Full wwPDB X-ray Structure Validation Report ⓘ

Aug 21, 2020 – 07:24 PM BST

PDB ID	:	5N2H
Title	:	Structure of the E9 DNA polymerase exonuclease deficient mutant (D166A+E168A) from vaccinia virus
Authors	:	Tarbouriech, N.; Burmeister, W.P.; Iseni, F.
Deposited on	:	2017-02-07
Resolution	:	2.81 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 following versions of software and data (see references ⓘ) were used in the production of this report:

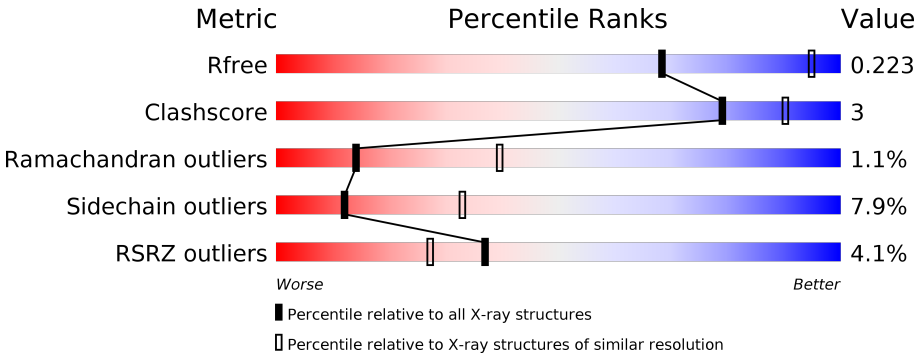
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.13.1
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.13.1

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 2.81 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}	130704	3617 (2.84-2.80)
Clashscore	141614	4060 (2.84-2.80)
Ramachandran outliers	138981	3978 (2.84-2.80)
Sidechain outliers	138945	3980 (2.84-2.80)
RSRZ outliers	127900	3552 (2.84-2.80)

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 >=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 <=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	1009	4% 86% 12%

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
5	EPE	A	1107	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8458 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.

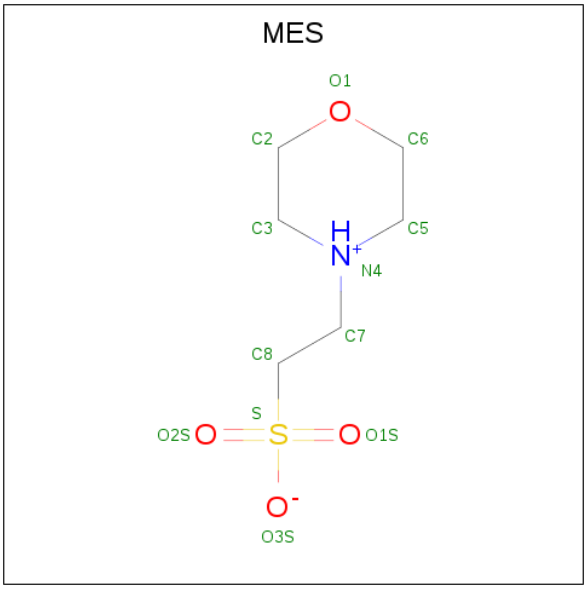
- Molecule 1 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	999	8173	5228	1364	1529	52	0	1	0

There are 7 discrepancies between the modelled and reference sequences:

