



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 12:33 PM UTC

PDB ID : 7WU1 / pdb_00007wu1
Title : Crystal structure of phospholipase D from Moritella sp. JT01
Authors : Wang, Y.H.; Mao, X.J.; Wang, J.; Wang, F.H.
Deposited on : 2022-02-05
Resolution : 2.30 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

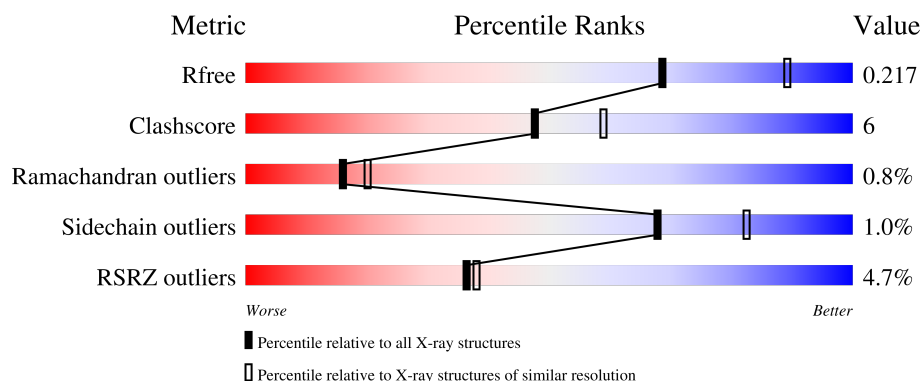
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	557	3% 89% 7% ..
1	B	557	6% 87% 9% ..
1	C	557	6% 88% 7% ..
1	D	557	5% 85% 11% ..
1	E	557	3% 89% 8% .

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Mol	Chain	Length	Quality of chain
1	F	557	 5% 87% 10% ..

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
3	NA	B	605	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 51186 atoms, of which 24695 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 Phospholipase D.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	538	Total	C	H	N	O	S	0	0	0
			8294	2661	4085	703	831	14			
1	B	542	Total	C	H	N	O	S	0	0	0
			8351	2679	4113	707	837	15			
1	C	542	Total	C	H	N	O	S	0	0	0
			8354	2682	4111	708	838	15			
1	D	542	Total	C	H	N	O	S	0	0	0
			8346	2677	4108	708	838	15			
1	E	545	Total	C	H	N	O	S	0	0	0
			8395	2694	4133	711	842	15			
1	F	545	Total	C	H	N	O	S	0	0	0
			8395	2694	4133	711	842	15			

There are 42 discrepancies between the modelled and reference sequences:

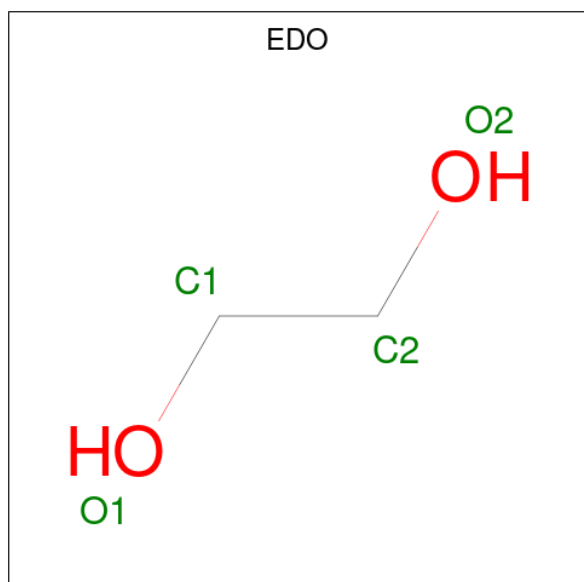
Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	expression tag	UNP A0A137SLD1
A	2	HIS	-	expression tag	UNP A0A137SLD1
A	3	HIS	-	expression tag	UNP A0A137SLD1
A	4	HIS	-	expression tag	UNP A0A137SLD1
A	5	HIS	-	expression tag	UNP A0A137SLD1
A	6	HIS	-	expression tag	UNP A0A137SLD1
A	7	HIS	-	expression tag	UNP A0A137SLD1
B	1	MET	-	expression tag	UNP A0A137SLD1
B	2	HIS	-	expression tag	UNP A0A137SLD1
B	3	HIS	-	expression tag	UNP A0A137SLD1
B	4	HIS	-	expression tag	UNP A0A137SLD1
B	5	HIS	-	expression tag	UNP A0A137SLD1
B	6	HIS	-	expression tag	UNP A0A137SLD1
B	7	HIS	-	expression tag	UNP A0A137SLD1
C	1	MET	-	expression tag	UNP A0A137SLD1
C	2	HIS	-	expression tag	UNP A0A137SLD1
C	3	HIS	-	expression tag	UNP A0A137SLD1

