



Full wwPDB X-ray Structure Validation Report

Feb 28, 2014 – 01:18 PM GMT

PDB ID : 4B3V
Title : Crystal structure of the Rubella virus glycoprotein E1 in its post-fusion form
crystallized in presence of 20mM of Calcium Acetate
Authors : Vaney, M.C.; Dubois, R.M.; Tortorici, M.A.; Rey, F.A.
Deposited on : 2012-07-26
Resolution : 1.98 Å(reported)

This is a full wwPDB validation report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at <http://wwpdb.org/ValidationPDFNotes.html>

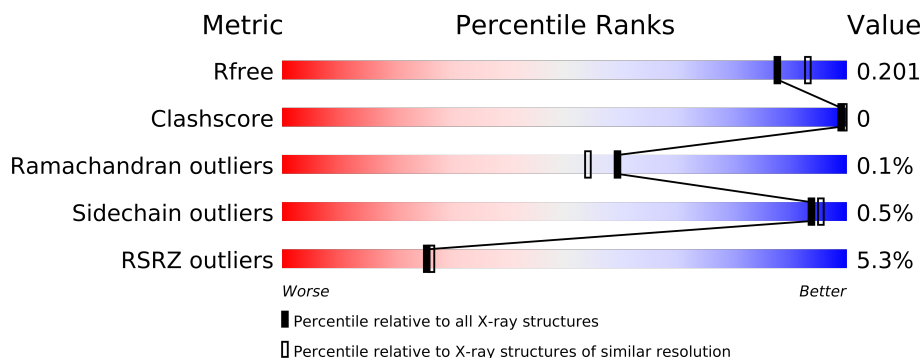
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.15 2013
Xtriage (Phenix) : dev-1323
EDS : stable22639
Percentile statistics : 21963
Refmac : 5.8.0049
CCP4 : 6.3.0 (Settle)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)
Validation Pipeline (wwPDB-VP) : stable22683

1 Overall quality at a glance

The reported resolution of this entry is 1.98 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}	66092	6577 (2.00-1.96)
Clashscore	79885	8091 (2.00-1.96)
Ramachandran outliers	78287	7989 (2.00-1.96)
Sidechain outliers	78261	7987 (2.00-1.96)
RSRZ outliers	66119	6578 (2.00-1.96)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	A	473	
1	B	473	
1	C	473	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
2	NAG	B	1436	-	X
2	NAG	C	1437	-	X
3	NGA	A	1437	-	X
3	NGA	C	1438	-	X
4	GOL	A	1438	-	X

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Mol	Type	Chain	Res	Geometry	Electron density
4	GOL	A	1439	-	X
4	GOL	A	1440	-	X
4	GOL	A	1441	-	X
4	GOL	B	1437	-	X
4	GOL	B	1438	-	X
4	GOL	B	1439	-	X
4	GOL	B	1440	-	X
4	GOL	B	1441	-	X
4	GOL	B	1442[A]	-	X
4	GOL	B	1442[B]	-	X
4	GOL	C	1439	-	X
4	GOL	C	1441	-	X
4	GOL	C	1442	-	X
4	GOL	C	1443	-	X
5	ACT	A	1445	-	X
5	ACT	B	1443	-	X
5	ACT	B	1444	-	X
5	ACT	C	1445	-	X
6	PG4	A	1447	-	X
7	PEG	A	1449	-	X
7	PEG	B	1446	-	X
7	PEG	C	1447	-	X
7	PEG	C	1448	-	X

2 Entry composition i

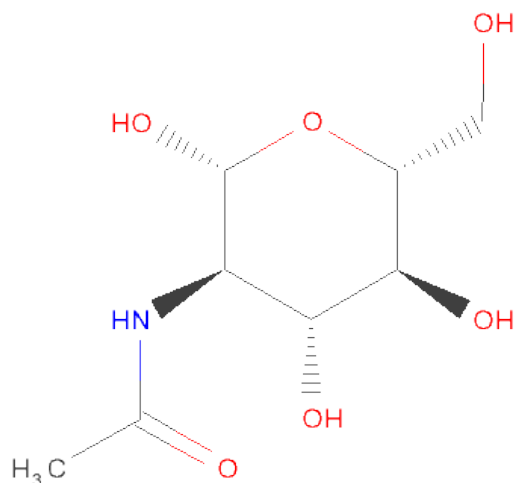
There are 10 unique types of molecules in this entry. The entry contains 11200 atoms, of which 0 are hydrogen and 0 are deuterium.