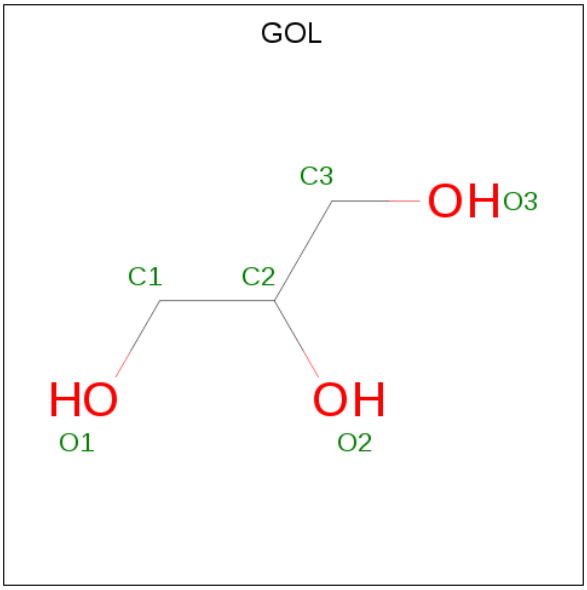
Chain	Residue	Modelled	Actual	Comment	Reference
A	-3	GLY	-	expression tag	UNP P20509
A	-2	ALA	-	expression tag	UNP P20509
A	-1	MET	-	expression tag	UNP P20509
A	0	ASP	-	expression tag	UNP P20509
A	1	PRO	-	expression tag	UNP P20509
A	166	ALA	ASP	engineered mutation	UNP P20509
A	168	ALA	GLU	engineered mutation	UNP P20509

- Molecule 2 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: $C_6H_{13}NO_4S$).



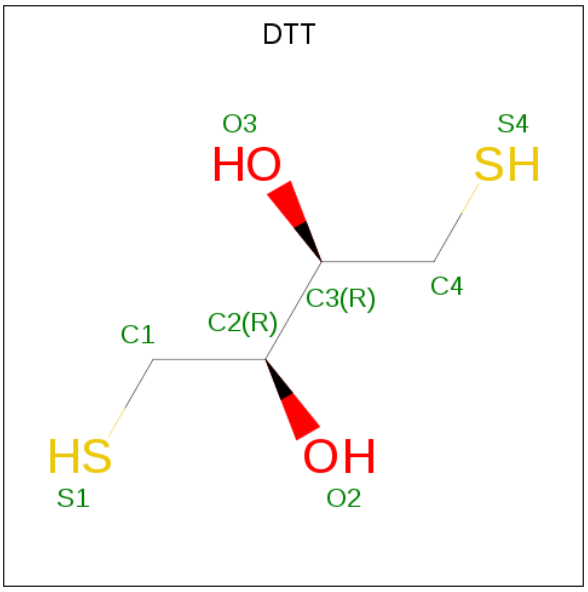
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
2	A	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



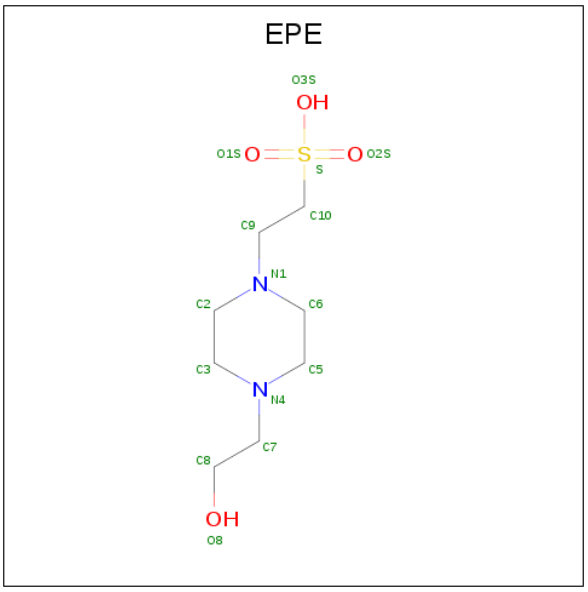
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O		0	0
			6	3	3			
3	A	1	Total	C	O		0	0
			6	3	3			

- Molecule 4 is 2,3-DIHYDROXY-1,4-DITHIOBUTANE (three-letter code: DTT) (formula: $C_4H_{10}O_2S_2$).



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

- Molecule 5 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	S		
5	A	1	15	8	2	4	1	0	0

- Molecule 6 is water.

