



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 04:51 AM GMT

PDB ID : 2OGE  
Title : x-ray structure of *S. venezuelae* DesV in its internal aldimine form  
Authors : Holden, H.M.; Burgie, E.S.  
Deposited on : 2007-01-05  
Resolution : 2.05 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](mailto:validation@mail.wwpdb.org)  
A user guide is available at  
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>  
with specific help available everywhere you see the ⓘ symbol.

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The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

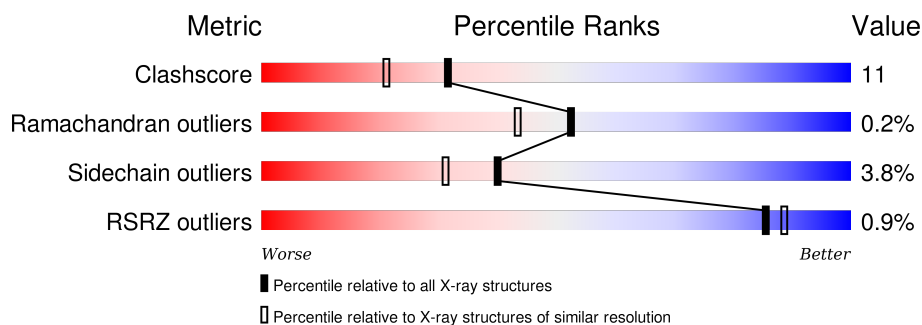
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.05 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))
Clashscore	102246	1269 (2.04-2.04)
Ramachandran outliers	100387	1258 (2.04-2.04)
Sidechain outliers	100360	1258 (2.04-2.04)
RSRZ outliers	91569	1194 (2.04-2.04)

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 on the lower bar indicate the fraction of residues that contain outliers for  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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	399	<div> <div></div> <div>60% 27% 5% 8%</div> </div>
1	B	399	<div> <div></div> <div>66% 21% 5% 8%</div> </div>
1	C	399	<div> <div></div> <div>66% 23% 8%</div> </div>
1	D	399	<div> <div></div> <div>60% 29% 8%</div> </div>

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	A	1299	-	-	-	X
3	NA	C	1304	-	-	-	X
4	EDO	A	1300	-	-	-	X
4	EDO	A	1302	-	-	-	X
4	EDO	A	1304	-	-	-	X
4	EDO	A	1305	-	-	-	X
4	EDO	A	1306	-	-	-	X
4	EDO	B	1304	-	-	-	X
4	EDO	C	1305	-	-	-	X
4	EDO	C	1307	-	-	-	X
4	EDO	C	1309	-	-	-	X
4	EDO	D	1307	-	-	-	X
4	EDO	D	1309	-	-	-	X
4	EDO	D	1310	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12743 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 Transaminase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	368	Total	C	N	O	P	S	0	0	0
			2840	1783	520	530	1	6			
1	B	369	Total	C	N	O	P	S	0	0	0
			2847	1788	521	531	1	6			
1	C	369	Total	C	N	O	P	S	0	0	0
			2847	1788	521	531	1	6			
1	D	368	Total	C	N	O	P	S	0	0	0
			2840	1783	520	530	1	6			

There are 80 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	INITIATING METHIONINE	UNP Q9ZGH4
A	-18	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-17	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-16	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-15	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
A	-14	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
A	-13	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
A	-12	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
A	-11	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
A	-10	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
A	-9	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-8	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-7	GLU	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-6	ASN	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-5	LEU	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-4	TYR	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-3	PHE	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-2	GLN	-	CLONING ARTIFACT	UNP Q9ZGH4
A	-1	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
A	0	HIS	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-19	MET	-	INITIATING METHIONINE	UNP Q9ZGH4

