1	1	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	5	SER	-	expression tag	UNP Q5ZYR7
A	6	ASN	-	expression tag	UNP Q5ZYR7
A	7	ALA	-	expression tag	UNP Q5ZYR7
B	5	SER	-	expression tag	UNP Q5ZYR7
B	6	ASN	-	expression tag	UNP Q5ZYR7
B	7	ALA	-	expression tag	UNP Q5ZYR7
C	5	SER	-	expression tag	UNP Q5ZYR7
C	6	ASN	-	expression tag	UNP Q5ZYR7
C	7	ALA	-	expression tag	UNP Q5ZYR7
D	5	SER	-	expression tag	UNP Q5ZYR7
D	6	ASN	-	expression tag	UNP Q5ZYR7
D	7	ALA	-	expression tag	UNP Q5ZYR7

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



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

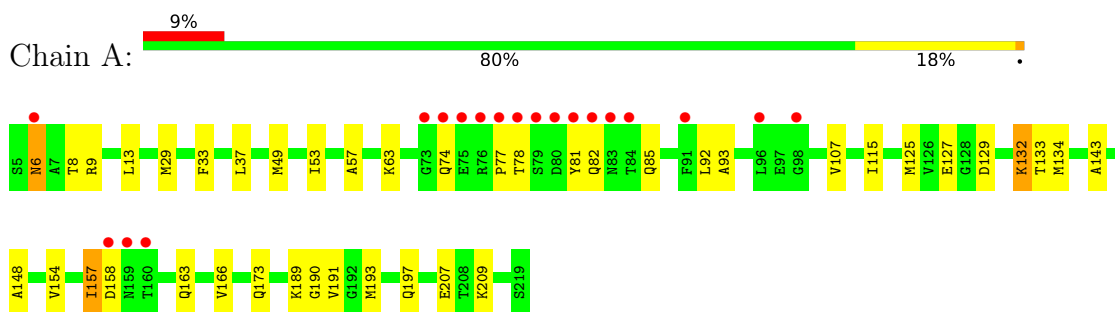
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	50	Total O 50 50	0	0
3	B	53	Total O 53 53	0	0
3	C	42	Total O 42 42	0	0
3	D	49	Total O 49 49	0	0

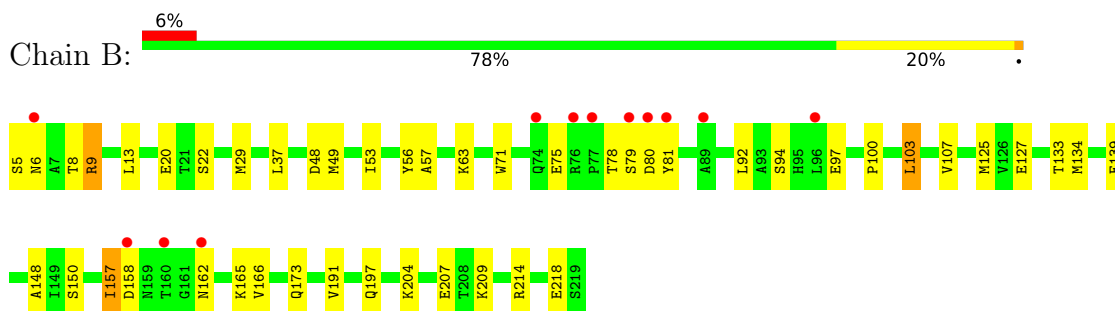
3 Residue-property plots [i](#)

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.

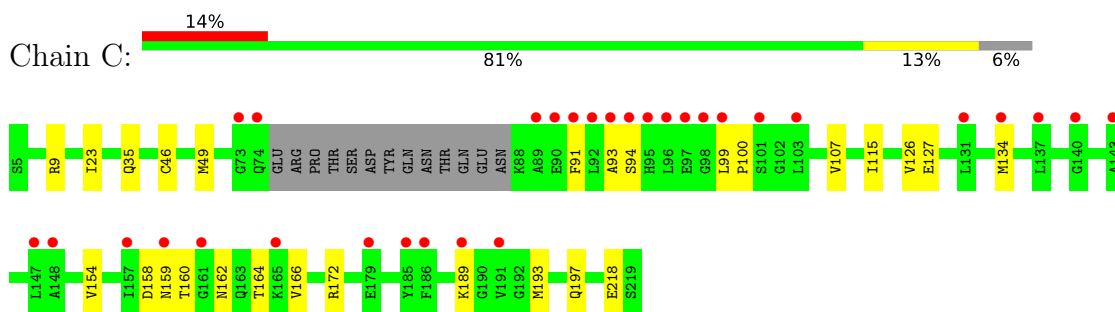
- Molecule 1: DotY (Lpg0294)



