



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 4, 2026 – 07:00 PM UTC

PDB ID : 3CDW / pdb_00003cdw
Title : Crystal structure of coxsackievirus B3 RNA-dependent RNA polymerase (3Dpol) in complex with protein primer VPg and a pyrophosphate
Authors : Gruez, A.; Selisko, B.; Roberts, M.; Bricogne, G.; Bussetta, C.; Canard, B.
Deposited on : 2008-02-27
Resolution : 2.50 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

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

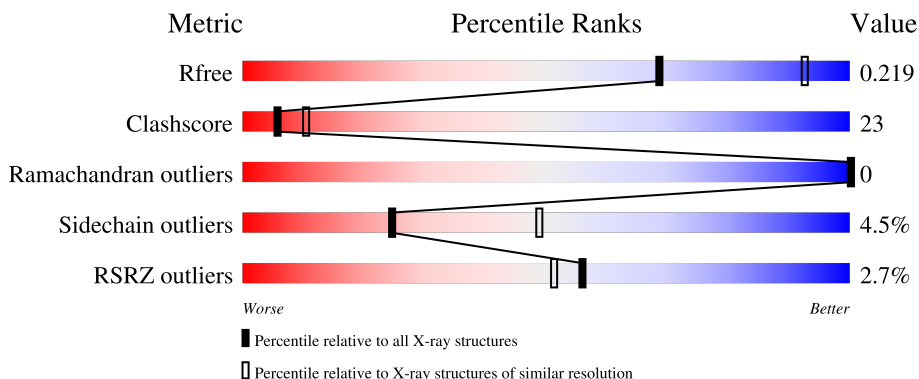
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)

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	468	 9% 27% 5% 59%
2	H	22	 9% 27% 5% 59%

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
4	ACT	A	477	-	-	X	-
4	ACT	A	478	-	X	X	-
6	GOL	A	484	-	-	X	-
6	GOL	A	488	-	-	X	-
6	GOL	A	495	-	-	X	-
6	GOL	A	496	-	-	X	-
6	GOL	A	497	-	-	X	-
6	GOL	A	498	-	-	X	-
6	GOL	A	501	-	-	X	-
6	GOL	A	502	-	-	X	-
6	GOL	A	507	-	-	X	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 4370 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 RNA-directed RNA polymerase 3D-POL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	468	3778	2420	641	695	22	0	6	0

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	463	HIS	-	expression tag	UNP P03313
A	464	HIS	-	expression tag	UNP P03313
A	465	HIS	-	expression tag	UNP P03313
A	466	HIS	-	expression tag	UNP P03313
A	467	HIS	-	expression tag	UNP P03313
A	468	HIS	-	expression tag	UNP P03313

- Molecule 2 is a protein called Protein 3B.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
			Total	C	N	O			
2	H	9	72	45	15	12	0	0	0

- Molecule 3 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

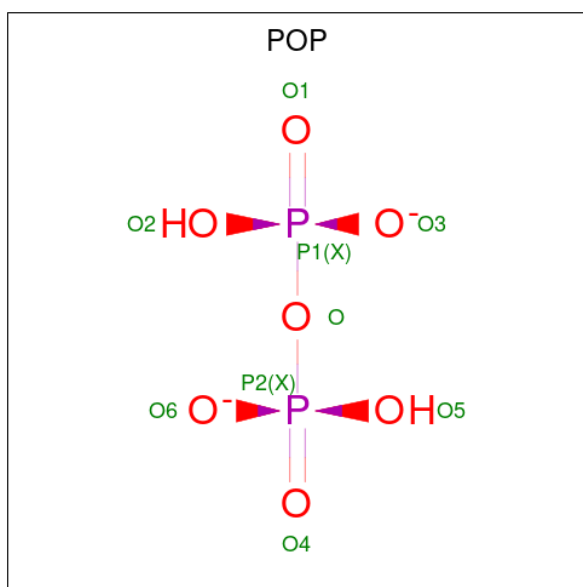
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	7	Total	Cl	0	0
			7	7		

- Molecule 4 is ACETATE ION (CCD ID: ACT) (formula: C₂H₃O₂).



