



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 01:11 PM UTC

PDB ID : 5B2T / pdb_00005b2t
Title : Crystal structure of the Streptococcus pyogenes Cas9 VRER variant in complex with sgRNA and target DNA (TGCG PAM)
Authors : Hirano, S.; Nishimasu, H.; Ishitani, R.; Nureki, O.
Deposited on : 2016-02-02
Resolution : 2.20 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)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

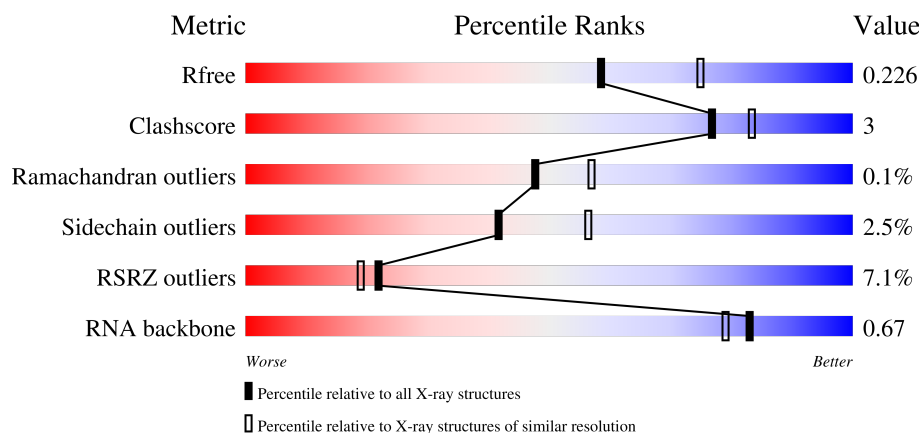
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)
RNA backbone	3983	1052 (2.50-1.90)

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	81	83% 17%
2	B	1372	7% 87% 9% ••
3	C	28	82% 18%
4	D	8	88% 12%

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 13608 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 RNA chain called Guide RNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	81	Total	C	N	O	P	0	0	0
			1739	778	319	561	81			

- Molecule 2 is a protein called CRISPR-associated endonuclease Cas9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	1326	Total	C	N	O	S	0	0	0
			10499	6699	1812	1968	20			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-3	GLY	-	expression tag	UNP Q99ZW2
B	-2	SER	-	expression tag	UNP Q99ZW2
B	-1	GLY	-	expression tag	UNP Q99ZW2
B	0	HIS	-	expression tag	UNP Q99ZW2
B	10	ALA	ASP	engineered mutation	UNP Q99ZW2
B	80	LEU	CYS	engineered mutation	UNP Q99ZW2
B	574	GLU	CYS	engineered mutation	UNP Q99ZW2
B	840	ALA	HIS	engineered mutation	UNP Q99ZW2
B	1135	VAL	ASP	engineered mutation	UNP Q99ZW2
B	1218	ARG	GLY	engineered mutation	UNP Q99ZW2
B	1335	GLU	ARG	engineered mutation	UNP Q99ZW2
B	1337	ARG	THR	engineered mutation	UNP Q99ZW2

- Molecule 3 is a DNA chain called Target DNA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	28	Total	C	N	O	P	0	0	0
			562	269	103	163	27			

- Molecule 4 is a DNA chain called Non-target DNA, DNA (5'-D(*TP*GP*CP*GP*AP*TP*

TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	8	Total	C	N	O	P	0	0	0
			163	79	29	48	7			

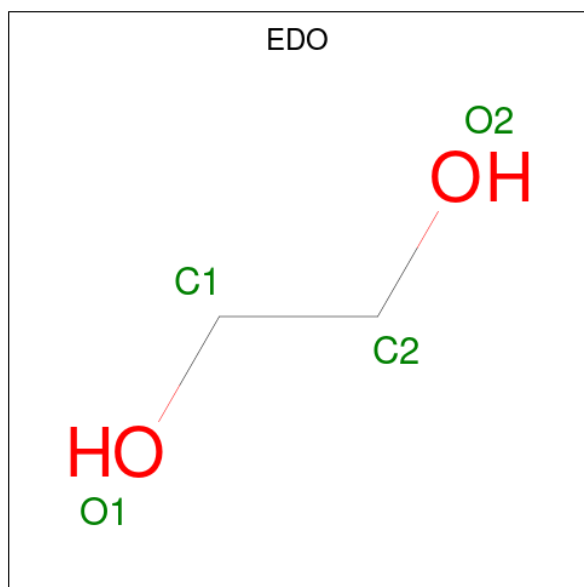
- Molecule 5 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	K	0	0
			3	3		
5	B	7	Total	K	0	0
			7	7		

- Molecule 6 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	3	Total	Mg	0	0
			3	3		

- Molecule 7 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: C₂H₆O₂).