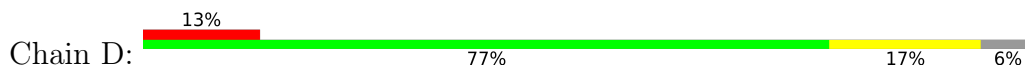
- Molecule 1: DotY (Lpg0294)

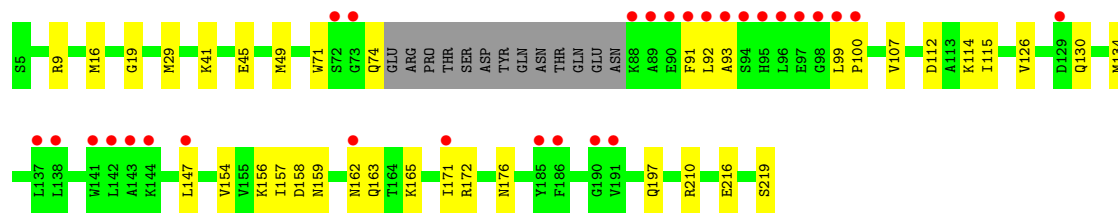


- Molecule 1: DotY (Lpg0294)



- Molecule 1: DotY (Lpg0294)





4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	153.20Å 75.62Å 101.20Å 90.00° 127.91° 90.00°	Depositor
Resolution (Å)	43.54 – 2.43 43.54 – 2.43	Depositor EDS
% Data completeness (in resolution range)	96.0 (43.54-2.43) 88.2 (43.54-2.43)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.22 (at 2.42Å)	Xtrriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.237 , 0.262 0.238 , 0.260	Depositor DCC
R_{free} test set	989 reflections (2.86%)	wwPDB-VP
Wilson B-factor (Å ²)	38.0	Xtrriage
Anisotropy	0.307	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 46.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	6495	wwPDB-VP
Average B, all atoms (Å ²)	52.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 10.04% 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: EDO

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	0.15	0/1655	0.33	0/2226
1	B	0.15	0/1668	0.33	0/2245
1	C	0.14	0/1509	0.35	0/2032
1	D	0.14	0/1523	0.32	0/2048
All	All	0.15	0/6355	0.33	0/8551

There are no bond length outliers.

There are no bond angle outliers.

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	1635	0	1611	22	0
1	B	1648	0	1602	27	0
1	C	1494	0	1435	12	0
1	D	1508	0	1486	15	0
2	A	4	0	6	0	0
2	B	4	0	6	1	0
2	C	4	0	6	1	0
2	D	4	0	6	1	0
3	A	50	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	53	0	0	2	0
3	C	42	0	0	0	0
3	D	49	0	0	0	0
All	All	6495	0	6158	73	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 6.