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 E1 ENVELOPE GLYCOPROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	10	1
			3299	2087	576	613	23			
1	B	432	Total	C	N	O	S	0	5	2
			3270	2067	575	605	23			
1	C	432	Total	C	N	O	S	0	4	2
			3252	2056	571	602	23			

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



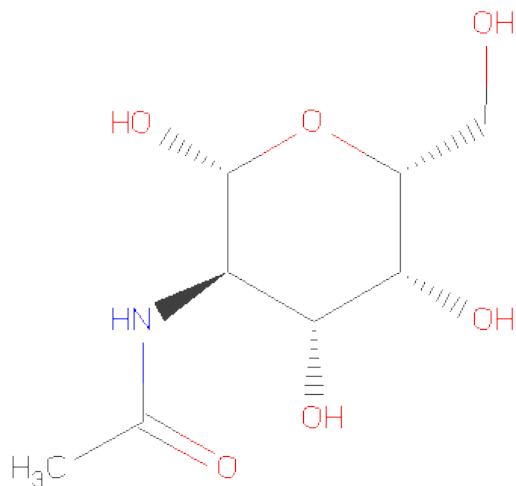
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is SUGAR (N-ACETYL-D-GALACTOSAMINE) (three-letter code: NGA) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



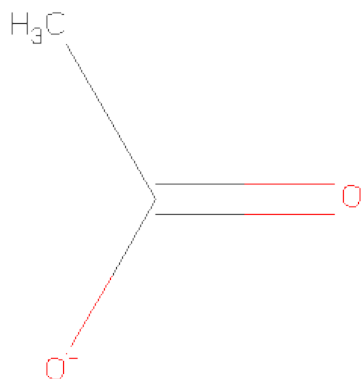
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	A	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	0
			6	3	3		
4	B	1	Total	C	O	0	1
			12	6	6		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		
4	C	1	Total	C	O	0	0
			6	3	3		

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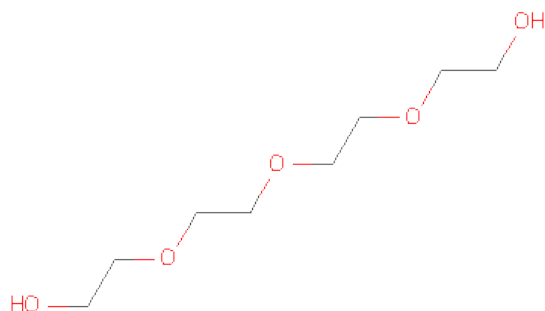
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	C	1	Total	C	O	0	0
			6	3	3		

- Molecule 5 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



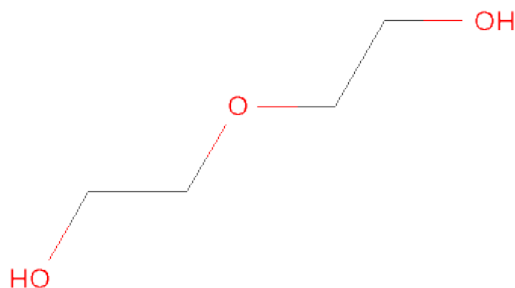
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	A	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	B	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		
5	C	1	Total	C	O	0	0
			4	2	2		

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			8	5	3		

- Molecule 7 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total	C	O	0	0
			7	4	3		
7	B	1	Total	C	O	0	0
			7	4	3		
7	C	1	Total	C	O	0	0
			7	4	3		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	C	1	Total	C	O	0	0
			7	4	3		

- Molecule 8 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	1	Total	Na	0	0
			1	1		

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	B	1	Total	Ca	0	0
			1	1		
9	A	1	Total	Ca	0	0
			1	1		
9	C	1	Total	Ca	0	0
			1	1		

- Molecule 10 is water.