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Chain	Residue	Modelled	Actual	Comment	Reference
C	4	HIS	-	expression tag	UNP A0A137SLD1
C	5	HIS	-	expression tag	UNP A0A137SLD1
C	6	HIS	-	expression tag	UNP A0A137SLD1
C	7	HIS	-	expression tag	UNP A0A137SLD1
D	1	MET	-	expression tag	UNP A0A137SLD1
D	2	HIS	-	expression tag	UNP A0A137SLD1
D	3	HIS	-	expression tag	UNP A0A137SLD1
D	4	HIS	-	expression tag	UNP A0A137SLD1
D	5	HIS	-	expression tag	UNP A0A137SLD1
D	6	HIS	-	expression tag	UNP A0A137SLD1
D	7	HIS	-	expression tag	UNP A0A137SLD1
E	1	MET	-	expression tag	UNP A0A137SLD1
E	2	HIS	-	expression tag	UNP A0A137SLD1
E	3	HIS	-	expression tag	UNP A0A137SLD1
E	4	HIS	-	expression tag	UNP A0A137SLD1
E	5	HIS	-	expression tag	UNP A0A137SLD1
E	6	HIS	-	expression tag	UNP A0A137SLD1
E	7	HIS	-	expression tag	UNP A0A137SLD1
F	1	MET	-	expression tag	UNP A0A137SLD1
F	2	HIS	-	expression tag	UNP A0A137SLD1
F	3	HIS	-	expression tag	UNP A0A137SLD1
F	4	HIS	-	expression tag	UNP A0A137SLD1
F	5	HIS	-	expression tag	UNP A0A137SLD1
F	6	HIS	-	expression tag	UNP A0A137SLD1
F	7	HIS	-	expression tag	UNP A0A137SLD1

- Molecule 2 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	H	O	0	0
			10	2	6	2		
2	A	1	Total	C	H	O	0	0
			10	2	6	2		

- Molecule 3 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	9	Total	Na	0	0
			9	9		
3	B	10	Total	Na	0	0
			10	10		
3	C	11	Total	Na	0	0
			11	11		
3	D	8	Total	Na	0	0
			8	8		
3	E	3	Total	Na	0	0
			3	3		
3	F	6	Total	Na	0	0
			6	6		

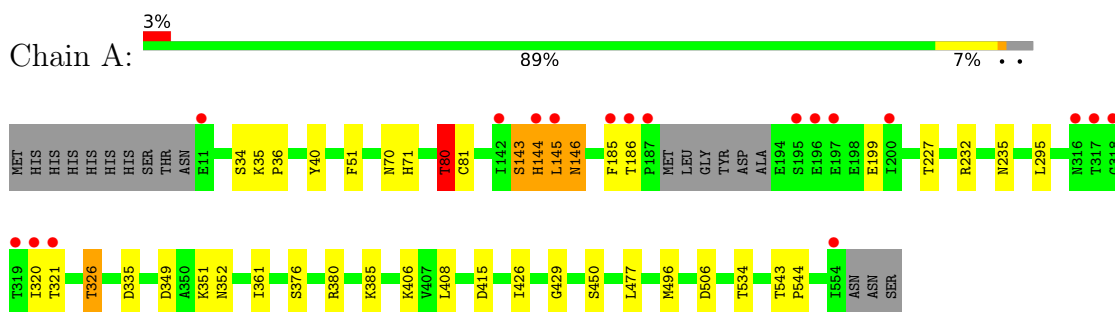
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	256	Total	O	0	0
			256	256		
4	B	146	Total	O	0	0
			146	146		
4	C	198	Total	O	0	0
			198	198		
4	D	144	Total	O	0	0
			144	144		
4	E	146	Total	O	0	0
			146	146		
4	F	94	Total	O	0	0
			94	94		

