



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 22, 2016 – 08:52 PM EDT

PDB ID : 5B2P  
Title : Crystal structure of Francisella novicida Cas9 in complex with sgRNA and target DNA (TGA PAM)  
Authors : Hirano, H.; Nishimasu, H.; Nakane, T.; Ishitani, R.; Nureki, O.  
Deposited on : 2016-02-01  
Resolution : 1.70 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 : 1.7.1 (RC1), CSD as537be (2016)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20027107  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0122  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : rb-20027107

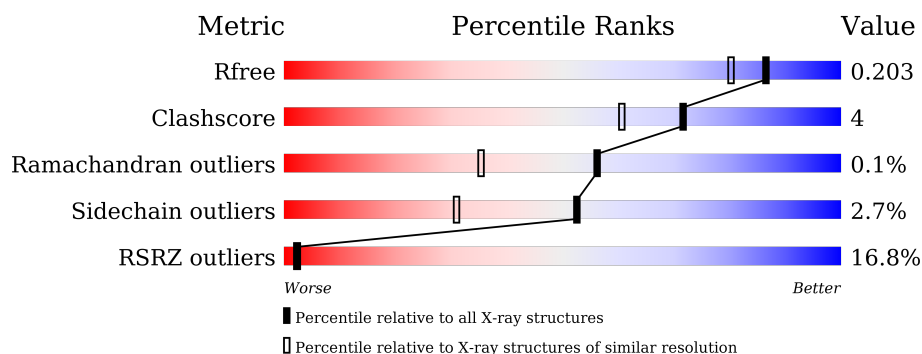
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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))
$R_{free}$	91344	3190 (1.70-1.70)
Clashscore	102246	3585 (1.70-1.70)
Ramachandran outliers	100387	3527 (1.70-1.70)
Sidechain outliers	100360	3527 (1.70-1.70)
RSRZ outliers	91569	3200 (1.70-1.70)

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	1632	<div> <div>16%</div> <div> <div>79%</div> <div>9%</div> <div>11%</div> </div> </div>
2	B	94	<div> <div>27%</div> <div>62%</div> <div>12%</div> </div>
3	C	30	<div> <div>7%</div> <div>47%</div> <div>43%</div> <div>10%</div> </div>
4	D	9	<div> <div>33%</div> <div>67%</div> <div>22%</div> <div>11%</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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
10	ACT	B	120	-	-	-	X
9	EDO	A	1724	-	-	-	X
9	EDO	A	1726	-	-	-	X
9	EDO	B	110	-	-	-	X
9	EDO	B	114	-	-	-	X
9	EDO	B	115	-	-	-	X

## 2 Entry composition

There are 11 unique types of molecules in this entry. The entry contains 15757 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 CRISPR-associated endonuclease Cas9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1455	Total	C	N	O	S	0	18	0
			11809	7555	2030	2193	31			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP A0Q5Y3
A	-1	SER	-	expression tag	UNP A0Q5Y3
A	0	HIS	-	expression tag	UNP A0Q5Y3
A	995	ALA	ASN	engineered mutation	UNP A0Q5Y3

- Molecule 2 is DNA/RNA hybrid called Guide RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	94	Total	C	N	O	P	0	0	0
			1991	886	350	661	94			

- Molecule 3 is a DNA chain called Target DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	30	Total	C	N	O	P	0	0	0
			596	286	104	177	29			

- Molecule 4 is a DNA chain called DNA (5'-D(\*TP\*GP\*AP\*TP\*AP\*TP\*CP\*GP\*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	9	Total	C	N	O	P	0	0	0
			184	89	34	53	8			

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Zn 1 1	0	0

- Molecule 6 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	2	Total Na 2 2	0	0
6	A	2	Total Na 2 2	0	0