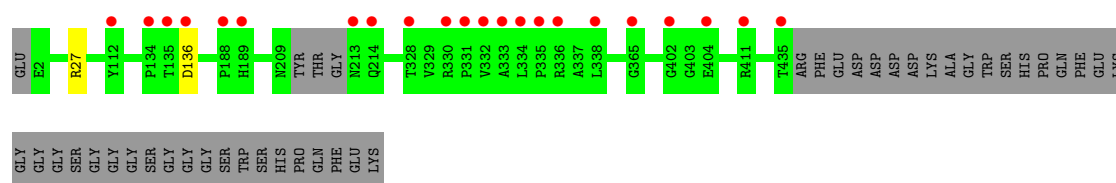
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	419	Total	O	0	0
			419	419		
10	B	378	Total	O	0	0
			378	378		
10	C	334	Total	O	0	0
			334	334		

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.

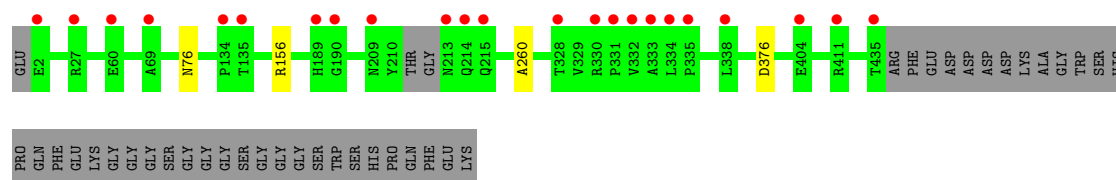
• Molecule 1: E1 ENVELOPE GLYCOPROTEIN

Chain A: 



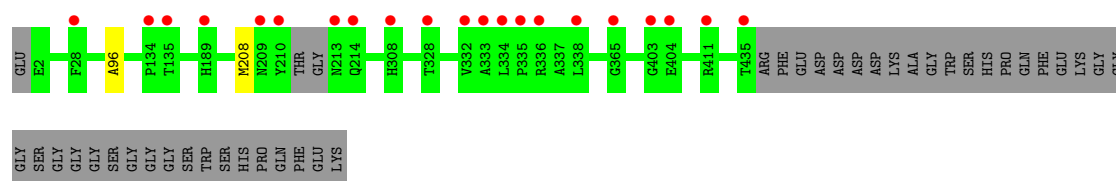
• Molecule 1: E1 ENVELOPE GLYCOPROTEIN

Chain B: 



• Molecule 1: E1 ENVELOPE GLYCOPROTEIN

Chain C: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	121.27Å 126.16Å 129.38Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.99 – 1.98 28.78 – 1.98	Depositor EDS
% Data completeness (in resolution range)	97.3 (28.99-1.98) 97.3 (28.78-1.98)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.89 (at 1.98Å)	Xtriage
Refinement program	BUSTER 2.11.2	Depositor
R, R_{free}	0.185 , 0.198 0.188 , 0.201	Depositor DCC
R_{free} test set	6752 reflections (5.29%)	DCC
Wilson B-factor (Å ²)	28.1	Xtriage
Anisotropy	0.051	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 42.0	EDS
Estimated twinning fraction	0.016 for -h,l,k	Xtriage
L-test for twinning	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	1 of 134445 reflections (0.001%)	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	11200	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.41% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, NAG, NA, CA, PG4, ACT, PEG, NGA

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	0.35	0/3421	0.58	0/4703
1	B	0.36	0/3391	0.59	0/4659
1	C	0.35	0/3372	0.58	0/4635
All	All	0.35	0/10184	0.58	0/13997

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3299	0	0	0	0
1	B	3270	0	0	1	0
1	C	3252	0	0	1	0
2	A	14	0	0	0	0
2	B	14	0	0	0	0
2	C	28	0	0	0	0
3	A	14	0	0	0	0
3	C	14	0	0	0	0
4	A	24	0	32	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	42	0	56	1	0
4	C	30	0	40	1	0
5	A	12	0	9	0	0
5	B	8	0	6	0	0
5	C	8	0	6	0	0
6	A	8	0	9	0	0
7	A	7	0	10	0	0
7	B	7	0	10	0	0
7	C	14	0	20	0	0
8	A	1	0	0	0	0
9	A	1	0	0	0	0
9	B	1	0	0	0	0
9	C	1	0	0	0	0
10	A	419	0	0	0	0
10	B	378	0	0	0	0
10	C	334	0	0	0	0
All	All	11200	0	198	2	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 0.