All (73) 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:C:23:ILE:H	2:C:301:EDO:H12	1.53	0.73
1:B:78:THR:HA	1:B:81:TYR:HB2	1.74	0.70
1:B:29:MET:HE3	1:B:53:ILE:HG23	1.75	0.69
1:C:158:ASP:OD1	1:C:162:ASN:N	2.26	0.68
1:B:63:LYS:NZ	3:B:402:HOH:O	2.21	0.68
1:A:125:MET:HE2	1:A:127:GLU:HG2	1.81	0.63
1:A:29:MET:HE3	1:A:53:ILE:HG23	1.79	0.63
1:A:74:GLN:HB3	1:A:77:PRO:HB2	1.81	0.62
1:B:125:MET:HE2	1:B:127:GLU:HG2	1.81	0.61
1:B:158:ASP:OD1	1:B:162:ASN:N	2.32	0.60
1:D:91:PHE:O	1:D:93:ALA:N	2.37	0.58
1:C:107:VAL:HG13	1:C:197:GLN:HG2	1.84	0.58
1:D:9:ARG:NH1	1:D:219:SER:O	2.38	0.57
1:B:22:SER:HA	2:B:301:EDO:H21	1.87	0.56
1:C:9:ARG:HD3	1:C:218:GLU:HA	1.87	0.56
1:A:63:LYS:NZ	3:A:403:HOH:O	2.39	0.56
1:D:115:ILE:HB	1:D:154:VAL:HG23	1.88	0.55
1:A:107:VAL:HG13	1:A:197:GLN:HG2	1.89	0.54
1:D:49:MET:HE2	1:D:216:GLU:HB3	1.89	0.54
1:A:148:ALA:HB2	1:A:157:ILE:HD13	1.91	0.53
1:D:107:VAL:HG13	1:D:197:GLN:HG2	1.90	0.53
1:B:92:LEU:HD13	1:B:133:THR:HA	1.91	0.52
1:B:78:THR:O	1:B:80:ASP:N	2.43	0.52
1:D:16:MET:HE1	1:D:210:ARG:HA	1.90	0.52
1:B:134:MET:HE1	1:B:191:VAL:HG11	1.92	0.52
1:C:172:ARG:O	1:C:197:GLN:NE2	2.43	0.52
1:A:13:LEU:HD21	1:B:207:GLU:HG3	1.92	0.52
1:D:126:VAL:HG11	1:D:134:MET:HE2	1.92	0.52
1:B:107:VAL:HG13	1:B:197:GLN:HG2	1.93	0.51
1:B:29:MET:HE2	1:B:57:ALA:HB2	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:100:PRO:HD3	1:D:130:GLN:HG2	1.94	0.49
1:B:100:PRO:HG2	1:B:103:LEU:HD11	1.94	0.49
1:B:214:ARG:O	1:B:218[B]:GLU:HG2	2.13	0.49
1:A:29:MET:HE2	1:A:57:ALA:HB2	1.95	0.49
1:A:134:MET:HE1	1:A:191:VAL:HG11	1.94	0.49
1:B:9:ARG:NE	1:B:218[B]:GLU:OE1	2.46	0.48
1:A:78:THR:HA	1:A:81:TYR:HB2	1.95	0.48
1:A:129:ASP:HA	1:A:132:LYS:HG3	1.96	0.47
1:B:148:ALA:HB2	1:B:157:ILE:HD13	1.96	0.47
1:A:134:MET:HE2	1:A:134:MET:HA	1.97	0.47
1:C:126:VAL:HG11	1:C:134:MET:SD	2.55	0.47
1:B:37:LEU:HD11	1:B:49:MET:HE2	1.96	0.46
1:B:71:TRP:CH2	1:B:139:GLU:HG3	2.50	0.46
1:B:5:SER:HB3	1:B:8:THR:HB	1.97	0.46
1:D:147:LEU:HD11	1:D:171:ILE:HD12	1.98	0.46
1:D:176:ASN:OD1	1:D:197:GLN:NE2	2.49	0.45
1:B:75:GLU:HG3	1:B:150:SER:HA	1.99	0.45
1:C:93:ALA:HB1	1:C:189:LYS:HD2	1.99	0.45
1:A:93:ALA:HB2	1:A:189:LYS:HG3	2.00	0.44
1:A:207:GLU:HG3	1:B:13:LEU:HD21	2.00	0.44
1:D:156:LYS:O	1:D:163:GLN:HA	2.17	0.44
1:A:6:ASN:ND2	1:A:8:THR:H	2.16	0.43
1:B:207:GLU:OE1	3:B:401:HOH:O	2.20	0.43
1:D:172:ARG:O	1:D:197:GLN:NE2	2.50	0.43
1:A:37:LEU:HD11	1:A:49:MET:HE2	2.01	0.42
1:D:112:ASP:OD2	1:D:114:LYS:HE2	2.19	0.42
1:A:33:PHE:CE2	1:A:49:MET:HE3	2.54	0.42
1:A:190:GLY:HA2	1:C:35:GLN:HE22	1.85	0.42
1:C:99:LEU:HA	1:C:100:PRO:HD3	1.94	0.42
1:C:134:MET:HE2	1:C:193:MET:HE1	2.02	0.41
1:D:19:GLY:HA3	1:D:29:MET:HE2	2.01	0.41
1:B:92:LEU:HB3	1:B:133:THR:HG23	2.02	0.41
1:A:115:ILE:HB	1:A:154:VAL:HG23	2.03	0.41
1:C:115:ILE:HB	1:C:154:VAL:HG22	2.01	0.41
1:B:103:LEU:HD12	1:B:103:LEU:HA	1.89	0.41
1:A:82:GLN:HA	1:A:143:ALA:HB1	2.02	0.41
1:C:46:CYS:HB3	1:C:49:MET:HE2	2.03	0.41
1:A:92:LEU:HD22	1:A:133:THR:HA	2.03	0.41
1:B:20:GLU:OE2	1:B:56:TYR:OH	2.35	0.40
1:B:173:GLN:HE21	1:B:173:GLN:HB2	1.70	0.40
1:B:6[B]:ASN:O	1:B:9:ARG:HG3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:71:TRP:HB2	2:D:301:EDO:H21	2.03	0.40
1:A:173:GLN:HE21	1:A:173:GLN:HB2	1.70	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	213/215 (99%)	208 (98%)	5 (2%)	0	100	100
1	B	215/215 (100%)	209 (97%)	5 (2%)	1 (0%)	24	29
1	C	198/215 (92%)	189 (96%)	7 (4%)	2 (1%)	12	13
1	D	199/215 (93%)	194 (98%)	4 (2%)	1 (0%)	24	29
All	All	825/860 (96%)	800 (97%)	21 (2%)	4 (0%)	24	29