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-18	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-17	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-16	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-15	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
B	-14	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
B	-13	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
B	-12	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
B	-11	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
B	-10	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
B	-9	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-8	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-7	GLU	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-6	ASN	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-5	LEU	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-4	TYR	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-3	PHE	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-2	GLN	-	CLONING ARTIFACT	UNP Q9ZGH4
B	-1	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
B	0	HIS	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-19	MET	-	INITIATING METHIONINE	UNP Q9ZGH4
C	-18	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-17	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-16	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-15	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
C	-14	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
C	-13	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
C	-12	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
C	-11	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
C	-10	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
C	-9	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-8	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-7	GLU	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-6	ASN	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-5	LEU	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-4	TYR	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-3	PHE	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-2	GLN	-	CLONING ARTIFACT	UNP Q9ZGH4
C	-1	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
C	0	HIS	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-19	MET	-	INITIATING METHIONINE	UNP Q9ZGH4
D	-18	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-17	SER	-	CLONING ARTIFACT	UNP Q9ZGH4

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Chain	Residue	Modelled	Actual	Comment	Reference
D	-16	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-15	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
D	-14	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
D	-13	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
D	-12	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
D	-11	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
D	-10	HIS	-	EXPRESSION TAG	UNP Q9ZGH4
D	-9	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-8	SER	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-7	GLU	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-6	ASN	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-5	LEU	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-4	TYR	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-3	PHE	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-2	GLN	-	CLONING ARTIFACT	UNP Q9ZGH4
D	-1	GLY	-	CLONING ARTIFACT	UNP Q9ZGH4
D	0	HIS	-	CLONING ARTIFACT	UNP Q9ZGH4

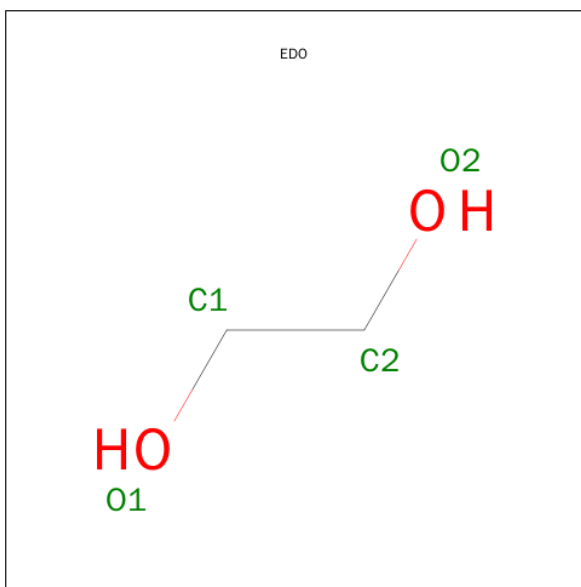
- Molecule 2 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Cl 2 2	0	0
2	A	2	Total Cl 2 2	0	0
2	D	2	Total Cl 2 2	0	0
2	C	2	Total Cl 2 2	0	0

- Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Na 1 1	0	0
3	C	1	Total Na 1 1	0	0

- Molecule 4 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



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

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

- Molecule 5 is water.

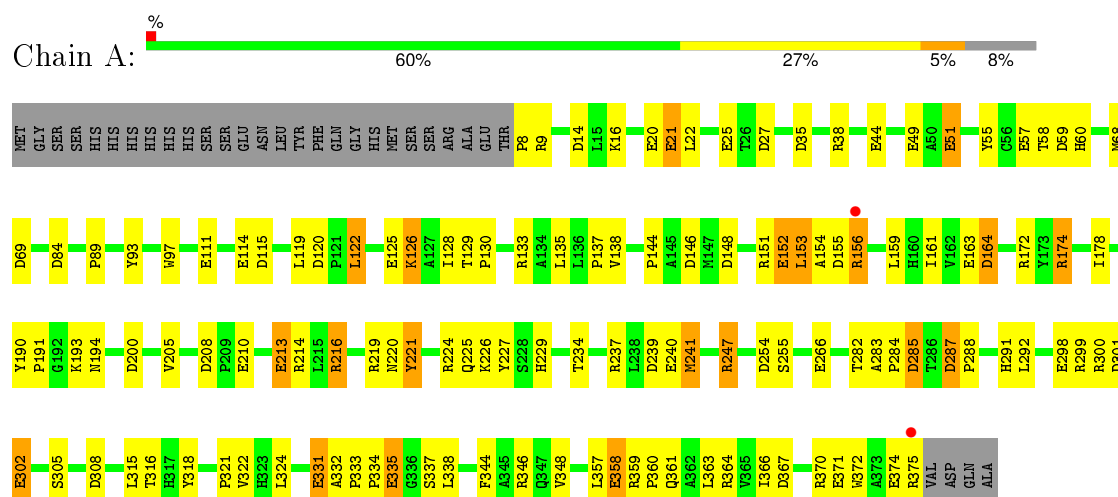
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	342	Total 342	O 342	0	0
5	B	302	Total 302	O 302	0	0
5	C	330	Total 330	O 330	0	0
5	D	301	Total 301	O 301	0	0