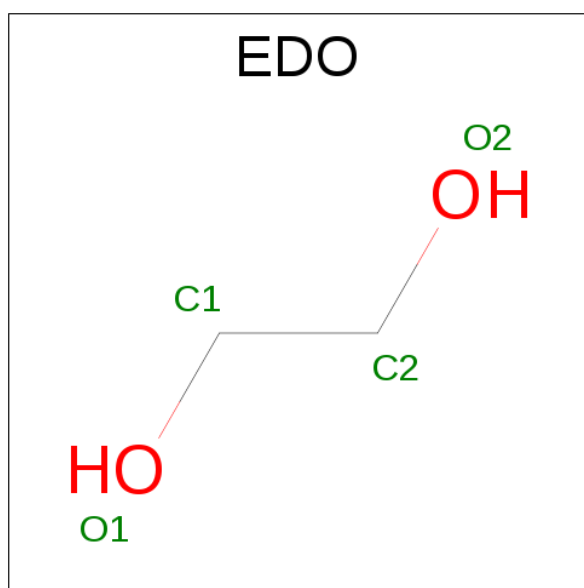
- Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	2	Total Cl 2 2	0	0

- Molecule 8 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	B	6	Total Ca 6 6	0	0
8	A	11	Total Ca 11 11	0	0

- Molecule 9 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C<sub>2</sub>H<sub>6</sub>O<sub>2</sub>).



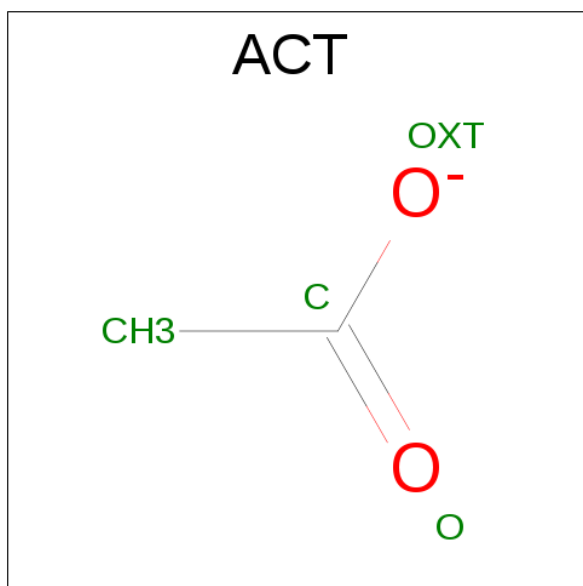
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0	0
9	A	1	Total 4	C 2	O 2	0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

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 10 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



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

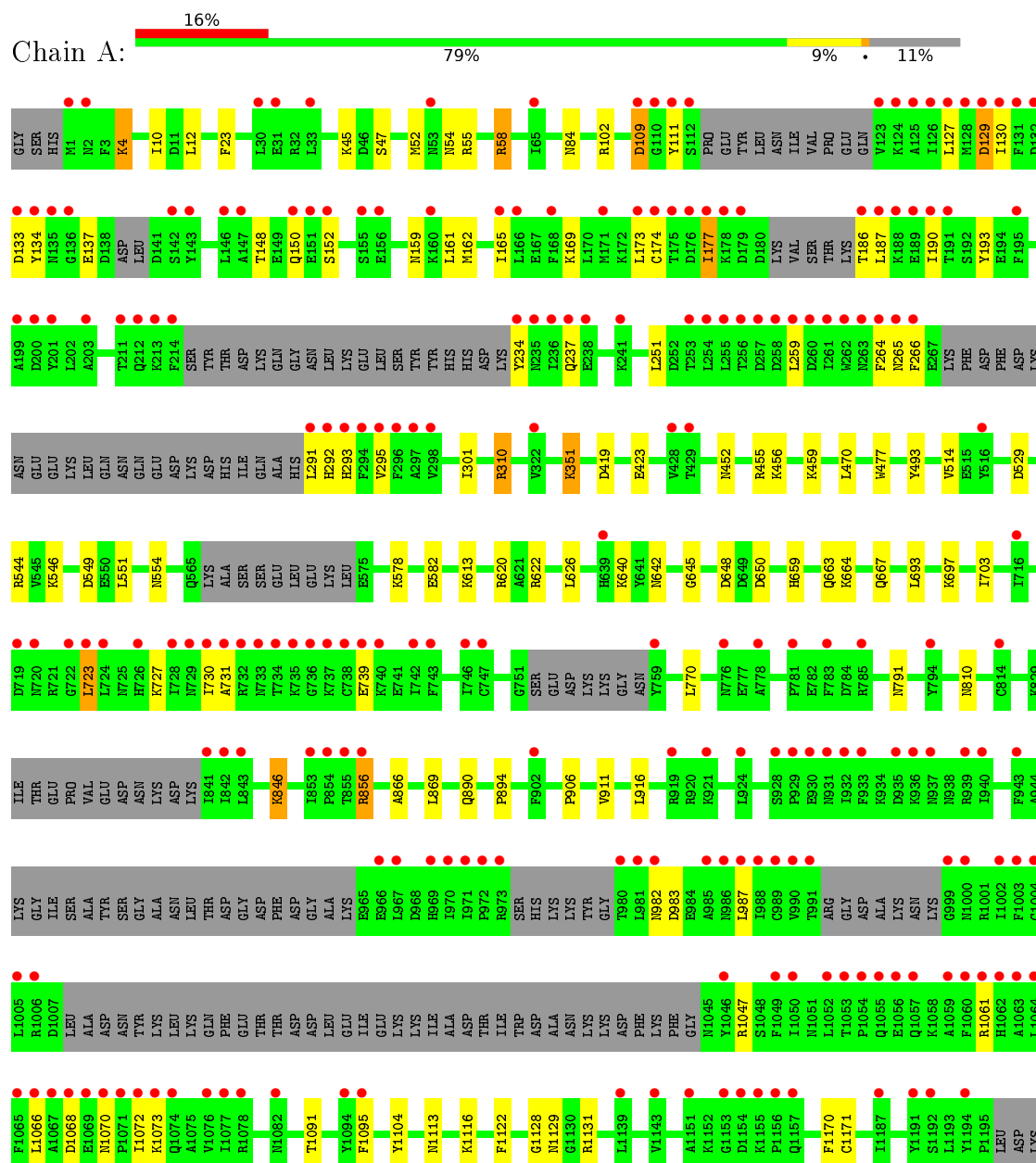
- Molecule 11 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	A	639	Total	O	0	0
			639	639		
11	B	342	Total	O	0	0
			342	342		
11	C	68	Total	O	0	0
			68	68		
11	D	4	Total	O	0	0
			4	4		