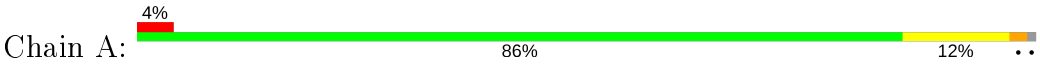
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	214	Total 214	O 214	0	0

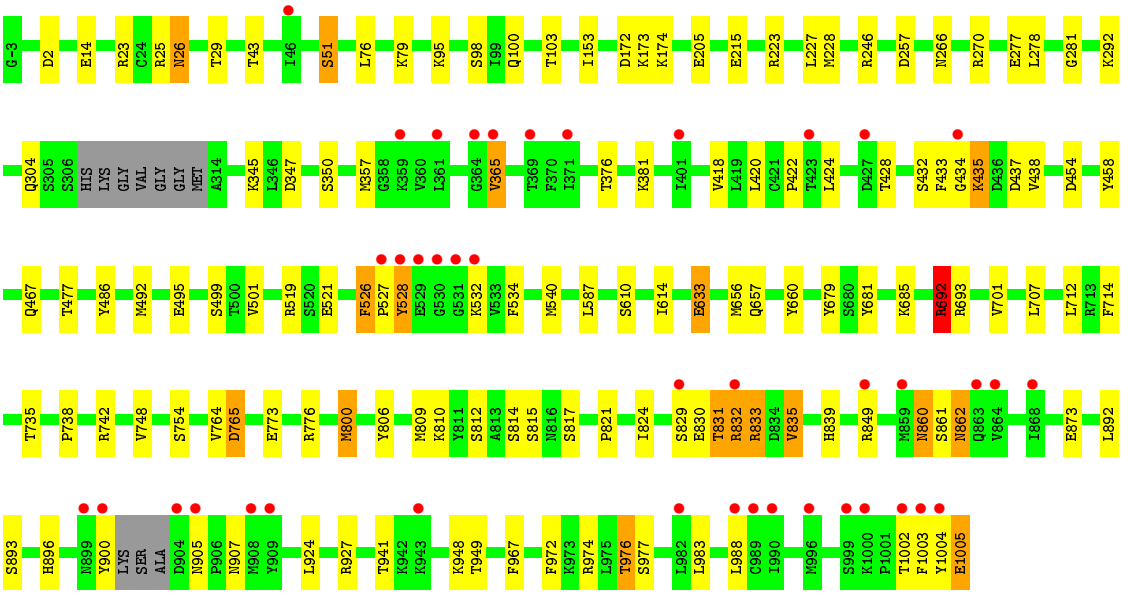
3 Residue-property plots (i)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density (RSRZ > 2). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: DNA polymerase

Chain A:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 31 2 1	Depositor
Cell constants a, b, c, α, β, γ	133.52Å 133.52Å 229.49Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	57.00 – 2.81 57.82 – 2.81	Depositor EDS
% Data completeness (in resolution range)	97.6 (57.00-2.81) 98.9 (57.82-2.81)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.80 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.185 , 0.222 0.189 , 0.223	Depositor DCC
R_{free} test set	2805 reflections (4.86%)	wwPDB-VP
Wilson B-factor (Å^2)	68.3	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 51.0	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.024 for -h,-k,l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	8458	wwPDB-VP
Average B, all atoms (Å^2)	78.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.64% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: GOL, EPE, MES, DTT

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	0.59	1/8353 (0.0%)	0.82	4/11283 (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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	347	ASP	CB-CG	5.51	1.63	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	246	ARG	NE-CZ-NH1	5.58	123.09	120.30
1	A	347	ASP	CB-CG-OD1	5.44	123.19	118.30
1	A	365	VAL	CB-CA-C	5.34	121.55	111.40
1	A	692	ARG	NE-CZ-NH1	5.14	122.87	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	281	GLY	Peptide
1	A	435	LYS	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	8173	0	8131	46	0
2	A	36	0	39	1	0
3	A	12	0	16	0	0
4	A	8	0	10	0	0
5	A	15	0	18	0	0
6	A	214	0	0	1	1
All	All	8458	0	8214	46	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 3.