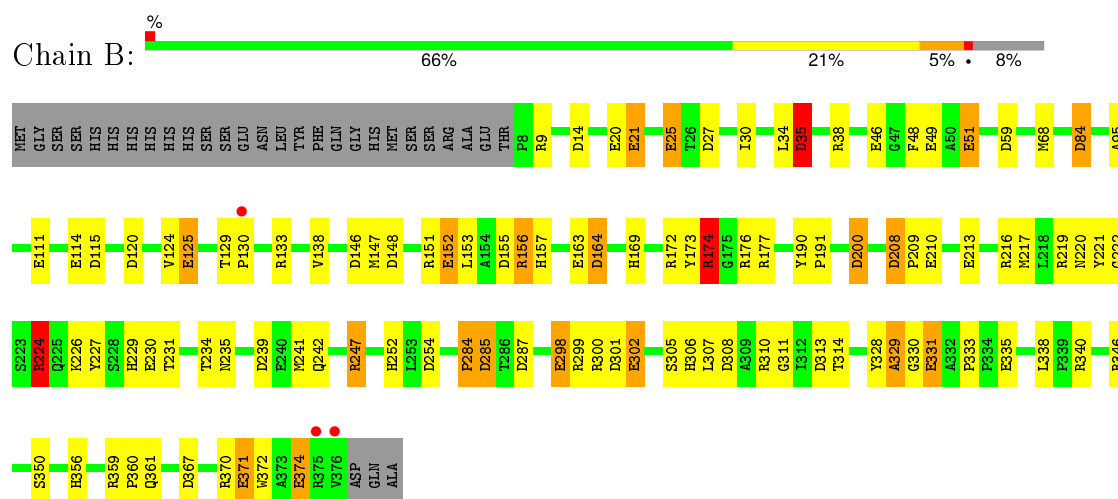
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