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

- Molecule 5 is PYROPHOSPHATE 2- (CCD ID: POP) (formula: H₂O₇P₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	O	P	0	0
			9	7	2		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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

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

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

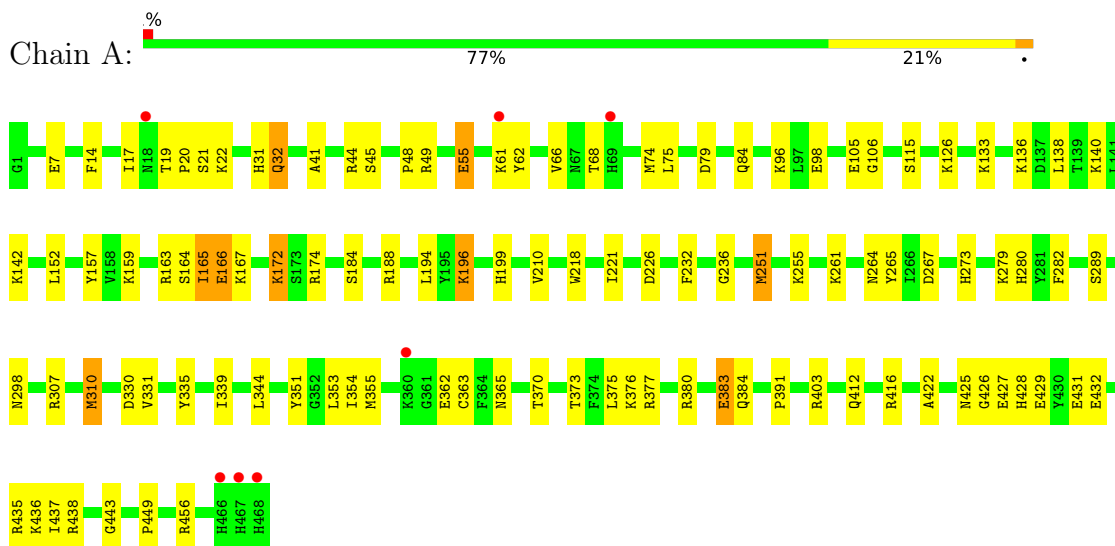
- Molecule 7 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	317	Total O 317 317	0	0
7	H	1	Total O 1 1	0	0

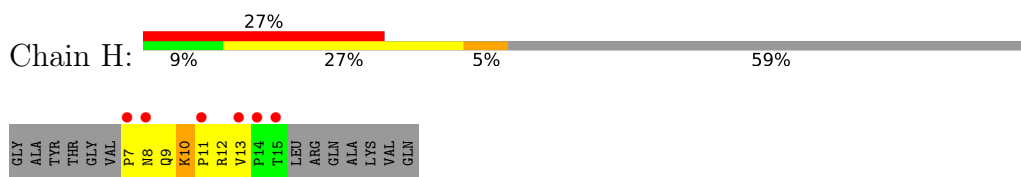
3 Residue-property plots [i](#)

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: RNA-directed RNA polymerase 3D-POL



- Molecule 2: Protein 3B



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	74.21Å 74.21Å 285.59Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.45 – 2.50 27.45 – 2.50	Depositor EDS
% Data completeness (in resolution range)	99.8 (27.45-2.50) 99.8 (27.45-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.10 (at 2.51Å)	Xtrriage
Refinement program	BUSTER-TNT 2.3.0	Depositor
R, R_{free}	0.175 , 0.220 0.181 , 0.219	Depositor DCC
R_{free} test set	1451 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	42.7	Xtrriage
Anisotropy	0.346	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	4370	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% 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: ACT, CL, POP, GOL

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	0.70	1/3905 (0.0%)	0.97	11/5284 (0.2%)
2	H	0.60	0/74	0.92	0/100
All	All	0.70	1/3979 (0.0%)	0.97	11/5384 (0.2%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	251	MET	SD-CE	5.81	1.94	1.79

The worst 5 of 11 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	152	LEU	CA-C-N	-7.51	112.59	120.03
1	A	152	LEU	C-N-CA	-7.51	112.59	120.03
1	A	66	VAL	N-CA-C	-7.20	98.07	108.36
1	A	422	ALA	N-CA-C	6.70	118.58	111.28
1	A	335	TYR	CA-C-N	-6.11	113.39	119.56

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	3778	0	3723	160	0
2	H	72	0	77	25	0
3	A	7	0	0	0	0
4	A	24	0	18	21	0
5	A	9	0	0	3	0
6	A	162	0	216	70	0
7	A	317	0	0	16	1
7	H	1	0	0	0	0
All	All	4370	0	4034	188	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 23.