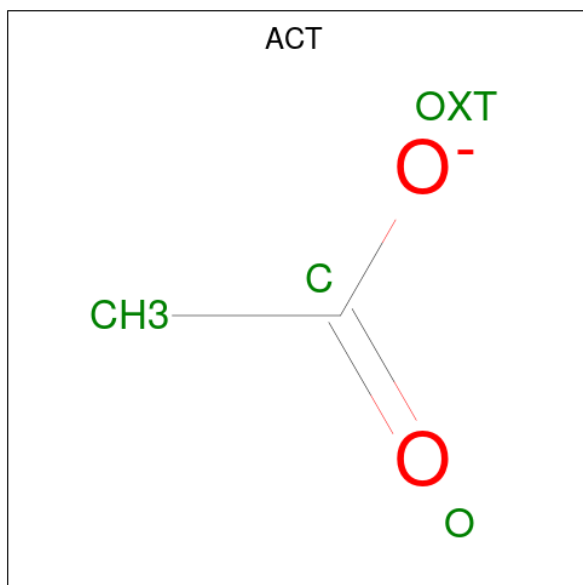
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			4	2	2		
7	B	1	Total	C	O	0	0
			4	2	2		

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

- Molecule 8 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$).



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

- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	180	Total	O	0	0
			180	180		
9	B	387	Total	O	0	0
			387	387		
9	C	35	Total	O	0	0
			35	35		
9	D	6	Total	O	0	0
			6	6		



- Molecule 4: Non-target DNA, DNA (5'-D(*TP*GP*CP*GP*AP*TP*TP*G)-3')

Chain D: 88% 12%



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	176.97Å 69.45Å 188.20Å 90.00° 109.67° 90.00°	Depositor
Resolution (Å)	49.01 – 2.20 49.01 – 2.20	Depositor EDS
% Data completeness (in resolution range)	94.5 (49.01-2.20) 94.5 (49.01-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.13 (at 2.20Å)	Xtriage
Refinement program	PHENIX 1.10_2155: ???	Depositor
R, R_{free}	0.204 , 0.223 0.207 , 0.226	Depositor DCC
R_{free} test set	5152 reflections (4.70%)	wwPDB-VP
Wilson B-factor (Å ²)	39.9	Xtriage
Anisotropy	0.364	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 43.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	13608	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% 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, MG, K, 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	0.09	0/1949	0.23	0/3037
2	B	0.10	0/10686	0.28	0/14425
3	C	0.19	0/629	0.38	0/966
4	D	0.22	0/182	0.43	0/280
All	All	0.11	0/13446	0.28	0/18708

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	1739	0	870	5	0
2	B	10499	0	10347	67	0
3	C	562	0	315	3	0
4	D	163	0	93	1	0
5	A	3	0	0	0	0
5	B	7	0	0	0	0
6	A	3	0	0	0	0
7	A	4	0	6	0	0
7	B	16	0	24	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
8	A	4	0	3	0	0
9	A	180	0	0	0	0
9	B	387	0	0	2	0
9	C	35	0	0	0	0
9	D	6	0	0	0	0
All	All	13608	0	11658	72	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 3.