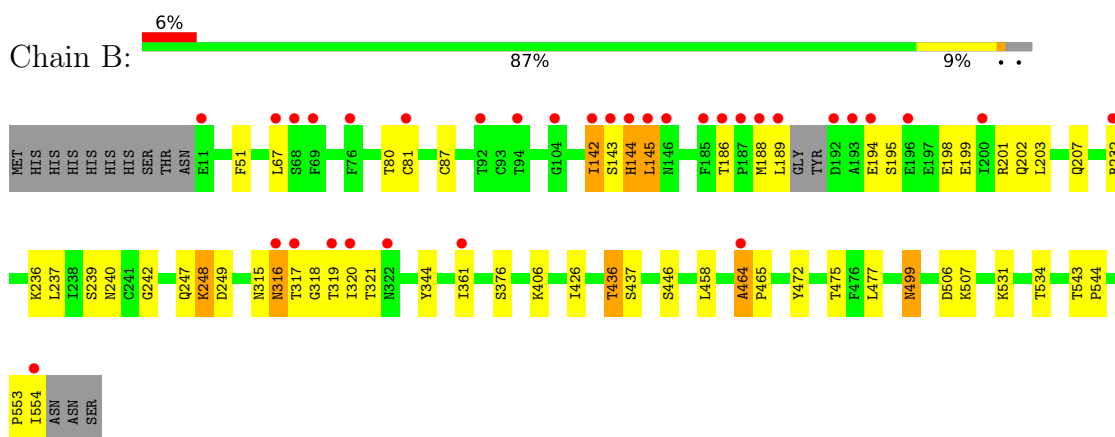
3 Residue-property plots

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.

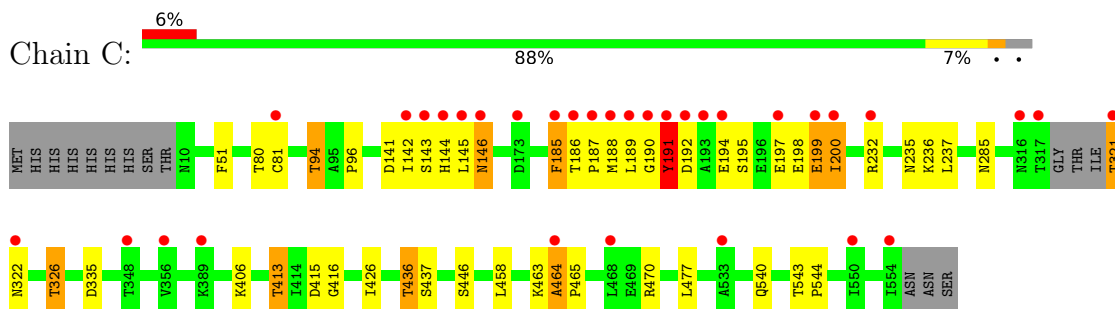
• Molecule 1: Phospholipase D



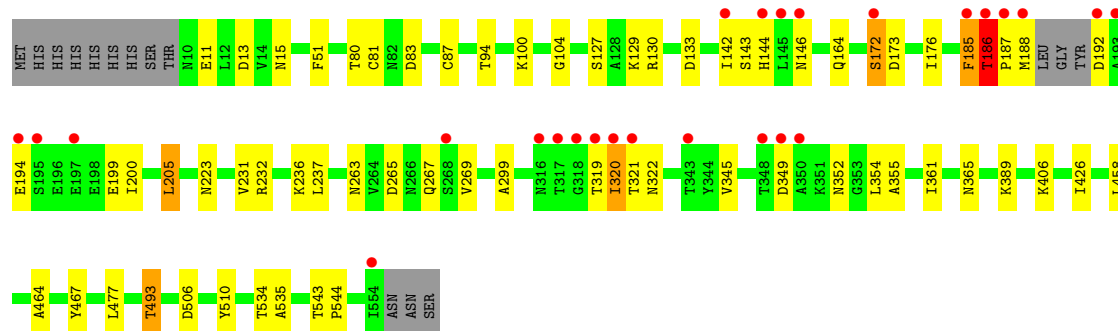
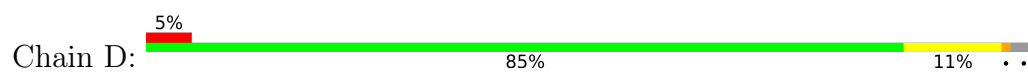
• Molecule 1: Phospholipase D



