



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 07:14 AM UTC

PDB ID : 6J1A / pdb_00006j1a
Title : Photoswitchable fluorescent protein Gamillus, off-state
Authors : Nakashima, R.; Sakurai, K.; shinoda, H.; Matsuda, T.; Nagai, T.
Deposited on : 2018-12-28
Resolution : 1.96 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

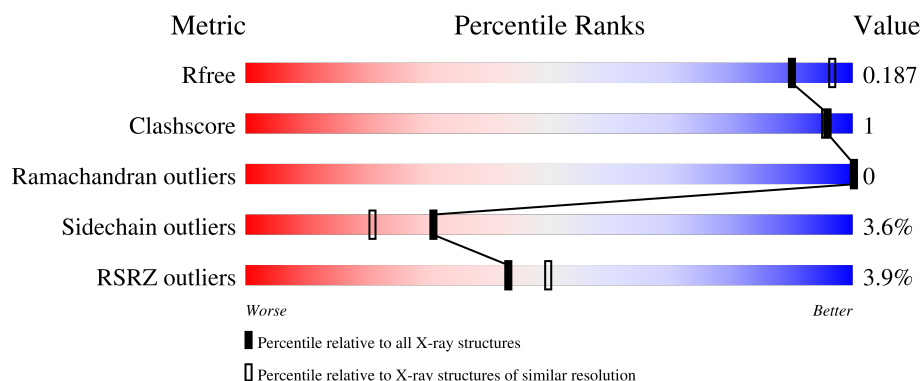
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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 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	271	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 2003 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.

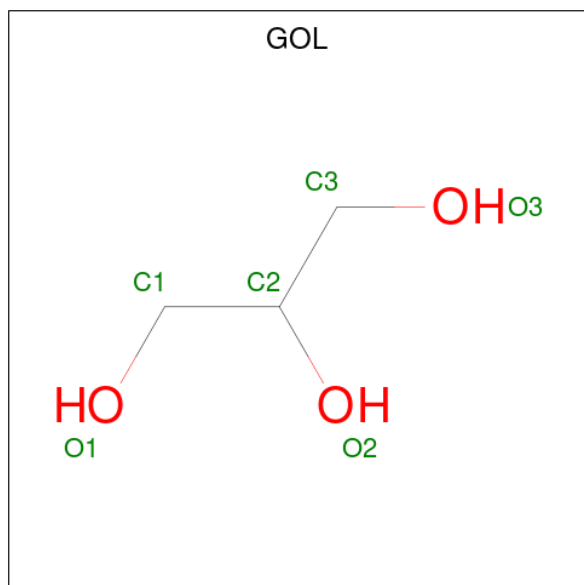
- Molecule 1 is a protein called Green fluorescent protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	230	Total	C	N	O	S	0	1	0
			1822	1154	311	346	11			

- Molecule 2 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

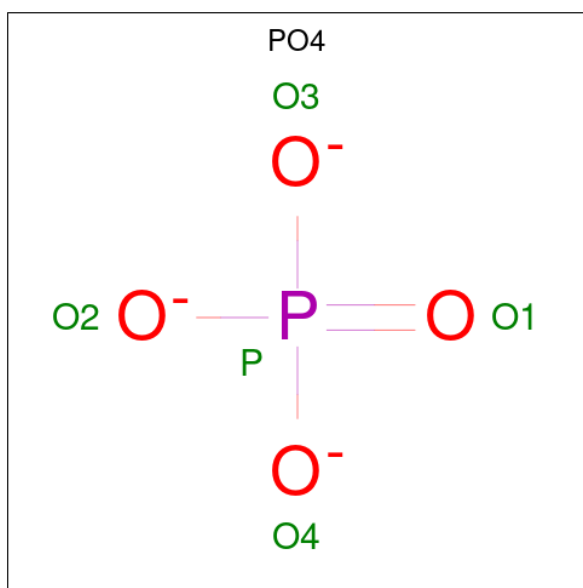
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Cl	0	0
			3	3		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