All (2) close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
1:C:96:ALA:N	4:C:1439:GOL:HO2	1.87	0.72
1:B:260:ALA:N	4:B:1437:GOL:HO3	2.19	0.40

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	437/473 (92%)	429 (98%)	6 (1%)	2 (0%)	38 27
1	B	433/473 (92%)	425 (98%)	8 (2%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	432/473 (91%)	425 (98%)	7 (2%)	0	100	100
All	All	1302/1419 (92%)	1279 (98%)	21 (2%)	2 (0%)	59	50

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	136[A]	ASP
1	A	136[B]	ASP

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	355/376 (94%)	354 (100%)	1 (0%)	96	97
1	B	350/376 (93%)	347 (99%)	3 (1%)	87	89
1	C	349/376 (93%)	348 (100%)	1 (0%)	96	97
All	All	1054/1128 (93%)	1049 (100%)	5 (0%)	94	95

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	27	ARG
1	B	76	ASN
1	B	156	ARG
1	B	376	ASP
1	C	208	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA chains 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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 38 ligands modelled in this entry, 4 are monoatomic - leaving 34 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# $ Z > 2$	Counts	RMSZ	# $ Z > 2$
2	NAG	A	1436	1	12,14,15	0.26	0	15,19,21	0.33	0
3	NGA	A	1437	1	12,14,15	0.26	0	15,19,21	0.29	0
4	GOL	A	1438	-	5,5,5	0.13	0	5,5,5	0.35	0
4	GOL	A	1439	-	5,5,5	0.14	0	5,5,5	0.33	0
4	GOL	A	1440	-	5,5,5	0.13	0	5,5,5	0.25	0
4	GOL	A	1441	-	5,5,5	0.12	0	5,5,5	0.32	0
5	ACT	A	1443	-	1,3,3	4.11	1 (100%)	0,3,3	0.00	-
5	ACT	A	1444	-	1,3,3	3.41	1 (100%)	0,3,3	0.00	-
5	ACT	A	1445	-	1,3,3	3.82	1 (100%)	0,3,3	0.00	-
6	PG4	A	1447	-	6,7,12	0.40	0	5,6,11	0.06	0
7	PEG	A	1449	-	6,6,6	0.10	0	5,5,5	0.07	0
2	NAG	B	1436	1	12,14,15	0.25	0	15,19,21	0.33	0
4	GOL	B	1437	-	5,5,5	0.13	0	5,5,5	0.34	0
4	GOL	B	1438	-	5,5,5	0.15	0	5,5,5	0.31	0
4	GOL	B	1439	-	5,5,5	0.12	0	5,5,5	0.25	0
4	GOL	B	1440	-	5,5,5	0.14	0	5,5,5	0.31	0
4	GOL	B	1441	-	5,5,5	0.13	0	5,5,5	0.33	0
4	GOL	B	1442[A]	-	5,5,5	0.12	0	5,5,5	0.40	0
4	GOL	B	1442[B]	-	5,5,5	0.12	0	5,5,5	0.43	0
5	ACT	B	1443	9	1,3,3	4.21	1 (100%)	0,3,3	0.00	-
5	ACT	B	1444	-	1,3,3	4.21	1 (100%)	0,3,3	0.00	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
7	PEG	B	1446	-	6,6,6	0.13	0	5,5,5	0.07	0
2	NAG	C	1436	1	12,14,15	0.25	0	15,19,21	0.34	0
2	NAG	C	1437	1	12,14,15	0.24	0	15,19,21	0.35	0
3	NGA	C	1438	1	12,14,15	0.24	0	15,19,21	0.32	0
4	GOL	C	1439	-	5,5,5	0.15	0	5,5,5	0.34	0
4	GOL	C	1440	-	5,5,5	0.15	0	5,5,5	0.25	0
4	GOL	C	1441	-	5,5,5	0.15	0	5,5,5	0.30	0
4	GOL	C	1442	-	5,5,5	0.12	0	5,5,5	0.32	0
4	GOL	C	1443	-	5,5,5	0.14	0	5,5,5	0.24	0
5	ACT	C	1444	9	1,3,3	4.12	1 (100%)	0,3,3	0.00	-
5	ACT	C	1445	-	1,3,3	4.20	1 (100%)	0,3,3	0.00	-
7	PEG	C	1447	-	6,6,6	0.11	0	5,5,5	0.02	0
7	PEG	C	1448	-	6,6,6	0.13	0	5,5,5	0.06	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1436	1	-	0/6/23/26	0/1/1/1
3	NGA	A	1437	1	-	0/6/23/26	0/1/1/1
4	GOL	A	1438	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1439	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1440	-	-	0/4/4/4	0/0/0/0
4	GOL	A	1441	-	-	0/4/4/4	0/0/0/0
5	ACT	A	1443	-	-	0/0/0/0	0/0/0/0
5	ACT	A	1444	-	-	0/0/0/0	0/0/0/0
5	ACT	A	1445	-	-	0/0/0/0	0/0/0/0
6	PG4	A	1447	-	-	0/5/5/10	0/0/0/0
7	PEG	A	1449	-	-	0/4/4/4	0/0/0/0
2	NAG	B	1436	1	-	0/6/23/26	0/1/1/1
4	GOL	B	1437	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1438	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1439	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1440	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1441	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1442[A]	-	-	0/4/4/4	0/0/0/0
4	GOL	B	1442[B]	-	-	0/4/4/4	0/0/0/0
5	ACT	B	1443	9	-	0/0/0/0	0/0/0/0
5	ACT	B	1444	-	-	0/0/0/0	0/0/0/0
7	PEG	B	1446	-	-	0/4/4/4	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	C	1436	1	-	0/6/23/26	0/1/1/1
2	NAG	C	1437	1	-	0/6/23/26	0/1/1/1
3	NGA	C	1438	1	-	0/6/23/26	0/1/1/1
4	GOL	C	1439	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1440	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1441	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1442	-	-	0/4/4/4	0/0/0/0
4	GOL	C	1443	-	-	0/4/4/4	0/0/0/0
5	ACT	C	1444	9	-	0/0/0/0	0/0/0/0
5	ACT	C	1445	-	-	0/0/0/0	0/0/0/0
7	PEG	C	1447	-	-	0/4/4/4	0/0/0/0
7	PEG	C	1448	-	-	0/4/4/4	0/0/0/0