All (72) 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)
2:B:1063:ILE:HD11	2:B:1072:ILE:HD12	1.64	0.79
2:B:817:GLN:O	2:B:882:TYR:OH	2.17	0.63
2:B:1357:GLU:OE1	2:B:1359:ARG:NH1	2.32	0.62
3:C:2:DA:H2'	3:C:3:DA:C8	2.39	0.58
2:B:1188:LYS:NZ	9:B:1505:HOH:O	2.36	0.58
1:A:33:G:N2	1:A:36:A:OP2	2.34	0.58
2:B:817:GLN:HE22	2:B:857:LEU:HB3	1.69	0.57
2:B:1114:ARG:NH1	4:D:9:DA:OP1	2.38	0.57
2:B:809:GLU:OE2	2:B:855:LYS:NZ	2.31	0.56
2:B:1215:ALA:HB2	2:B:1221:GLN:HG3	1.88	0.56
1:A:44:U:O2'	2:B:402:GLN:NE2	2.40	0.55
2:B:780:ARG:NH1	2:B:806:LEU:O	2.39	0.55
2:B:898:ASP:O	2:B:905:ARG:NH2	2.41	0.54
2:B:614:ASP:OD1	2:B:664:ARG:NH2	2.41	0.54
2:B:1278:LYS:HA	7:B:1409:EDO:H21	1.88	0.54
2:B:342:GLN:HB2	2:B:383:MET:HE3	1.89	0.54
2:B:600:ILE:HG22	2:B:647:VAL:HG23	1.91	0.52
2:B:342:GLN:NE2	2:B:384:ASP:O	2.40	0.52
2:B:102:GLU:OE2	9:B:1501:HOH:O	2.19	0.52
2:B:584:GLU:O	2:B:586:ARG:N	2.43	0.52
2:B:762:GLU:OE2	2:B:960:SER:OG	2.26	0.52
2:B:1177:ASN:ND2	2:B:1180:ASP:OD2	2.43	0.51
2:B:305:ILE:HG13	2:B:306:LEU:HG	1.93	0.50
2:B:339:VAL:HG21	2:B:351:PHE:HE2	1.75	0.50
2:B:944:ASP:HB2	2:B:948:LYS:H	1.76	0.50
2:B:787:GLY:HA3	2:B:891:LEU:HD21	1.94	0.50
2:B:826:GLN:NE2	2:B:859:ARG:HG3	2.27	0.50
1:A:18:G:N7	2:B:71:ARG:NH2	2.60	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:353:ASP:OD1	2:B:355:SER:OG	2.30	0.49
2:B:974:LYS:HD3	2:B:976:ARG:HD3	1.94	0.49
2:B:551:LEU:O	2:B:555:THR:OG1	2.29	0.48
2:B:944:ASP:HB3	2:B:946:ASN:H	1.79	0.47
2:B:489:GLN:HG3	2:B:625:LEU:HD21	1.95	0.47
2:B:618:ASP:OD2	2:B:639:TYR:OH	2.27	0.47
2:B:758:ASN:HD22	2:B:995:THR:HG22	1.78	0.47
2:B:836:TYR:CE1	2:B:859:ARG:HD3	2.51	0.45
2:B:643:PHE:HB3	2:B:647:VAL:HG13	1.99	0.45
2:B:869:ASN:OD1	2:B:870:VAL:N	2.44	0.45
2:B:531:THR:HG23	2:B:533:GLY:H	1.81	0.45
2:B:554:LYS:HD3	2:B:594:TYR:CZ	2.52	0.44
2:B:601:ILE:HG13	2:B:603:ASP:H	1.83	0.44
2:B:745:ASP:OD2	2:B:938:ARG:NH2	2.51	0.44
2:B:1000:LYS:HB2	2:B:1073:VAL:HG11	2.00	0.44
2:B:1047:LYS:O	2:B:1076:LYS:NZ	2.37	0.43
3:C:16:DG:H2'	3:C:17:DC:C6	2.53	0.43
2:B:508:LEU:HD21	2:B:664:ARG:HB2	2.01	0.43
2:B:901:THR:O	2:B:904:GLU:HG2	2.18	0.43
1:A:45:U:H5'	2:B:402:GLN:HE21	1.83	0.43
2:B:390:LEU:HD13	2:B:390:LEU:HA	1.90	0.43
2:B:870:VAL:HG21	2:B:902:LYS:HD3	2.01	0.43
2:B:923:GLU:HA	2:B:959:LYS:HE3	2.00	0.43
2:B:550:ASP:HA	2:B:554:LYS:HG3	2.02	0.42
2:B:30:LYS:HE3	2:B:30:LYS:HB2	1.91	0.42
2:B:1078:ARG:HE	2:B:1078:ARG:HB3	1.79	0.42
2:B:384:ASP:HA	2:B:385:GLY:HA2	1.66	0.41
2:B:249:THR:HG22	2:B:265:GLN:HB3	2.02	0.41
2:B:534:MET:H	2:B:534:MET:HG2	1.59	0.41
2:B:557:ARG:NH2	2:B:596:ASP:OD1	2.31	0.41
2:B:568:TYR:O	2:B:572:ILE:HG22	2.18	0.41
2:B:843:PRO:HG2	2:B:868:ASP:O	2.20	0.41
2:B:1339:THR:O	2:B:1342:VAL:HG22	2.21	0.41
2:B:849:ASP:HB3	2:B:854:ASN:HD22	1.85	0.41
2:B:962:LEU:HD12	2:B:962:LEU:HA	1.94	0.41
2:B:961:LYS:NZ	2:B:965:ASP:OD2	2.51	0.41
2:B:1037:PHE:O	2:B:1041:ASN:ND2	2.48	0.41
3:C:1:DC:H2'	3:C:2:DA:C8	2.55	0.41
2:B:633:GLU:HB2	2:B:652:LYS:HD2	2.01	0.40
2:B:258:LEU:HB3	2:B:260:GLU:OE2	2.20	0.40
2:B:902:LYS:HE2	2:B:908:LEU:HD23	2.02	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:46:A:H2'	1:A:47:A:C8	2.57	0.40
2:B:178:ASN:HB2	2:B:310:THR:H	1.85	0.40
2:B:1075:ASP:OD2	2:B:1078:ARG:HD2	2.21	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
2	B	1314/1372 (96%)	1278 (97%)	35 (3%)	1 (0%)	48 57