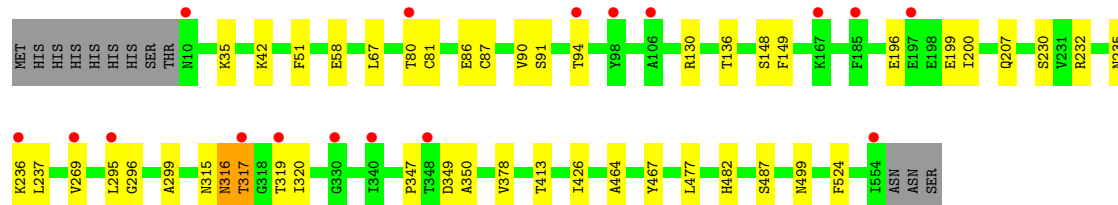
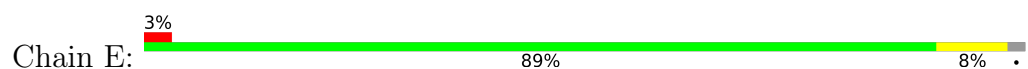
• Molecule 1: Phospholipase D



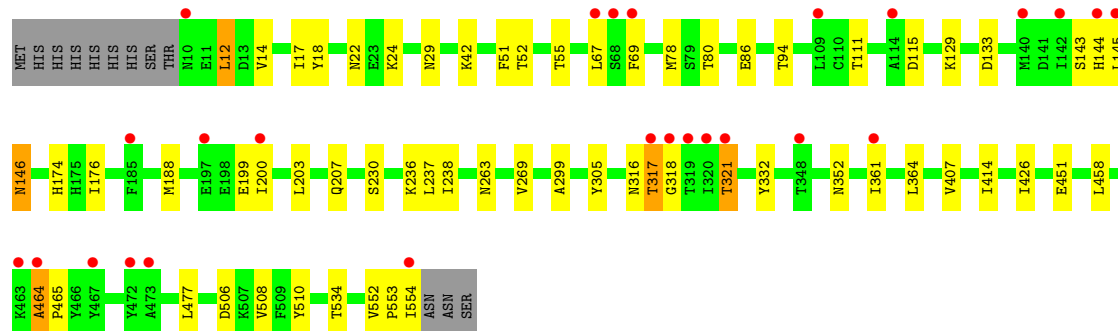
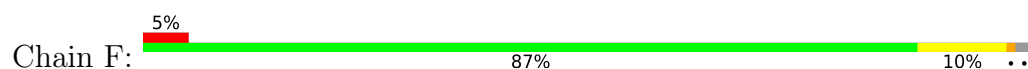
• Molecule 1: Phospholipase D



• Molecule 1: Phospholipase D



• Molecule 1: Phospholipase D



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	93.90Å 216.64Å 277.71Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.81 – 2.30 19.81 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.9 (19.81-2.30) 99.7 (19.81-2.30)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.37 (at 2.30Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874	Depositor
R, R_{free}	0.212 , 0.216 0.213 , 0.217	Depositor DCC
R_{free} test set	2000 reflections (0.80%)	wwPDB-VP
Wilson B-factor (Å ²)	66.3	Xtriage
Anisotropy	0.217	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 50.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	51186	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.06% 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: NA, 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	0.53	2/4299 (0.0%)	0.60	0/5850
1	B	0.46	0/4328	0.56	0/5889
1	C	0.50	2/4334 (0.0%)	0.60	0/5897
1	D	0.42	0/4328	0.58	3/5889 (0.1%)
1	E	0.40	0/4354	0.52	0/5926
1	F	0.37	0/4354	0.50	0/5926
All	All	0.45	4/25997 (0.0%)	0.56	3/35377 (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	2
1	B	0	3
1	C	0	4
1	D	0	2
1	E	0	1
1	F	0	1
All	All	0	13

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	285	ASN	C-O	9.12	1.28	1.23
1	A	81	CYS	CB-SG	-6.50	1.59	1.81
1	A	185	PHE	C-N	6.17	1.46	1.33
1	C	81	CYS	CB-SG	-5.13	1.64	1.81

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	186	THR	C-N-CD	-8.19	102.58	120.60
1	D	186	THR	CA-C-N	8.10	146.43	127.00
1	D	186	THR	C-N-CA	8.10	146.43	127.00

There are no chirality outliers.