All (46) 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:519:ARG:NH2	1:A:679:TYR:O	1.98	0.95
1:A:833:ARG:HG3	1:A:893:SER:OG	1.69	0.93
1:A:833:ARG:HG3	1:A:893:SER:CB	2.24	0.67
1:A:833:ARG:HB3	1:A:893:SER:H	1.59	0.66
1:A:454:ASP:O	1:A:458[B]:TYR:CD1	2.55	0.60
1:A:681:TYR:CZ	1:A:685:LYS:HD2	2.39	0.58
1:A:23:ARG:NH1	1:A:29:THR:OG1	2.37	0.57
1:A:266:ASN:OD1	1:A:270:ARG:NH1	2.38	0.56
1:A:773:GLU:OE2	1:A:776:ARG:NH1	2.39	0.56
1:A:26:ASN:N	1:A:26:ASN:OD1	2.40	0.54
1:A:833:ARG:NH1	1:A:835:VAL:O	2.41	0.53
1:A:350:SER:CB	1:A:434:GLY:HA2	2.37	0.53
1:A:862:ASN:OD1	1:A:862:ASN:N	2.42	0.52
1:A:532:LYS:HE2	1:A:534:PHE:CE1	2.44	0.52
1:A:712:LEU:HD23	1:A:714:PHE:CZ	2.47	0.50
1:A:1003:PHE:O	1:A:1005:GLU:N	2.45	0.50
1:A:860:ASN:HB2	1:A:862:ASN:H	1.77	0.48
1:A:831:THR:O	1:A:832:ARG:C	2.53	0.47
1:A:656:MET:HE3	6:A:1306:HOH:O	2.15	0.47
1:A:833:ARG:HB3	1:A:893:SER:N	2.27	0.47
1:A:633:GLU:HG2	1:A:660:TYR:CZ	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:810:LYS:HD3	1:A:824:ILE:HD11	1.97	0.46
1:A:972:PHE:O	1:A:976:THR:HG23	2.15	0.46
1:A:800:MET:HB2	1:A:806:TYR:HB2	1.98	0.45
1:A:830:GLU:HG3	1:A:831:THR:N	2.31	0.44
1:A:227:LEU:C	1:A:227:LEU:HD23	2.38	0.44
1:A:765:ASP:CG	1:A:817:SER:HB2	2.38	0.44
1:A:76:LEU:HD21	1:A:587:LEU:HA	1.99	0.44
1:A:764:VAL:CG2	1:A:817:SER:HA	2.47	0.44
1:A:896:HIS:CE1	1:A:924:LEU:HD12	2.52	0.44
1:A:486:TYR:CG	1:A:501:VAL:HB	2.53	0.43
1:A:23:ARG:NH2	1:A:257:ASP:OD2	2.52	0.43
1:A:681:TYR:CE1	1:A:685:LYS:HD2	2.53	0.43
1:A:701:VAL:HG13	1:A:714:PHE:CD1	2.54	0.43
1:A:707:LEU:O	1:A:742:ARG:HA	2.19	0.43
1:A:833:ARG:HD3	1:A:892:LEU:HA	2.01	0.43
1:A:350:SER:HB2	1:A:434:GLY:HA2	2.00	0.42
1:A:587:LEU:HD21	1:A:614:ILE:HD11	2.01	0.42
1:A:832:ARG:O	1:A:833:ARG:HB2	2.19	0.42
1:A:907:ASN:OD1	1:A:948:LYS:NZ	2.39	0.42
1:A:812:SER:O	1:A:815:SER:HB3	2.19	0.42
1:A:495:GLU:OE1	2:A:1103:MES:H61	2.19	0.41
1:A:205:GLU:OE2	1:A:223:ARG:NE	2.53	0.41
1:A:532:LYS:NZ	1:A:692:ARG:HG2	2.37	0.40
1:A:835:VAL:HG13	1:A:839:HIS:HB3	2.03	0.40
1:A:2:ASP:OD2	1:A:25:ARG:NH1	2.54	0.40

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)
6:A:1251:HOH:O	6:A:1251:HOH:O[6_555]	1.21	0.99