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 PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	P	0	0
			5	4	1		

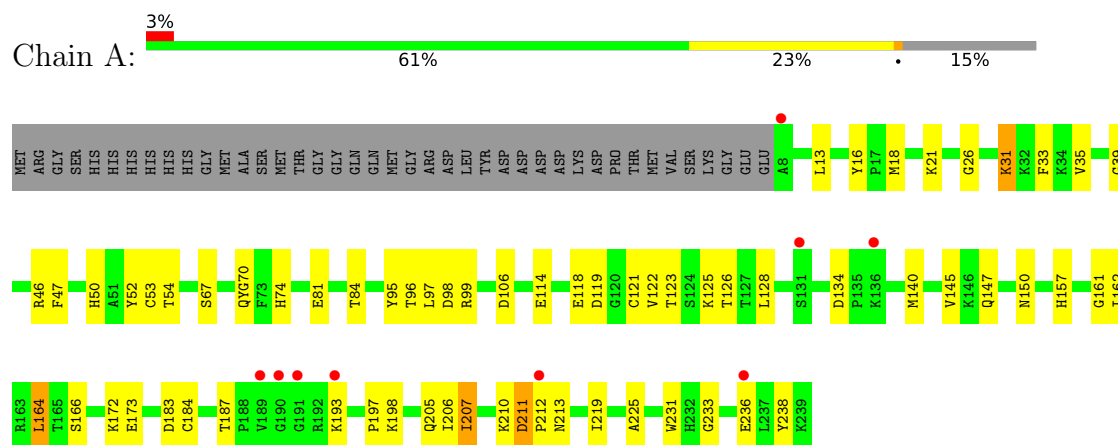
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	161	Total	O	0	0
			161	161		

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: Green fluorescent protein



4 Data and refinement statistics

Property	Value	Source
Space group	I 21 3	Depositor
Cell constants a, b, c, α , β , γ	161.54Å 161.54Å 161.54Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	114.23 – 1.96 114.23 – 1.96	Depositor EDS
% Data completeness (in resolution range)	99.8 (114.23-1.96) 99.8 (114.23-1.96)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.00 (at 1.95Å)	Xtriage
Refinement program	REFMAC 5.8.0135	Depositor
R, R_{free}	0.152 , 0.180 0.163 , 0.187	Depositor DCC
R_{free} test set	2492 reflections (4.95%)	wwPDB-VP
Wilson B-factor (Å ²)	26.3	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 38.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.028 for -l,-k,-h	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	2003	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.84% 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: QYG, PO4, GOL, CL

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	2.12	56/1843 (3.0%)	1.55	12/2495 (0.5%)

All (56) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	95	TYR	CA-C	-9.38	1.41	1.52
1	A	122	VAL	CA-C	-8.18	1.42	1.52
1	A	238	TYR	N-CA	8.10	1.55	1.46
1	A	219	ILE	CA-C	-7.49	1.43	1.52
1	A	97	LEU	CA-C	-7.38	1.43	1.52
1	A	96	THR	N-CA	-7.32	1.37	1.45
1	A	118	GLU	C-O	7.26	1.32	1.23
1	A	39	GLY	CA-C	-7.12	1.44	1.51
1	A	172	LYS	N-CA	-6.94	1.36	1.45
1	A	13	LEU	N-CA	-6.94	1.37	1.46
1	A	21	LYS	CA-C	-6.89	1.44	1.52
1	A	33	PHE	CA-C	-6.78	1.44	1.52
1	A	74	HIS	CA-C	-6.45	1.43	1.52
1	A	106	ASP	CG-OD2	-6.42	1.13	1.25
1	A	81	GLU	C-O	-6.22	1.16	1.24
1	A	173	GLU	N-CA	6.11	1.54	1.46
1	A	161	GLY	N-CA	6.09	1.50	1.44
1	A	126	THR	CA-C	-6.08	1.45	1.52
1	A	53	CYS	N-CA	-6.00	1.38	1.46
1	A	16	TYR	CA-C	5.98	1.60	1.52
1	A	134	ASP	CA-C	-5.89	1.46	1.52
1	A	211	ASP	CA-C	5.88	1.59	1.52
1	A	35	VAL	CA-C	-5.84	1.45	1.52
1	A	26	GLY	N-CA	-5.83	1.38	1.44
1	A	210	LYS	C-O	-5.82	1.17	1.23
1	A	16	TYR	C-O	-5.81	1.17	1.23