The worst 5 of 188 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:H:9:GLN:HG2	2:H:12:ARG:HG3	1.40	1.02
1:A:273[A]:HIS:NE2	1:A:280:HIS:NE2	2.06	1.01
6:A:509:GOL:H2	2:H:7:PRO:HD2	1.48	0.93
1:A:31:HIS:CE1	6:A:501:GOL:H31	2.06	0.90
1:A:45:SER:H	6:A:495:GOL:H32	1.35	0.89

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)
7:A:659:HOH:O	7:A:659:HOH:O[8_555]	2.18	0.02

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	472/468 (101%)	463 (98%)	9 (2%)	0	100	100
2	H	7/22 (32%)	6 (86%)	1 (14%)	0	100	100
All	All	479/490 (98%)	469 (98%)	10 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	415/409 (102%)	397 (96%)	18 (4%)	26	51
2	H	9/18 (50%)	8 (89%)	1 (11%)	6	12
All	All	424/427 (99%)	405 (96%)	19 (4%)	24	49

5 of 19 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	298	ASN
1	A	383	GLU
2	H	10	LYS
1	A	362	GLU
1	A	166	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	H	8	ASN
1	A	468	HIS
1	A	298	ASN
1	A	271	ASN
1	A	466	HIS

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 41 ligands modelled in this entry, 7 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	$\# Z > 2$
6	GOL	A	496	-	5,5,5	0.38	0	5,5,5	0.29	0
6	GOL	A	503	-	5,5,5	0.28	0	5,5,5	0.37	0
6	GOL	A	489	-	5,5,5	0.48	0	5,5,5	0.29	0
6	GOL	A	492	-	5,5,5	0.29	0	5,5,5	0.42	0
4	ACT	A	481	-	3,3,3	0.94	0	3,3,3	1.07	0
4	ACT	A	478	-	3,3,3	1.70	1 (33%)	3,3,3	2.27	2 (66%)
6	GOL	A	491	-	5,5,5	0.48	0	5,5,5	0.27	0
6	GOL	A	493	-	5,5,5	0.25	0	5,5,5	0.36	0
6	GOL	A	486	-	5,5,5	0.35	0	5,5,5	0.45	0
6	GOL	A	498	-	5,5,5	0.57	0	5,5,5	0.20	0
4	ACT	A	476	-	3,3,3	1.29	0	3,3,3	0.58	0
6	GOL	A	494	-	5,5,5	0.30	0	5,5,5	0.35	0
6	GOL	A	505	-	5,5,5	0.52	0	5,5,5	0.24	0
6	GOL	A	509	-	5,5,5	0.36	0	5,5,5	0.27	0
6	GOL	A	487	-	5,5,5	0.62	0	5,5,5	0.09	0
6	GOL	A	501	-	5,5,5	0.64	0	5,5,5	0.26	0
4	ACT	A	477	-	3,3,3	1.02	0	3,3,3	1.00	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	POP	A	482	-	6,8,8	1.13	0	12,13,13	2.23	6 (50%)
6	GOL	A	499	-	5,5,5	0.35	0	5,5,5	0.34	0
6	GOL	A	507	-	5,5,5	0.64	0	5,5,5	0.29	0
6	GOL	A	506	-	5,5,5	0.33	0	5,5,5	0.61	0
6	GOL	A	508	-	5,5,5	0.32	0	5,5,5	0.31	0
6	GOL	A	497	-	5,5,5	0.89	0	5,5,5	0.25	0
4	ACT	A	480	-	3,3,3	0.83	0	3,3,3	0.80	0
6	GOL	A	485	-	5,5,5	0.27	0	5,5,5	0.35	0
6	GOL	A	490	-	5,5,5	0.40	0	5,5,5	0.39	0
4	ACT	A	479	-	3,3,3	1.25	0	3,3,3	1.14	0
6	GOL	A	483	-	5,5,5	0.82	0	5,5,5	0.19	0
6	GOL	A	488	-	5,5,5	0.70	0	5,5,5	0.30	0
6	GOL	A	502	-	5,5,5	0.22	0	5,5,5	0.40	0