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	994/1009 (98%)	927 (93%)	56 (6%)	11 (1%)	14 39

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	51	SER
1	A	422	PRO
1	A	435	LYS
1	A	526	PHE
1	A	528	TYR
1	A	821	PRO
1	A	527	PRO
1	A	831	THR
1	A	1004	TYR
1	A	365	VAL
1	A	832	ARG

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	921/926 (100%)	848 (92%)	73 (8%)	12 33

All (73) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	14	GLU
1	A	26	ASN
1	A	43	THR
1	A	51	SER
1	A	79	LYS
1	A	95	LYS
1	A	98	SER
1	A	100	GLN

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Mol	Chain	Res	Type
1	A	103	THR
1	A	153	ILE
1	A	172	ASP
1	A	173	LYS
1	A	174	LYS
1	A	215	GLU
1	A	228	MET
1	A	277	GLU
1	A	278	LEU
1	A	292	LYS
1	A	304	GLN
1	A	345	LYS
1	A	357	MET
1	A	376	THR
1	A	381	LYS
1	A	418	VAL
1	A	420	LEU
1	A	424	LEU
1	A	428	THR
1	A	432	SER
1	A	433	PHE
1	A	437	ASP
1	A	438	VAL
1	A	467	GLN
1	A	477	THR
1	A	492	MET
1	A	499	SER
1	A	521	GLU
1	A	526	PHE
1	A	528	TYR
1	A	540	MET
1	A	610	SER
1	A	633	GLU
1	A	657	GLN
1	A	692	ARG
1	A	693	ARG
1	A	735	THR
1	A	738	PRO
1	A	748	VAL
1	A	754	SER
1	A	765	ASP
1	A	800	MET

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Mol	Chain	Res	Type
1	A	809	MET
1	A	814	SER
1	A	829	SER
1	A	833	ARG
1	A	835	VAL
1	A	849	ARG
1	A	860	ASN
1	A	861	SER
1	A	862	ASN
1	A	873	GLU
1	A	900	TYR
1	A	905	ASN
1	A	927	ARG
1	A	941	THR
1	A	949	THR
1	A	967	PHE
1	A	974	ARG
1	A	976	THR
1	A	977	SER
1	A	983	LEU
1	A	988	LEU
1	A	1002	THR
1	A	1005	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	860	ASN
1	A	897	HIS

5.3.3 RNA

There are no RNA molecules in this entry.

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 (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

7 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	MES	A	1103	-	12,12,12	2.10	1 (8%)	14,16,16	2.29	4 (28%)
2	MES	A	1101	-	12,12,12	1.93	1 (8%)	14,16,16	1.96	2 (14%)
3	GOL	A	1104	-	5,5,5	0.59	0	5,5,5	0.49	0
3	GOL	A	1105	-	5,5,5	0.41	0	5,5,5	0.66	0
4	DTT	A	1106	-	7,7,7	0.86	0	4,8,8	1.16	0
5	EPE	A	1107	-	15,15,15	1.76	1 (6%)	18,20,20	1.56	4 (22%)
2	MES	A	1102	-	12,12,12	1.87	1 (8%)	14,16,16	1.88	5 (35%)

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	MES	A	1103	-	-	0/6/14/14	0/1/1/1
2	MES	A	1101	-	-	0/6/14/14	0/1/1/1
3	GOL	A	1104	-	-	4/4/4/4	-
3	GOL	A	1105	-	-	2/4/4/4	-
4	DTT	A	1106	-	-	2/8/8/8	-
5	EPE	A	1107	-	-	2/9/19/19	0/1/1/1
2	MES	A	1102	-	-	3/6/14/14	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1103	MES	C8-S	-6.54	1.68	1.77
2	A	1101	MES	C8-S	-6.30	1.68	1.77
5	A	1107	EPE	C10-S	-6.24	1.68	1.77
2	A	1102	MES	C8-S	-5.83	1.69	1.77