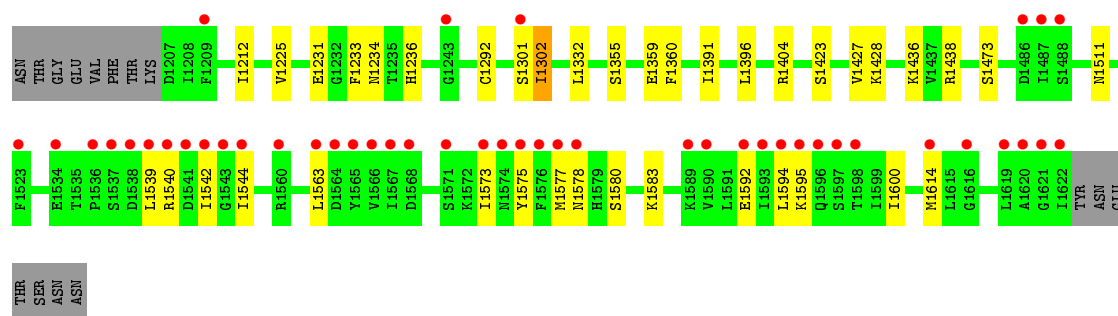
### 3 Residue-property plots

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: CRISPR-associated endonuclease Cas9

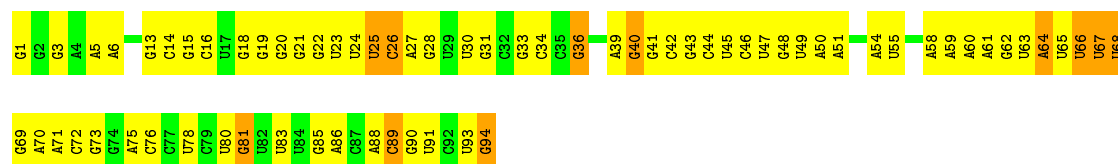






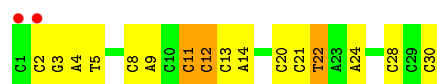
• Molecule 2: Guide RNA

Chain B: 27% 62% 12%



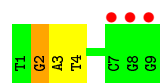
• Molecule 3: Target DNA

Chain C: 7% 47% 43% 10%



• Molecule 4: DNA (5'-D(\*TP\*GP\*AP\*TP\*AP\*TP\*CP\*GP\*G)-3')