6	GOL	A	495	-	5,5,5	0.72	0	5,5,5	0.14	0
6	GOL	A	500	-	5,5,5	0.39	0	5,5,5	0.37	0
6	GOL	A	504	-	5,5,5	0.63	0	5,5,5	0.22	0
6	GOL	A	484	-	5,5,5	0.58	0	5,5,5	0.45	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
6	GOL	A	496	-	-	2/4/4/4	-
6	GOL	A	503	-	-	2/4/4/4	-
6	GOL	A	489	-	-	4/4/4/4	-
6	GOL	A	492	-	-	3/4/4/4	-
6	GOL	A	491	-	-	0/4/4/4	-
6	GOL	A	493	-	-	2/4/4/4	-
6	GOL	A	486	-	-	2/4/4/4	-
6	GOL	A	498	-	-	0/4/4/4	-
6	GOL	A	494	-	-	2/4/4/4	-
6	GOL	A	505	-	-	0/4/4/4	-
6	GOL	A	509	-	-	4/4/4/4	-
6	GOL	A	487	-	-	4/4/4/4	-
6	GOL	A	501	-	-	2/4/4/4	-
5	POP	A	482	-	-	4/6/6/6	-
6	GOL	A	499	-	-	2/4/4/4	-
6	GOL	A	507	-	-	1/4/4/4	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	GOL	A	506	-	-	3/4/4/4	-
6	GOL	A	508	-	-	2/4/4/4	-
6	GOL	A	497	-	-	2/4/4/4	-
6	GOL	A	485	-	-	2/4/4/4	-
6	GOL	A	490	-	-	4/4/4/4	-
6	GOL	A	483	-	-	4/4/4/4	-
6	GOL	A	488	-	-	4/4/4/4	-
6	GOL	A	502	-	-	4/4/4/4	-
6	GOL	A	495	-	-	4/4/4/4	-
6	GOL	A	500	-	-	2/4/4/4	-
6	GOL	A	504	-	-	2/4/4/4	-
6	GOL	A	484	-	-	4/4/4/4	-

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	478	ACT	OXT-C	-2.33	1.20	1.30

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	482	POP	O3-P1-O1	-3.84	95.88	110.83
5	A	482	POP	O5-P2-O	3.65	116.86	104.64
5	A	482	POP	O6-P2-O4	-3.32	97.88	110.83
4	A	478	ACT	OXT-C-CH3	2.87	127.07	115.05
4	A	478	ACT	OXT-C-O	-2.64	112.22	122.03

There are no chirality outliers.

5 of 71 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	A	482	POP	P1-O-P2-O6
6	A	486	GOL	O1-C1-C2-C3
6	A	487	GOL	O1-C1-C2-O2
6	A	487	GOL	O1-C1-C2-C3
6	A	488	GOL	O1-C1-C2-C3

There are no ring outliers.

26 monomers are involved in 93 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	496	GOL	6	0
6	A	503	GOL	3	0
6	A	489	GOL	1	0
6	A	492	GOL	2	0
4	A	478	ACT	11	0
6	A	493	GOL	2	0
6	A	486	GOL	2	0
6	A	498	GOL	4	0
4	A	476	ACT	1	0
6	A	494	GOL	2	0
6	A	509	GOL	2	0
6	A	487	GOL	3	0
6	A	501	GOL	6	0
4	A	477	ACT	8	0
5	A	482	POP	3	0
6	A	507	GOL	7	0
6	A	506	GOL	2	0
6	A	508	GOL	1	0
6	A	497	GOL	6	0
4	A	480	ACT	1	0
6	A	483	GOL	3	0
6	A	488	GOL	4	0
6	A	502	GOL	8	0
6	A	495	GOL	6	0
6	A	500	GOL	1	0
6	A	484	GOL	4	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, 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	468/468 (100%)	-0.31	7 (1%) 72 68	20, 41, 67, 95	6 (1%)
2	H	9/22 (40%)	2.56	6 (66%) 0 0	57, 71, 77, 78	0
All	All	477/490 (97%)	-0.26	13 (2%) 56 51	20, 41, 70, 95	6 (1%)