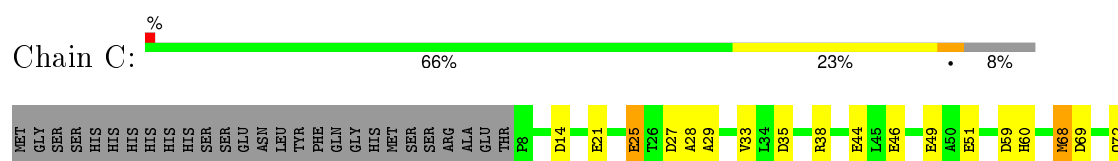
#### • Molecule 1: Transaminase

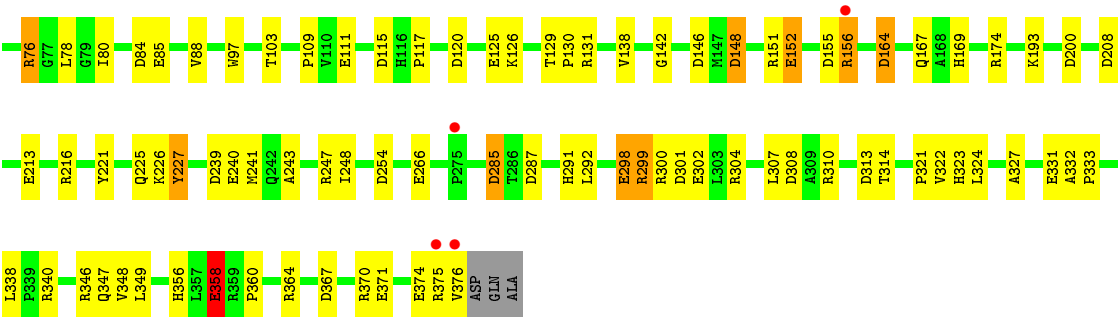


#### • Molecule 1: Transaminase

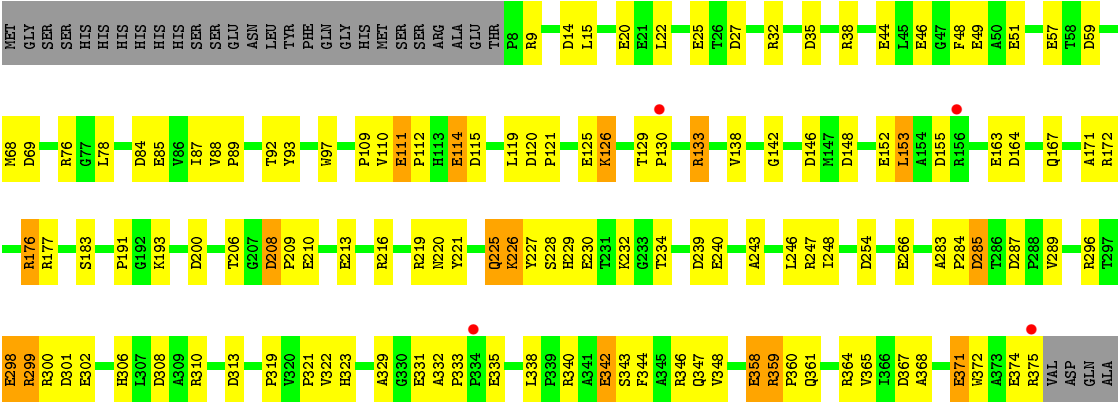


#### • Molecule 1: Transaminase





• Molecule 1: Transaminase



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.80Å 143.82Å 81.13Å 90.00° 106.95° 90.00°	Depositor
Resolution (Å)	30.50 – 2.05 30.51 – 2.05	Depositor EDS
% Data completeness (in resolution range)	92.0 (30.50-2.05) 94.0 (30.51-2.05)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.08	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	0.89 (at 2.05Å)	Xtriage
Refinement program	TNT	Depositor
R, $R_{free}$	0.159 , 0.234 0.160 , (Not available)	Depositor DCC
$R_{free}$ test set	No test flags present.	DCC
Wilson B-factor (Å <sup>2</sup> )	17.5	Xtriage
Anisotropy	0.469	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 91.1	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 92487 reflections	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	12743	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	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 60.17 % 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 1.5835e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<sup>1</sup> Intensities estimated from amplitudes.

<sup>2</sup> Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 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, LLP, 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	0.87	22/2886 (0.8%)	1.30	46/3932 (1.2%)
1	B	0.86	19/2893 (0.7%)	1.28	45/3942 (1.1%)
1	C	0.86	17/2893 (0.6%)	1.31	50/3942 (1.3%)
1	D	0.87	26/2886 (0.9%)	1.27	46/3932 (1.2%)
All	All	0.86	84/11558 (0.7%)	1.29	187/15748 (1.2%)

The worst 5 of 84 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	266	GLU	CD-OE2	6.53	1.32	1.25
1	D	25	GLU	CD-OE2	6.46	1.32	1.25
1	A	57	GLU	CD-OE2	6.28	1.32	1.25
1	D	374	GLU	CD-OE2	6.18	1.32	1.25
1	D	298	GLU	CD-OE2	6.10	1.32	1.25