5 of 13 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	145	LEU	Peptide
1	A	80	THR	Peptide
1	B	145	LEU	Peptide
1	B	248	LYS	Peptide
1	B	80	THR	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	4209	4085	4084	33	0
1	B	4238	4113	4113	56	0
1	C	4243	4111	4109	52	0
1	D	4238	4108	4108	63	0
1	E	4262	4133	4132	33	0
1	F	4262	4133	4132	49	0
2	A	8	12	12	3	0
3	A	9	0	0	0	0
3	B	10	0	0	0	0
3	C	11	0	0	0	0
3	D	8	0	0	0	0
3	E	3	0	0	0	0
3	F	6	0	0	0	0
4	A	256	0	0	5	0
4	B	146	0	0	7	0
4	C	198	0	0	2	1
4	D	144	0	0	6	0
4	E	146	0	0	7	1
4	F	94	0	0	1	0
All	All	26491	24695	24690	281	1

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.

The worst 5 of 281 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:100:LYS:NZ	1:D:164:GLN:OE1	1.83	1.11
1:D:186:THR:HG23	1:D:187:PRO:HA	1.35	1.08
1:B:344:TYR:OH	4:B:701:HOH:O	1.85	0.95
1:D:127:SER:OG	4:D:701:HOH:O	1.85	0.93
1:D:186:THR:HG23	1:D:187:PRO:CA	2.00	0.91

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:C:894:HOH:O	4:E:843:HOH:O[3_656]	1.99	0.21

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	534/557 (96%)	501 (94%)	29 (5%)	4 (1%)	18	23
1	B	538/557 (97%)	501 (93%)	34 (6%)	3 (1%)	21	27
1	C	538/557 (97%)	499 (93%)	34 (6%)	5 (1%)	14	17
1	D	538/557 (97%)	506 (94%)	27 (5%)	5 (1%)	14	17
1	E	543/557 (98%)	515 (95%)	26 (5%)	2 (0%)	30	38
1	F	543/557 (98%)	509 (94%)	28 (5%)	6 (1%)	11	13
All	All	3234/3342 (97%)	3031 (94%)	178 (6%)	25 (1%)	16	20

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	144	HIS
1	A	146	ASN
1	B	144	HIS
1	B	316	ASN
1	B	464	ALA

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	475/492 (96%)	471 (99%)	4 (1%)	73	86
1	B	478/492 (97%)	474 (99%)	4 (1%)	73	86
1	C	478/492 (97%)	469 (98%)	9 (2%)	50	69
1	D	478/492 (97%)	473 (99%)	5 (1%)	68	82
1	E	480/492 (98%)	476 (99%)	4 (1%)	73	86
1	F	480/492 (98%)	477 (99%)	3 (1%)	78	89
All	All	2869/2952 (97%)	2840 (99%)	29 (1%)	68	82

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	413	THR
1	F	94	THR
1	D	51	PHE
1	E	94	THR
1	C	540	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	70	ASN
1	E	480	ASN
1	F	409	HIS
1	E	409	HIS

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Mol	Chain	Res	Type
1	E	523	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](#)

Of 49 ligands modelled in this entry, 47 are monoatomic - leaving 2 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	EDO	A	601	-	3,3,3	0.56	0	2,2,2	0.25	0
2	EDO	A	602	-	3,3,3	0.69	0	2,2,2	0.70	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	601	-	-	0/1/1/1	-
2	EDO	A	602	-	-	1/1/1/1	-

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	602	EDO	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	EDO	1	0
2	A	602	EDO	2	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 [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	538/557 (96%)	0.24	18 (3%) 49 51	53, 69, 102, 154	0
1	B	542/557 (97%)	0.63	33 (6%) 27 29	58, 80, 122, 167	0
1	C	542/557 (97%)	0.66	33 (6%) 27 29	58, 74, 109, 199	0
1	D	542/557 (97%)	0.47	26 (4%) 35 37	58, 84, 126, 165	0
1	E	545/557 (97%)	0.59	17 (3%) 51 53	62, 85, 117, 150	0
1	F	545/557 (97%)	0.59	26 (4%) 35 37	66, 90, 119, 164	0
All	All	3254/3342 (97%)	0.53	153 (4%) 36 38	53, 81, 119, 199	0