Chain D: 33% 67% 22% 11%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	81.61Å 159.27Å 96.67Å 90.00° 106.86° 90.00°	Depositor
Resolution (Å)	46.26 – 1.70 46.26 – 1.70	Depositor EDS
% Data completeness (in resolution range)	98.8 (46.26-1.70) 98.8 (46.26-1.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.31 (at 1.70Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.180 , 0.203 0.179 , 0.203	Depositor DCC
$R_{free}$ test set	12758 reflections (5.00%)	DCC
Wilson B-factor (Å <sup>2</sup> )	28.6	Xtriage
Anisotropy	0.036	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 50.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 255174 reflections	Xtriage
$F_o, F_c$ correlation	0.97	EDS
Total number of atoms	15757	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.18% of the height of the origin peak. No significant pseudotranslation is detected.*

<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: ZN, CL, NA, CA, EDO, ACT

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	0.66	2/12080 (0.0%)	0.73	11/16292 (0.1%)
2	B	1.61	30/2224 (1.3%)	1.98	122/3465 (3.5%)
3	C	1.62	10/665 (1.5%)	1.55	10/1020 (1.0%)
4	D	1.24	0/206	1.11	1/317 (0.3%)
All	All	0.93	42/15175 (0.3%)	1.09	144/21094 (0.7%)

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
2	B	0	1

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	9	DA	N3-C4	-9.14	1.29	1.34
2	B	43	G	N7-C5	9.11	1.44	1.39
2	B	46	C	N1-C6	8.56	1.42	1.37
2	B	76	C	N1-C6	7.11	1.41	1.37
3	C	20	DC	N3-C4	-6.90	1.29	1.33

The worst 5 of 144 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	12	DC	O5'-P-OP2	-12.73	94.24	105.70
2	B	24	U	C5-C6-N1	-11.26	117.07	122.70
2	B	27	A	O5'-P-OP2	-10.63	96.13	105.70
3	C	11	DC	O5'-P-OP2	-9.59	97.07	105.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	68	U	C4-C5-C6	9.31	125.29	119.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	B	36	G	Sidechain

## 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	11809	0	11590	101	0
2	B	1991	0	997	14	0
3	C	596	0	338	12	0
4	D	184	0	104	2	0
5	A	1	0	0	0	0
6	A	2	0	0	0	0
6	B	2	0	0	0	0
7	A	2	0	0	0	0
8	A	11	0	0	0	0
8	B	6	0	0	0	0
9	A	44	0	66	3	0
9	B	44	0	66	8	0
9	C	4	0	6	0	0
10	A	4	0	3	0	0
10	B	4	0	3	0	0
11	A	639	0	0	14	0
11	B	342	0	0	2	0
11	C	68	0	0	0	0
11	D	4	0	0	0	0
All	All	15757	0	13173	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 4.

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:A:54[B]:ASN:OD1	1:A:58[B]:ARG:NH1	1.91	1.03
1:A:169:LYS:HB3	1:A:187:LEU:HD21	1.63	0.79
3:C:22:DT:H5"	3:C:22:DT:H6	1.46	0.79
1:A:906:PRO:HA	1:A:916:LEU:HD21	1.64	0.78
1:A:578:LYS:NZ	1:A:582:GLU:OE2	2.17	0.77

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	1445/1632 (88%)	1407 (97%)	37 (3%)	1 (0%)	56 35