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	585	ASP

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
2	B	1103/1228 (90%)	1075 (98%)	28 (2%)	42 56

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	67	THR
2	B	123	VAL
2	B	141	LYS
2	B	225	LEU
2	B	269	ASP
2	B	334	LEU
2	B	348	LYS
2	B	384	ASP
2	B	390	LEU
2	B	419	LEU
2	B	493	GLU
2	B	514	LEU
2	B	566	GLU
2	B	572	ILE
2	B	586	ARG
2	B	615	ILE
2	B	635	ARG
2	B	642	LEU
2	B	647	VAL
2	B	804	THR
2	B	868	ASP
2	B	881	ASN
2	B	917	ILE
2	B	976	ARG
2	B	1063	ILE
2	B	1078	ARG
2	B	1154	SER
2	B	1260	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
2	B	402	GLN
2	B	412	HIS
2	B	511	HIS
2	B	881	ASN
2	B	926	GLN
2	B	930	HIS
2	B	983	HIS
2	B	1044	ASN
2	B	1241	HIS
2	B	1261	GLN
2	B	1317	ASN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	A	80/81 (98%)	7 (8%)	0

All (7) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
1	A	28	A
1	A	40	C
1	A	51	A
1	A	56	U
1	A	59	U
1	A	68	A
1	A	77	A

There are no RNA pucker outliers to report.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 19 ligands modelled in this entry, 13 are monoatomic - leaving 6 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	$\# Z > 2$
7	EDO	B	1409	-	3,3,3	0.41	0	2,2,2	0.32	0
7	EDO	A	107	-	3,3,3	0.44	0	2,2,2	0.33	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	EDO	B	1408	-	3,3,3	0.45	0	2,2,2	0.36	0
8	ACT	A	108	-	3,3,3	0.81	0	3,3,3	1.36	0
7	EDO	B	1410	-	3,3,3	0.43	0	2,2,2	0.41	0
7	EDO	B	1411	-	3,3,3	0.41	0	2,2,2	0.42	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
7	EDO	B	1409	-	-	0/1/1/1	-
7	EDO	A	107	-	-	0/1/1/1	-
7	EDO	B	1408	-	-	0/1/1/1	-
7	EDO	B	1410	-	-	0/1/1/1	-
7	EDO	B	1411	-	-	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
7	B	1411	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	B	1409	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	81/81 (100%)	-0.61	0 100 100	27, 45, 92, 101	0
2	B	1326/1372 (96%)	0.57	102 (7%) 19 17	27, 55, 97, 115	0
3	C	28/28 (100%)	-0.25	0 100 100	37, 53, 74, 75	0
4	D	8/8 (100%)	-0.31	0 100 100	39, 51, 88, 100	0
All	All	1443/1489 (96%)	0.49	102 (7%) 22 19	27, 55, 96, 115	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	203	ALA	5.4
2	B	803	ASN	5.4
2	B	776	ASN	5.4
2	B	1012	ASP	4.3
2	B	1251	ASP	4.2
2	B	551	LEU	3.9
2	B	296	LEU	3.9
2	B	204	SER	3.8
2	B	1011	GLY	3.6
2	B	765	ARG	3.6
2	B	199	ASN	3.6
2	B	271	TYR	3.5
2	B	1250	GLU	3.4
2	B	225	LEU	3.4
2	B	1068	GLU	3.4
2	B	784	ILE	3.4
2	B	1249	PRO	3.3
2	B	729	GLY	3.3
2	B	178	ASN	3.3
2	B	688	PHE	3.3
2	B	842	VAL	3.3