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1443	ACT	CH3-C	4.21	1.54	1.48
5	B	1444	ACT	CH3-C	4.21	1.54	1.48
5	C	1445	ACT	CH3-C	4.20	1.54	1.48
5	C	1444	ACT	CH3-C	4.12	1.54	1.48
5	A	1443	ACT	CH3-C	4.11	1.54	1.48
5	A	1445	ACT	CH3-C	3.82	1.54	1.48
5	A	1444	ACT	CH3-C	3.41	1.53	1.48

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

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 ⓘ

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	431/473 (91%)	0.22	22 (5%) 27 28	19, 29, 53, 81	0
1	B	432/473 (91%)	0.16	23 (5%) 25 26	19, 28, 51, 74	0
1	C	432/473 (91%)	0.08	21 (4%) 28 29	19, 28, 49, 66	1 (0%)
All	All	1295/1419 (91%)	0.15	66 (5%) 25 28	19, 28, 51, 81	1 (0%)

All (66) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	333	ALA	6.1
1	A	189	HIS	6.1
1	A	335	PRO	5.9
1	C	333	ALA	5.2
1	B	333	ALA	5.1
1	A	135[A]	THR	4.9
1	B	189	HIS	4.8
1	C	213	ASN	4.6
1	B	335	PRO	4.5
1	C	335	PRO	4.4
1	B	330	ARG	4.4
1	A	188	PRO	4.3
1	A	134[A]	PRO	4.2
1	B	213	ASN	4.1
1	C	210	TYR	4.1
1	B	135	THR	3.7
1	A	331	PRO	3.6
1	A	334	LEU	3.6
1	B	331	PRO	3.5
1	B	134	PRO	3.4
1	C	134	PRO	3.4
1	A	365	GLY	3.4
1	C	209	ASN	3.4