The worst 5 of 187 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	239	ASP	CB-CG-OD1	10.13	127.42	118.30
1	B	224	ARG	NE-CZ-NH1	9.71	125.15	120.30
1	B	239	ASP	CB-CG-OD2	-9.69	109.58	118.30
1	C	340	ARG	NE-CZ-NH1	9.35	124.97	120.30
1	C	76	ARG	NE-CZ-NH1	9.29	124.95	120.30

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	2840	0	2782	81	0
1	B	2847	0	2791	69	0
1	C	2847	0	2791	59	0
1	D	2840	0	2782	64	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	1	0	0	0	0
3	C	1	0	0	0	0
4	A	28	0	33	4	0
4	B	12	0	16	1	0
4	C	20	0	21	3	0
4	D	24	0	26	5	0
5	A	342	0	0	5	0
5	B	302	0	0	7	0
5	C	330	0	0	8	0
5	D	301	0	0	3	0
All	All	12743	0	11242	243	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 11.

The worst 5 of 243 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:15:LEU:HB2	4:D:1310:EDO:H11	1.38	1.05
1:C:68:MET:HE3	1:D:234:THR:HA	1.54	0.89
1:C:299:ARG:HG2	1:C:299:ARG:HH11	1.39	0.87
1:B:306:HIS:CD2	1:B:372:TRP:HB2	2.21	0.77
1:A:315:LEU:HD22	1:B:226:LYS:HE2	1.68	0.76

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	365/399 (92%)	350 (96%)	15 (4%)	0	100	100
1	B	366/399 (92%)	351 (96%)	14 (4%)	1 (0%)	46	36
1	C	366/399 (92%)	347 (95%)	18 (5%)	1 (0%)	46	36
1	D	365/399 (92%)	351 (96%)	13 (4%)	1 (0%)	46	36
All	All	1462/1596 (92%)	1399 (96%)	60 (4%)	3 (0%)	52	43

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	329	ALA
1	D	299	ARG
1	C	117	PRO

### 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	287/314 (91%)	274 (96%)	13 (4%)	34	25
1	B	288/314 (92%)	277 (96%)	11 (4%)	40	31
1	C	288/314 (92%)	282 (98%)	6 (2%)	61	56
1	D	287/314 (91%)	273 (95%)	14 (5%)	31	21
All	All	1150/1256 (92%)	1106 (96%)	44 (4%)	40	31

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	284	PRO
1	C	25	GLU
1	D	344	PHE
1	B	300	ARG
1	B	331	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	169	HIS
1	B	229	HIS
1	D	72	GLN
1	B	157	HIS
1	C	306	HIS

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

4 non-standard protein/DNA/RNA residues 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
1	LLP	A	193	1	23,24,25	1.51	2 (8%)	28,32,34	1.04	2 (7%)
1	LLP	B	193	1	23,24,25	1.62	4 (17%)	28,32,34	0.97	0
1	LLP	C	193	1	23,24,25	1.44	2 (8%)	28,32,34	1.07	1 (3%)
1	LLP	D	193	1	23,24,25	1.30	2 (8%)	28,32,34	1.04	3 (10%)

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
1	LLP	A	193	1	-	0/15/17/19	0/1/1/1
1	LLP	B	193	1	-	0/15/17/19	0/1/1/1
1	LLP	C	193	1	-	0/15/17/19	0/1/1/1
1	LLP	D	193	1	-	0/15/17/19	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	193	LLP	C3-C2	-3.61	1.38	1.40
1	B	193	LLP	CB-CA	-2.04	1.51	1.53
1	B	193	LLP	P-OP1	2.36	1.58	1.51
1	C	193	LLP	P-OP1	2.41	1.59	1.51
1	A	193	LLP	P-OP1	2.60	1.59	1.51

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	193	LLP	O-C-CA	-2.27	119.58	125.49
1	A	193	LLP	O-C-CA	-2.21	119.73	125.49
1	D	193	LLP	O3-C3-C2	2.03	121.19	117.66
1	A	193	LLP	CD-CE-NZ	2.45	114.98	110.98
1	C	193	LLP	CD-CE-NZ	2.50	115.07	110.98

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	193	LLP	4	0
1	C	193	LLP	1	0
1	D	193	LLP	2	0

## 5.5 Carbohydrates

There are no carbohydrates in this entry.