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	1128	GLY

### 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	1259/1484 (85%)	1226 (97%)	33 (3%)	54 32

5 of 33 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	723	LEU
1	A	856	ARG
1	A	1578	ASN
1	A	730	ILE
1	A	791	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	642	ASN
1	A	659	HIS
1	A	1157	GLN
1	A	604	GLN
1	A	1234	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 carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 49 ligands modelled in this entry, 24 are monoatomic - leaving 25 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
9	EDO	A	1717	-	3,3,3	0.37	0	2,2,2	0.84	0
9	EDO	A	1718	-	3,3,3	0.47	0	2,2,2	0.82	0
9	EDO	A	1719	-	3,3,3	0.60	0	2,2,2	0.39	0
9	EDO	A	1720	-	3,3,3	1.00	0	2,2,2	0.21	0
9	EDO	A	1721	-	3,3,3	0.79	0	2,2,2	0.78	0
9	EDO	A	1722	-	3,3,3	0.41	0	2,2,2	0.80	0
9	EDO	A	1723	-	3,3,3	0.63	0	2,2,2	0.38	0
9	EDO	A	1724	-	3,3,3	0.58	0	2,2,2	0.16	0
9	EDO	A	1725	-	3,3,3	0.60	0	2,2,2	0.25	0
9	EDO	A	1726	-	3,3,3	0.47	0	2,2,2	0.34	0
9	EDO	A	1727	-	3,3,3	0.40	0	2,2,2	0.84	0
10	ACT	A	1728	-	0,3,3	0.00	-	0,3,3	0.00	-
9	EDO	B	109	-	3,3,3	0.56	0	2,2,2	0.51	0
9	EDO	B	110	-	3,3,3	0.68	0	2,2,2	0.85	0
9	EDO	B	111	-	3,3,3	0.66	0	2,2,2	0.23	0
9	EDO	B	112	-	3,3,3	0.80	0	2,2,2	0.14	0
9	EDO	B	113	-	3,3,3	0.48	0	2,2,2	0.33	0
9	EDO	B	114	-	3,3,3	0.72	0	2,2,2	0.35	0
9	EDO	B	115	-	3,3,3	0.59	0	2,2,2	0.16	0
9	EDO	B	116	-	3,3,3	0.40	0	2,2,2	0.77	0
9	EDO	B	117	-	3,3,3	0.55	0	2,2,2	0.37	0
9	EDO	B	118	-	3,3,3	0.36	0	2,2,2	0.42	0
9	EDO	B	119	-	3,3,3	0.49	0	2,2,2	0.27	0
10	ACT	B	120	-	0,3,3	0.00	-	0,3,3	0.00	-
9	EDO	C	101	-	3,3,3	0.57	0	2,2,2	0.24	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
9	EDO	A	1717	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1718	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1719	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1720	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1721	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1722	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1723	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1724	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1725	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1726	-	-	0/1/1/1	0/0/0/0
9	EDO	A	1727	-	-	0/1/1/1	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
10	ACT	A	1728	-	-	0/0/0/0	0/0/0/0
9	EDO	B	109	-	-	0/1/1/1	0/0/0/0
9	EDO	B	110	-	-	0/1/1/1	0/0/0/0
9	EDO	B	111	-	-	0/1/1/1	0/0/0/0
9	EDO	B	112	-	-	0/1/1/1	0/0/0/0
9	EDO	B	113	-	-	0/1/1/1	0/0/0/0
9	EDO	B	114	-	-	0/1/1/1	0/0/0/0
9	EDO	B	115	-	-	0/1/1/1	0/0/0/0
9	EDO	B	116	-	-	0/1/1/1	0/0/0/0
9	EDO	B	117	-	-	0/1/1/1	0/0/0/0
9	EDO	B	118	-	-	0/1/1/1	0/0/0/0
9	EDO	B	119	-	-	0/1/1/1	0/0/0/0
10	ACT	B	120	-	-	0/0/0/0	0/0/0/0
9	EDO	C	101	-	-	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.

6 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
9	A	1722	EDO	2	0
9	A	1726	EDO	1	0
9	B	116	EDO	3	0
9	B	117	EDO	1	0
9	B	118	EDO	3	0
9	B	119	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 [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	1455/1632 (89%)	0.83	262 (18%) <b>2</b> <b>2</b>	20, 44, 95, 129	0
2	B	94/94 (100%)	-0.21	0 <b>100</b> <b>100</b>	20, 30, 59, 80	0
3	C	30/30 (100%)	0.01	2 (6%) <b>21</b> <b>23</b>	24, 46, 92, 133	0
4	D	9/9 (100%)	0.96	3 (33%) <b>0</b> <b>0</b>	39, 52, 111, 119	0
All	All	1588/1765 (89%)	0.75	267 (16%) <b>2</b> <b>2</b>	20, 43, 94, 133	0

The worst 5 of 267 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1542	ILE	10.9
1	A	1573	ILE	9.5
1	A	131	PHE	9.5
1	A	723	LEU	8.8
1	A	1565	TYR	8.8