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	91	PHE
1	D	92	LEU
1	B	79	SER
1	C	94	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	167/179 (93%)	157 (94%)	10 (6%)	17	23
1	B	167/179 (93%)	157 (94%)	10 (6%)	17	23
1	C	147/179 (82%)	142 (97%)	5 (3%)	32	45
1	D	149/179 (83%)	140 (94%)	9 (6%)	17	23
All	All	630/716 (88%)	596 (95%)	34 (5%)	20	27

All (34) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	6	ASN
1	A	9	ARG
1	A	85	GLN
1	A	132	LYS
1	A	157	ILE
1	A	158	ASP
1	A	163	GLN
1	A	166	VAL
1	A	193	MET
1	A	209	LYS
1	B	9	ARG
1	B	48	ASP
1	B	94	SER
1	B	97	GLU
1	B	103	LEU
1	B	157	ILE
1	B	165	LYS
1	B	166	VAL
1	B	204	LYS
1	B	209	LYS
1	C	127	GLU
1	C	159	ASN
1	C	160	THR
1	C	164	THR
1	C	166	VAL
1	D	41	LYS
1	D	45	GLU
1	D	74	GLN
1	D	99	LEU
1	D	157	ILE
1	D	158	ASP
1	D	159	ASN
1	D	162	ASN

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Mol	Chain	Res	Type
1	D	165	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	197	GLN
1	B	58	GLN
1	B	122	ASN
1	B	169	GLN
1	B	173	GLN
1	B	197	GLN
1	C	122	ASN
1	C	159	ASN
1	D	122	ASN
1	D	197	GLN

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](#)

4 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	EDO	A	301	-	3,3,3	0.42	0	2,2,2	0.40	0
2	EDO	D	301	-	3,3,3	0.40	0	2,2,2	0.41	0
2	EDO	B	301	-	3,3,3	0.44	0	2,2,2	0.37	0
2	EDO	C	301	-	3,3,3	0.43	0	2,2,2	0.39	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	EDO	A	301	-	-	1/1/1/1	-
2	EDO	D	301	-	-	0/1/1/1	-
2	EDO	B	301	-	-	0/1/1/1	-
2	EDO	C	301	-	-	0/1/1/1	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	301	EDO	O1-C1-C2-O2

There are no ring outliers.