## 5.6 Ligand geometry

Of 31 ligands modelled in this entry, 10 are monoatomic - leaving 21 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
4	EDO	A	1300	-	3,3,3	1.02	0	2,2,2	0.52	0
4	EDO	A	1301	-	3,3,3	1.18	0	2,2,2	0.33	0
4	EDO	A	1302	-	3,3,3	1.10	0	2,2,2	0.52	0
4	EDO	A	1303	-	3,3,3	1.09	0	2,2,2	0.49	0
4	EDO	A	1304	-	3,3,3	1.09	0	2,2,2	0.44	0
4	EDO	A	1305	-	3,3,3	1.02	0	2,2,2	0.46	0
4	EDO	A	1306	-	3,3,3	1.04	0	2,2,2	0.52	0
4	EDO	B	1302	-	3,3,3	1.05	0	2,2,2	0.48	0
4	EDO	B	1303	-	3,3,3	1.06	0	2,2,2	0.48	0
4	EDO	B	1304	-	3,3,3	1.01	0	2,2,2	0.49	0
4	EDO	C	1305	-	3,3,3	1.11	0	2,2,2	0.50	0
4	EDO	C	1306	-	3,3,3	1.09	0	2,2,2	0.49	0
4	EDO	C	1307	-	3,3,3	1.09	0	2,2,2	0.46	0
4	EDO	C	1308	-	3,3,3	1.15	0	2,2,2	0.54	0
4	EDO	C	1309	-	3,3,3	1.09	0	2,2,2	0.58	0
4	EDO	D	1307	-	3,3,3	1.05	0	2,2,2	0.57	0
4	EDO	D	1308	-	3,3,3	1.07	0	2,2,2	0.39	0
4	EDO	D	1309	-	3,3,3	1.06	0	2,2,2	0.62	0
4	EDO	D	1310	-	3,3,3	1.05	0	2,2,2	0.49	0
4	EDO	D	1311	-	3,3,3	1.18	0	2,2,2	0.38	0
4	EDO	D	1312	-	3,3,3	1.08	0	2,2,2	0.47	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
4	EDO	A	1300	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1301	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1302	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1303	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	EDO	A	1304	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1305	-	-	0/1/1/1	0/0/0/0
4	EDO	A	1306	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1302	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1303	-	-	0/1/1/1	0/0/0/0
4	EDO	B	1304	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1305	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1306	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1307	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1308	-	-	0/1/1/1	0/0/0/0
4	EDO	C	1309	-	-	0/1/1/1	0/0/0/0
4	EDO	D	1307	-	-	0/1/1/1	0/0/0/0
4	EDO	D	1308	-	-	0/1/1/1	0/0/0/0
4	EDO	D	1309	-	-	0/1/1/1	0/0/0/0
4	EDO	D	1310	-	-	0/1/1/1	0/0/0/0
4	EDO	D	1311	-	-	0/1/1/1	0/0/0/0
4	EDO	D	1312	-	-	0/1/1/1	0/0/0/0

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.