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Mol	Chain	Res	Type	RSRZ
2	B	181	VAL	3.2
2	B	871	PRO	3.2
2	B	568	TYR	3.2
2	B	779	GLU	3.2
2	B	778	ARG	3.1
2	B	1056	GLU	3.1
2	B	870	VAL	3.1
2	B	3	LYS	3.1
2	B	1115	ASN	3.1
2	B	1054	ASN	3.0
2	B	805	GLN	3.0
2	B	855	LYS	3.0
2	B	1037	PHE	3.0
2	B	238	PHE	2.9
2	B	1116	SER	2.9
2	B	1366	GLY	2.9
2	B	312	ILE	2.9
2	B	1053	ALA	2.8
2	B	1244	LYS	2.8
2	B	569	PHE	2.8
2	B	799	HIS	2.7
2	B	794	GLN	2.7
2	B	850	ASP	2.7
2	B	174	LEU	2.7
2	B	190	GLN	2.7
2	B	302	LEU	2.7
2	B	292	ALA	2.7
2	B	788	ILE	2.6
2	B	576	ASP	2.6
2	B	530	VAL	2.6
2	B	804	THR	2.6
2	B	611	GLU	2.6
2	B	777	SER	2.6
2	B	782	LYS	2.6
2	B	783	ARG	2.6
2	B	538	ALA	2.6
2	B	176	PRO	2.5
2	B	346	LYS	2.5
2	B	343	LEU	2.5
2	B	1069	THR	2.4
2	B	535	ARG	2.4
2	B	647	VAL	2.4

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Mol	Chain	Res	Type	RSRZ
2	B	192	TYR	2.4
2	B	337	ALA	2.4
2	B	906	GLY	2.4
2	B	1067	GLY	2.4
2	B	201	ILE	2.4
2	B	179	SER	2.3
2	B	800	PRO	2.3
2	B	1034	ALA	2.3
2	B	580	ILE	2.3
2	B	856	VAL	2.3
2	B	639	TYR	2.3
2	B	905	ARG	2.3
2	B	944	ASP	2.2
2	B	297	SER	2.2
2	B	851	SER	2.2
2	B	877	LYS	2.2
2	B	720	LEU	2.2
2	B	579	GLU	2.2
2	B	885	GLN	2.2
2	B	728	ALA	2.2
2	B	806	LEU	2.2
2	B	578	VAL	2.2
2	B	868	ASP	2.2
2	B	891	LEU	2.1
2	B	384	ASP	2.1
2	B	394	ASN	2.1
2	B	907	GLY	2.1
2	B	249	THR	2.1
2	B	796	LEU	2.1
2	B	606	PHE	2.1
2	B	594	TYR	2.1
2	B	787	GLY	2.1
2	B	807	GLN	2.1
2	B	841	ILE	2.1
2	B	308	VAL	2.1
2	B	1252	ASN	2.0
2	B	1057	ILE	2.0
2	B	867	SER	2.0
2	B	572	ILE	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($\text{\AA}^2$)	Q<0.9
5	K	B	1405	1/1	0.84	0.14	70,70,70,70	0
5	K	B	1407	1/1	0.84	0.25	143,143,143,143	0
5	K	B	1406	1/1	0.86	0.10	101,101,101,101	0
7	EDO	B	1409	4/4	0.90	0.15	48,48,49,49	0
7	EDO	B	1410	4/4	0.90	0.15	44,45,46,47	0
8	ACT	A	108	4/4	0.91	0.15	52,53,54,54	0
5	K	B	1404	1/1	0.93	0.09	70,70,70,70	0
5	K	B	1403	1/1	0.94	0.09	70,70,70,70	0
6	MG	A	104	1/1	0.94	0.05	61,61,61,61	0
6	MG	A	105	1/1	0.94	0.20	57,57,57,57	0
6	MG	A	106	1/1	0.96	0.07	49,49,49,49	0
7	EDO	A	107	4/4	0.96	0.07	38,40,40,41	0
7	EDO	B	1408	4/4	0.96	0.11	37,38,39,40	0
7	EDO	B	1411	4/4	0.97	0.08	42,42,42,42	0
5	K	B	1402	1/1	0.97	0.06	48,48,48,48	0
5	K	B	1401	1/1	0.98	0.06	49,49,49,49	0
5	K	A	101	1/1	0.98	0.06	29,29,29,29	0
5	K	A	102	1/1	0.98	0.07	36,36,36,36	0
5	K	A	103	1/1	0.98	0.05	39,39,39,39	0

6.5 Other polymers [i](#)

There are no such residues in this entry.