The worst 5 of 153 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	145	LEU	6.8
1	F	145	LEU	6.5
1	A	187	PRO	6.0
1	C	191	TYR	5.9
1	F	69	PHE	5.8

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

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	601	4/4	0.77	0.23	68,79,91,91	0
3	NA	B	605	1/1	0.77	0.42	75,75,75,75	0
3	NA	C	610	1/1	0.79	0.26	83,83,83,83	0
3	NA	C	605	1/1	0.81	0.36	88,88,88,88	0
3	NA	F	606	1/1	0.83	0.20	86,86,86,86	0
3	NA	B	607	1/1	0.86	0.19	80,80,80,80	0
3	NA	D	606	1/1	0.87	0.24	80,80,80,80	0
3	NA	E	601	1/1	0.88	0.25	76,76,76,76	0
3	NA	F	601	1/1	0.88	0.24	74,74,74,74	0
3	NA	F	602	1/1	0.88	0.24	79,79,79,79	0
3	NA	C	604	1/1	0.88	0.28	73,73,73,73	0
3	NA	F	605	1/1	0.89	0.26	73,73,73,73	0
3	NA	C	611	1/1	0.89	0.17	71,71,71,71	0
2	EDO	A	602	4/4	0.90	0.14	60,71,81,82	0
3	NA	C	609	1/1	0.90	0.16	76,76,76,76	0
3	NA	A	606	1/1	0.90	0.17	65,65,65,65	0
3	NA	C	602	1/1	0.90	0.17	59,59,59,59	0
3	NA	A	609	1/1	0.90	0.19	63,63,63,63	0
3	NA	C	606	1/1	0.91	0.17	74,74,74,74	0
3	NA	C	603	1/1	0.91	0.41	72,72,72,72	0
3	NA	D	608	1/1	0.92	0.14	81,81,81,81	0
3	NA	B	602	1/1	0.92	0.33	77,77,77,77	0
3	NA	B	606	1/1	0.92	0.19	58,58,58,58	0
3	NA	C	601	1/1	0.93	0.14	56,56,56,56	0
3	NA	A	604	1/1	0.93	0.18	63,63,63,63	0
3	NA	B	609	1/1	0.93	0.27	69,69,69,69	0
3	NA	B	610	1/1	0.93	0.15	95,95,95,95	0
3	NA	A	607	1/1	0.94	0.16	43,43,43,43	0
3	NA	A	608	1/1	0.94	0.18	58,58,58,58	0
3	NA	A	605	1/1	0.94	0.11	63,63,63,63	0
3	NA	E	602	1/1	0.94	0.20	107,107,107,107	0
3	NA	A	611	1/1	0.94	0.26	65,65,65,65	0
3	NA	B	601	1/1	0.94	0.08	64,64,64,64	0
3	NA	F	604	1/1	0.94	0.16	79,79,79,79	0
3	NA	A	603	1/1	0.94	0.11	57,57,57,57	0
3	NA	B	603	1/1	0.94	0.22	68,68,68,68	0
3	NA	D	603	1/1	0.95	0.17	80,80,80,80	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	NA	C	608	1/1	0.95	0.20	68,68,68,68	0
3	NA	F	603	1/1	0.95	0.14	84,84,84,84	0
3	NA	B	608	1/1	0.95	0.19	69,69,69,69	0
3	NA	D	601	1/1	0.95	0.10	78,78,78,78	0
3	NA	D	602	1/1	0.95	0.18	75,75,75,75	0
3	NA	B	604	1/1	0.96	0.17	74,74,74,74	0
3	NA	D	604	1/1	0.96	0.28	61,61,61,61	0
3	NA	D	605	1/1	0.96	0.10	70,70,70,70	0
3	NA	E	603	1/1	0.96	0.13	69,69,69,69	0
3	NA	C	607	1/1	0.96	0.16	47,47,47,47	0
3	NA	D	607	1/1	0.97	0.30	81,81,81,81	0
3	NA	A	610	1/1	0.98	0.11	76,76,76,76	0

6.5 Other polymers [i](#)

There are no such residues in this entry.