9 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1301	EDO	1	0
4	A	1304	EDO	2	0
4	A	1305	EDO	1	0
4	B	1304	EDO	1	0
4	C	1308	EDO	1	0
4	C	1309	EDO	2	0
4	D	1308	EDO	1	0
4	D	1310	EDO	3	0
4	D	1311	EDO	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	367/399 (91%)	-0.39	2 (0%) 91 93	11, 20, 44, 81	0
1	B	368/399 (92%)	-0.44	3 (0%) 87 90	10, 20, 46, 80	0
1	C	368/399 (92%)	-0.49	4 (1%) 82 86	10, 18, 43, 77	0
1	D	367/399 (91%)	-0.38	4 (1%) 82 86	11, 21, 48, 95	0
All	All	1470/1596 (92%)	-0.42	13 (0%) 85 89	10, 20, 46, 95	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	375	ARG	5.5
1	B	376	VAL	4.6
1	B	375	ARG	3.4
1	C	375	ARG	3.4
1	D	130	PRO	3.1

### 6.2 Non-standard residues in protein, DNA, RNA chains [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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
1	LLP	A	193	24/25	0.97	0.12	-	10,16,26,54	0
1	LLP	B	193	24/25	0.98	0.11	-	5,15,22,38	0
1	LLP	C	193	24/25	0.97	0.12	-	5,14,21,37	0
1	LLP	D	193	24/25	0.98	0.12	-	8,14,22,41	0

## 6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
4	EDO	A	1306	4/4	0.83	0.28	15.29	43,47,100,100	0
4	EDO	D	1310	4/4	0.91	0.24	10.01	13,32,45,78	0
4	EDO	C	1305	4/4	0.90	0.18	9.89	29,34,39,76	0
4	EDO	B	1304	4/4	0.78	0.24	8.55	51,58,64,88	0
4	EDO	C	1309	4/4	0.73	0.28	6.68	34,51,61,90	0
4	EDO	A	1300	4/4	0.92	0.19	6.50	38,39,39,43	0
3	NA	C	1304	1/1	0.99	0.20	5.06	12,12,12,12	0
4	EDO	C	1307	4/4	0.87	0.17	4.45	37,45,55,67	0
3	NA	A	1299	1/1	0.98	0.17	4.15	14,14,14,14	0
4	EDO	D	1307	4/4	0.94	0.13	3.09	25,30,32,33	0
4	EDO	A	1304	4/4	0.90	0.17	2.99	26,36,56,100	0
4	EDO	D	1309	4/4	0.94	0.13	2.78	21,37,40,42	0
4	EDO	A	1302	4/4	0.94	0.13	2.55	27,34,52,54	0
4	EDO	A	1305	4/4	0.91	0.15	2.28	30,34,44,49	0
4	EDO	A	1301	4/4	0.94	0.12	1.99	24,37,41,44	0
4	EDO	A	1303	4/4	0.97	0.11	1.68	21,23,28,32	0
4	EDO	C	1306	4/4	0.96	0.11	1.06	24,31,33,43	0
4	EDO	D	1308	4/4	0.95	0.11	0.46	20,20,21,28	0
4	EDO	B	1303	4/4	0.97	0.10	0.28	22,23,28,29	0
2	CL	A	1298	1/1	0.99	0.08	-0.42	22,22,22,22	0
2	CL	C	1303	1/1	0.98	0.06	-1.39	30,30,30,30	0
2	CL	D	1305	1/1	0.98	0.07	-1.51	27,27,27,27	0
2	CL	C	1302	1/1	1.00	0.04	-2.86	23,23,23,23	0
2	CL	B	1300	1/1	1.00	0.05	-3.65	27,27,27,27	0
2	CL	A	1297	1/1	0.98	0.04	-3.91	30,30,30,30	0
4	EDO	B	1302	4/4	0.93	0.17	-	27,36,43,45	0
4	EDO	C	1308	4/4	0.88	0.18	-	38,52,60,62	0
2	CL	B	1301	1/1	0.98	0.07	-	38,38,38,38	0
2	CL	D	1306	1/1	1.00	0.06	-	23,23,23,23	0
4	EDO	D	1311	4/4	0.83	0.22	-	43,51,83,100	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	EDO	D	1312	4/4	0.93	0.20	-	26,33,41,51	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.