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	467	HIS	5.3
2	H	15	THR	4.2
2	H	8	ASN	4.2
2	H	11	PRO	3.6
1	A	466	HIS	3.4

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(\AA^2)	Q<0.9
4	ACT	A	479	4/4	-0.14	0.32	111,111,111,112	0
6	GOL	A	507	6/6	0.52	0.25	99,99,100,100	0
4	ACT	A	477	4/4	0.58	0.33	99,99,99,99	0
6	GOL	A	502	6/6	0.62	0.37	107,108,109,110	0
4	ACT	A	478	4/4	0.64	0.24	91,91,91,92	0
6	GOL	A	495	6/6	0.68	0.27	89,91,92,92	0
6	GOL	A	501	6/6	0.68	0.18	68,71,72,74	0
6	GOL	A	486	6/6	0.69	0.20	69,69,69,69	0
4	ACT	A	476	4/4	0.72	0.17	76,77,77,78	0
6	GOL	A	484	6/6	0.75	0.23	93,95,96,98	0
6	GOL	A	504	6/6	0.75	0.27	89,90,90,90	0
4	ACT	A	480	4/4	0.75	0.28	94,95,95,96	0
6	GOL	A	503	6/6	0.76	0.20	76,78,79,81	0
6	GOL	A	483	6/6	0.78	0.22	52,58,59,63	0
6	GOL	A	505	6/6	0.79	0.18	78,80,80,82	0
3	CL	A	475	1/1	0.79	0.22	106,106,106,106	0
6	GOL	A	492	6/6	0.80	0.22	84,85,85,86	0
4	ACT	A	481	4/4	0.80	0.17	81,81,82,82	0
6	GOL	A	508	6/6	0.80	0.25	99,100,100,102	0
6	GOL	A	506	6/6	0.81	0.21	79,80,81,82	0
6	GOL	A	491	6/6	0.81	0.21	88,89,90,90	0
5	POP	A	482	9/9	0.81	0.20	54,55,59,59	9
6	GOL	A	509	6/6	0.81	0.25	96,97,97,97	0
6	GOL	A	488	6/6	0.82	0.17	63,66,67,68	0
6	GOL	A	498	6/6	0.83	0.19	81,85,86,87	0
6	GOL	A	496	6/6	0.84	0.27	86,86,87,87	0
6	GOL	A	487	6/6	0.85	0.17	65,66,66,67	0
6	GOL	A	500	6/6	0.87	0.19	64,67,68,69	0
6	GOL	A	489	6/6	0.88	0.13	59,63,64,66	0
6	GOL	A	493	6/6	0.88	0.19	69,71,72,73	0
6	GOL	A	494	6/6	0.88	0.23	77,77,77,78	0
6	GOL	A	485	6/6	0.88	0.19	55,59,61,61	0
6	GOL	A	490	6/6	0.89	0.16	67,67,68,69	0
6	GOL	A	497	6/6	0.91	0.20	80,81,81,82	0
3	CL	A	473	1/1	0.91	0.30	83,83,83,83	0
6	GOL	A	499	6/6	0.93	0.09	47,50,51,53	0
3	CL	A	474	1/1	0.96	0.06	62,62,62,62	0
3	CL	A	470	1/1	0.97	0.05	45,45,45,45	0
3	CL	A	469	1/1	0.97	0.05	43,43,43,43	0
3	CL	A	472	1/1	0.98	0.07	49,49,49,49	0
3	CL	A	471	1/1	0.98	0.06	50,50,50,50	0

6.5 Other polymers [i](#)

There are no such residues in this entry.