3 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	301	EDO	1	0
2	B	301	EDO	1	0
2	C	301	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	215/215 (100%)	0.62	19 (8%) 15 13	33, 45, 92, 110	0
1	B	215/215 (100%)	0.49	12 (5%) 30 27	27, 43, 85, 103	2 (0%)
1	C	202/215 (93%)	0.93	31 (15%) 5 3	35, 53, 93, 114	0
1	D	202/215 (93%)	0.87	29 (14%) 6 4	31, 50, 94, 101	2 (0%)
All	All	834/860 (96%)	0.72	91 (10%) 10 8	27, 46, 93, 114	4 (0%)

All (91) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	159	ASN	4.8
1	D	89	ALA	4.6
1	A	80	ASP	4.5
1	A	83	ASN	4.4
1	B	77	PRO	4.3
1	D	96	LEU	4.3
1	D	138	LEU	4.2
1	A	77	PRO	4.1
1	D	88	LYS	4.0
1	A	79	SER	3.7
1	C	89	ALA	3.6
1	C	96	LEU	3.6
1	D	137	LEU	3.6
1	D	97	GLU	3.6
1	D	92	LEU	3.5
1	A	81	TYR	3.4
1	D	98	GLY	3.3
1	C	95	HIS	3.3
1	C	92	LEU	3.2
1	A	158	ASP	3.2
1	C	97	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	76	ARG	3.1
1	C	90	GLU	3.1
1	C	137	LEU	3.1
1	C	73	GLY	3.0
1	A	98	GLY	3.0
1	C	157	ILE	3.0
1	B	79	SER	3.0
1	D	99	LEU	2.9
1	B	74	GLN	2.9
1	B	6[A]	ASN	2.9
1	A	78	THR	2.9
1	D	144	LYS	2.9
1	C	148	ALA	2.9
1	A	6	ASN	2.8
1	C	131	LEU	2.8
1	C	159	ASN	2.7
1	C	94	SER	2.7
1	D	100	PRO	2.7
1	A	91	PHE	2.6
1	C	91	PHE	2.6
1	C	93	ALA	2.6
1	C	143	ALA	2.6
1	A	160	THR	2.6
1	D	90	GLU	2.6
1	C	191	VAL	2.6
1	B	81	TYR	2.6
1	B	76	ARG	2.6
1	C	98	GLY	2.6
1	C	140	GLY	2.6
1	C	134	MET	2.6
1	C	99	LEU	2.5
1	D	162	ASN	2.5
1	D	95	HIS	2.4
1	D	191	VAL	2.4
1	D	93	ALA	2.4
1	C	165	LYS	2.4
1	C	185	TYR	2.4
1	D	141	TRP	2.4
1	D	143	ALA	2.4
1	B	160	THR	2.4
1	C	161	GLY	2.3
1	D	142	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	189	LYS	2.3
1	C	179	GLU	2.3
1	D	94	SER	2.3
1	B	96	LEU	2.3
1	D	91	PHE	2.3
1	A	82	GLN	2.2
1	B	89	ALA	2.2
1	A	84	THR	2.2
1	C	74	GLN	2.2
1	D	190	GLY	2.2
1	A	75	GLU	2.2
1	D	72	SER	2.2
1	D	129	ASP	2.2
1	C	103	LEU	2.1
1	B	162	ASN	2.1
1	A	73	GLY	2.1
1	D	185	TYR	2.1
1	A	74	GLN	2.1
1	C	186	PHE	2.1
1	C	147	LEU	2.1
1	B	80	ASP	2.1
1	B	158	ASP	2.1
1	A	96	LEU	2.0
1	D	73	GLY	2.0
1	D	186	PHE	2.0
1	D	147	LEU	2.0
1	D	171	ILE	2.0
1	C	101	SER	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	EDO	A	301	4/4	0.66	0.17	54,55,60,65	0
2	EDO	C	301	4/4	0.85	0.12	38,45,47,51	0
2	EDO	B	301	4/4	0.92	0.10	45,48,49,52	0
2	EDO	D	301	4/4	0.92	0.11	42,46,53,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.