### 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 carbohydrates 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. 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( $\text{\AA}^2$ )	Q<0.9
10	ACT	B	120	4/4	0.94	0.18	5.33	76,77,77,77	0
9	EDO	B	115	4/4	0.92	0.10	3.13	43,47,52,55	0
9	EDO	B	114	4/4	0.85	0.19	2.98	46,49,52,52	0
9	EDO	A	1726	4/4	0.94	0.14	2.80	49,49,56,58	0
9	EDO	B	110	4/4	0.95	0.11	2.56	32,33,33,37	0
9	EDO	A	1724	4/4	0.91	0.12	2.26	44,45,45,46	0
9	EDO	A	1727	4/4	0.78	0.18	1.68	62,62,63,65	0
9	EDO	A	1721	4/4	0.90	0.15	1.00	32,32,36,36	0
9	EDO	A	1718	4/4	0.95	0.12	0.75	36,40,43,48	0
9	EDO	B	112	4/4	0.98	0.11	0.57	28,29,32,32	0
9	EDO	B	109	4/4	0.97	0.09	0.55	30,31,33,36	0
9	EDO	A	1722	4/4	0.92	0.17	0.42	48,49,52,53	0
9	EDO	B	117	4/4	0.89	0.13	0.32	43,45,46,46	0
5	ZN	A	1701	1/1	0.99	0.13	0.17	26,26,26,26	0
10	ACT	A	1728	4/4	0.96	0.11	0.11	32,33,34,35	0
9	EDO	A	1719	4/4	0.96	0.07	-0.06	31,34,37,39	0
9	EDO	A	1720	4/4	0.92	0.15	-0.15	30,36,38,39	0
8	CA	A	1715	1/1	0.98	0.08	-0.24	52,52,52,52	0
9	EDO	A	1723	4/4	0.97	0.08	-0.24	27,32,37,42	0
7	CL	A	1705	1/1	0.99	0.09	-0.24	28,28,28,28	0
9	EDO	C	101	4/4	0.88	0.13	-0.38	45,49,50,52	0
9	EDO	B	111	4/4	0.98	0.13	-0.40	23,24,24,27	0
9	EDO	B	116	4/4	0.92	0.13	-0.49	37,47,50,51	0
8	CA	B	108	1/1	0.93	0.11	-0.55	80,80,80,80	0
9	EDO	B	113	4/4	0.93	0.08	-0.55	36,36,39,40	0
7	CL	A	1704	1/1	0.98	0.06	-0.79	43,43,43,43	0
8	CA	A	1706	1/1	0.97	0.05	-1.12	67,67,67,67	0
6	NA	A	1702	1/1	0.95	0.07	-1.19	43,43,43,43	0
8	CA	B	103	1/1	0.99	0.05	-1.49	33,33,33,33	0
6	NA	B	101	1/1	1.00	0.07	-1.76	27,27,27,27	0
9	EDO	A	1717	4/4	0.97	0.08	-1.77	40,42,44,45	0
8	CA	A	1709	1/1	0.99	0.07	-3.63	50,50,50,50	0
9	EDO	A	1725	4/4	0.70	0.17	-	60,61,61,62	0
8	CA	A	1708	1/1	0.98	0.04	-	42,42,42,42	0
8	CA	B	106	1/1	0.93	0.07	-	54,54,54,54	0
9	EDO	B	119	4/4	0.85	0.20	-	44,46,47,49	0
8	CA	B	107	1/1	0.92	0.09	-	84,84,84,84	0
8	CA	A	1713	1/1	0.90	0.12	-	96,96,96,96	0
8	CA	B	104	1/1	0.88	0.05	-	73,73,73,73	0
8	CA	A	1707	1/1	1.00	0.03	-	34,34,34,34	0
8	CA	A	1710	1/1	0.94	0.09	-	48,48,48,48	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
8	CA	A	1712	1/1	0.95	0.11	-	61,61,61,61	0
6	NA	A	1703	1/1	0.87	0.08	-	61,61,61,61	0
9	EDO	B	118	4/4	0.84	0.18	-	56,57,58,58	0
8	CA	B	105	1/1	0.99	0.06	-	35,35,35,35	0
6	NA	B	102	1/1	0.95	0.15	-	46,46,46,46	0
8	CA	A	1711	1/1	0.92	0.06	-	79,79,79,79	0
8	CA	A	1714	1/1	0.96	0.13	-	60,60,60,60	0
8	CA	A	1716	1/1	0.96	0.08	-	56,56,56,56	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.