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Mol	Chain	Res	Type	RSRZ
1	B	332	VAL	3.3
1	A	332	VAL	3.2
1	C	135	THR	3.2
1	C	336	ARG	3.1
1	C	338	LEU	3.1
1	B	328	THR	3.1
1	C	404	GLU	2.9
1	C	189	HIS	2.9
1	A	435	THR	2.9
1	C	214	GLN	2.8
1	C	334	LEU	2.8
1	A	330	ARG	2.8
1	A	328	THR	2.7
1	A	213	ASN	2.7
1	B	215	GLN	2.6
1	A	336	ARG	2.5
1	B	190	GLY	2.5
1	C	365	GLY	2.5
1	C	328	THR	2.5
1	C	308	HIS	2.4
1	A	402	GLY	2.4
1	A	404	GLU	2.3
1	C	332	VAL	2.3
1	A	411	ARG	2.3
1	B	209	ASN	2.3
1	C	403	GLY	2.3
1	B	60	GLU	2.3
1	A	112	TYR	2.3
1	B	334	LEU	2.2
1	C	411	ARG	2.2
1	C	28	PHE	2.2
1	B	411	ARG	2.2
1	C	435	THR	2.1
1	B	404	GLU	2.1
1	B	2	GLU	2.1
1	A	338	LEU	2.1
1	A	136[A]	ASP	2.1
1	B	435	THR	2.0
1	B	214	GLN	2.0
1	B	69	ALA	2.0
1	B	27	ARG	2.0
1	B	338	LEU	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	214	GLN	2.0

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

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

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, 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	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	NGA	C	1438	14/15	0.49	19.67	74,77,80,80	0
7	PEG	C	1448	7/7	0.22	16.64	41,45,48,48	0
2	NAG	C	1437	14/15	0.35	16.55	73,74,76,76	0
3	NGA	A	1437	14/15	0.53	16.42	76,78,80,80	0
5	ACT	A	1445	4/4	0.35	15.42	84,84,84,84	0
4	GOL	B	1442[A]	6/6	0.32	11.93	42,45,45,46	6
4	GOL	B	1442[B]	6/6	0.32	11.93	26,29,29,29	6
4	GOL	C	1442	6/6	0.34	11.22	69,70,70,71	0
6	PG4	A	1447	8/13	0.27	10.76	65,66,67,67	0
4	GOL	B	1439	6/6	0.35	7.28	51,54,55,56	0
4	GOL	C	1443	6/6	0.22	6.22	74,74,75,75	0
4	GOL	A	1441	6/6	0.27	6.19	70,71,71,71	0
2	NAG	B	1436	14/15	0.23	5.68	45,47,50,51	0
4	GOL	C	1441	6/6	0.28	5.21	57,58,58,59	0
5	ACT	B	1444	4/4	0.35	5.14	77,77,77,78	0
4	GOL	A	1440	6/6	0.27	5.03	66,67,67,67	0
4	GOL	B	1440	6/6	0.24	4.50	60,61,61,61	0
7	PEG	B	1446	7/7	0.25	4.38	45,49,52,52	0
4	GOL	B	1438	6/6	0.31	4.35	50,50,52,52	0

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Mol	Type	Chain	Res	Atoms	RSR	LLDF	B-factors(Å ²)	Q<0.9
5	ACT	C	1445	4/4	0.30	4.28	80,80,80,80	0
7	PEG	A	1449	7/7	0.21	3.76	62,63,63,63	0
4	GOL	B	1437	6/6	0.17	3.40	33,34,35,35	0
4	GOL	A	1438	6/6	0.22	3.13	49,51,51,51	0
7	PEG	C	1447	7/7	0.29	3.10	82,83,83,83	0
4	GOL	B	1441	6/6	0.17	2.78	69,70,70,70	0
4	GOL	A	1439	6/6	0.17	2.64	59,61,61,61	0
4	GOL	C	1439	6/6	0.14	2.43	33,36,37,39	0
5	ACT	B	1443	4/4	0.35	2.29	65,65,65,65	0
5	ACT	C	1444	4/4	0.27	1.39	71,71,71,71	0
4	GOL	C	1440	6/6	0.13	1.37	39,39,39,40	0
5	ACT	A	1444	4/4	0.21	1.28	62,62,62,62	0
2	NAG	C	1436	14/15	0.19	1.25	43,47,50,50	0
2	NAG	A	1436	14/15	0.21	1.16	42,45,47,48	0
5	ACT	A	1443	4/4	0.29	0.71	47,48,48,48	4
9	CA	B	1445	1/1	0.08	-0.92	36,36,36,36	0
9	CA	C	1446	1/1	0.07	-1.07	36,36,36,36	0
9	CA	A	1451	1/1	0.05	-1.48	33,33,33,33	1
8	NA	A	1450	1/1	0.03	-1.67	41,41,41,41	1

6.5 Other polymers ⓘ

There are no such residues in this entry.