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1103	MES	C6-C5-N4	4.57	117.03	110.10
2	A	1101	MES	O1S-S-C8	4.53	112.37	106.92
2	A	1101	MES	O3S-S-C8	4.29	112.70	105.77
2	A	1103	MES	O3S-S-C8	4.27	112.68	105.77
2	A	1103	MES	O1S-S-C8	3.93	111.64	106.92
5	A	1107	EPE	O3S-S-C10	3.71	111.76	105.77
2	A	1102	MES	O3S-S-C8	3.61	111.61	105.77
2	A	1103	MES	C2-C3-N4	3.12	114.84	110.10
2	A	1102	MES	O1S-S-C8	2.97	110.50	106.92
5	A	1107	EPE	O2S-S-C10	2.93	110.45	106.92
2	A	1102	MES	O2S-S-C8	2.80	110.28	106.92
2	A	1102	MES	C6-O1-C2	2.48	118.18	109.89
5	A	1107	EPE	O3S-S-O2S	-2.19	105.92	111.27
2	A	1102	MES	O2S-S-O1S	-2.18	106.39	113.95
5	A	1107	EPE	O1S-S-C10	2.04	109.37	106.92

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	1104	GOL	O1-C1-C2-C3
4	A	1106	DTT	C2-C3-C4-S4
4	A	1106	DTT	O3-C3-C4-S4
2	A	1102	MES	C7-C8-S-O2S
2	A	1102	MES	C7-C8-S-O3S
5	A	1107	EPE	N4-C7-C8-O8
3	A	1104	GOL	C1-C2-C3-O3
3	A	1104	GOL	O1-C1-C2-O2
5	A	1107	EPE	C9-C10-S-O3S
3	A	1104	GOL	O2-C2-C3-O3
2	A	1102	MES	C7-C8-S-O1S
3	A	1105	GOL	O1-C1-C2-O2
3	A	1105	GOL	O1-C1-C2-C3

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1103	MES	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, 95^{th} 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	999/1009 (99%)	0.21	41 (4%) 37 27	39, 70, 134, 177	0

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	900	TYR	6.5
1	A	864	VAL	6.2
1	A	988	LEU	5.5
1	A	527	PRO	4.5
1	A	531	GLY	4.3
1	A	1004	TYR	4.2
1	A	989	CYS	4.2
1	A	829	SER	4.0
1	A	863	GLN	3.9
1	A	832	ARG	3.7
1	A	904	ASP	3.3
1	A	401	ILE	3.3
1	A	359	LYS	3.3
1	A	532	LYS	3.2
1	A	364	GLY	3.0
1	A	528	TYR	2.9
1	A	899	ASN	2.9
1	A	990	ILE	2.9
1	A	868	ILE	2.9
1	A	361	LEU	2.7
1	A	982	LEU	2.6
1	A	996	MET	2.5
1	A	427	ASP	2.5
1	A	1002	THR	2.5
1	A	46	ILE	2.4
1	A	423	THR	2.4
1	A	905	ASN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	369	THR	2.4
1	A	943	LYS	2.3
1	A	1000	LYS	2.3
1	A	908	MET	2.3
1	A	859	MET	2.3
1	A	530	GLY	2.2
1	A	999	SER	2.2
1	A	529	GLU	2.2
1	A	371	ILE	2.1
1	A	909	TYR	2.1
1	A	1003	PHE	2.1
1	A	434	GLY	2.0
1	A	365	VAL	2.0
1	A	849	ARG	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 monosaccharides 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, 95^{th} 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
3	GOL	A	1104	6/6	0.58	0.38	104,119,120,123	0
4	DTT	A	1106	8/8	0.73	0.39	110,126,139,140	0
5	EPE	A	1107	15/15	0.74	0.43	107,135,155,159	0
2	MES	A	1102	12/12	0.81	0.26	109,121,144,158	0
2	MES	A	1103	12/12	0.88	0.47	123,139,153,154	0
3	GOL	A	1105	6/6	0.91	0.34	78,81,85,86	0
2	MES	A	1101	12/12	0.96	0.22	63,75,91,97	0

6.5 Other polymers (i)

There are no such residues in this entry.