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	122	VAL	CA-CB	5.78	1.60	1.54
1	A	187	THR	N-CA	5.76	1.53	1.46
1	A	236	GLU	C-O	-5.69	1.17	1.24
1	A	123	THR	CA-CB	5.69	1.61	1.53
1	A	225	ALA	CA-C	-5.68	1.45	1.52
1	A	206	ILE	C-O	-5.67	1.18	1.24
1	A	231	TRP	N-CA	5.58	1.53	1.46
1	A	46	ARG	C-O	5.55	1.30	1.24
1	A	197	PRO	CA-C	5.51	1.58	1.52
1	A	18	MET	CA-CB	5.46	1.61	1.53
1	A	98	ASP	N-CA	-5.43	1.39	1.46
1	A	183	ASP	CA-C	5.40	1.58	1.52
1	A	54	THR	N-CA	5.36	1.53	1.46
1	A	50	HIS	CA-C	-5.31	1.46	1.52
1	A	162	ILE	CA-C	-5.30	1.46	1.52
1	A	99	ARG	CA-C	-5.28	1.46	1.52
1	A	166	SER	CA-CB	5.22	1.62	1.53
1	A	121	CYS	C-O	5.18	1.30	1.24
1	A	84	THR	CA-CB	5.17	1.61	1.53
1	A	238	TYR	CG-CD1	-5.16	1.28	1.39
1	A	207	ILE	N-CA	5.15	1.52	1.46
1	A	119	ASP	C-O	5.14	1.30	1.23
1	A	52	TYR	CA-CB	5.12	1.62	1.53
1	A	157	HIS	N-CA	-5.12	1.40	1.46
1	A	67	SER	CA-CB	5.10	1.61	1.53
1	A	147	GLN	N-CA	5.07	1.51	1.45
1	A	46	ARG	CD-NE	5.07	1.53	1.46
1	A	213	ASN	N-CA	-5.07	1.39	1.46
1	A	31	LYS	CA-C	-5.04	1.46	1.52
1	A	96	THR	CA-C	5.01	1.58	1.52

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	140	MET	CG-SD-CE	-10.14	78.60	100.90
1	A	211	ASP	N-CA-C	-7.31	99.08	109.24
1	A	46	ARG	NE-CZ-NH2	6.99	125.49	119.20
1	A	233	GLY	N-CA-C	6.87	122.22	114.67
1	A	46	ARG	NE-CZ-NH1	-6.56	114.94	121.50
1	A	145	VAL	CB-CA-C	-6.13	104.50	111.55
1	A	213	ASN	N-CA-C	6.02	120.82	112.45
1	A	46	ARG	CD-NE-CZ	-5.79	116.30	124.40

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	114	GLU	CA-CB-CG	-5.54	103.02	114.10
1	A	207	ILE	CB-CA-C	-5.31	102.78	110.63
1	A	205	GLN	N-CA-CB	-5.14	101.70	111.00
1	A	205	GLN	CA-CB-CG	-5.08	103.93	114.10

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	1822	0	1751	4	0
2	A	3	0	0	0	0
3	A	12	0	16	0	0
4	A	5	0	0	0	0
5	A	161	0	0	1	0
All	All	2003	0	1767	4	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 1.

All (4) 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:207:ILE:HG12	5:A:541:HOH:O	1.83	0.77
1:A:164:LEU:HB2	1:A:184:CYS:HB2	1.92	0.52
1:A:211:ASP:OD1	1:A:212:PRO:HD2	2.17	0.44
1:A:128:LEU:HD23	1:A:128:LEU:C	2.46	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	226/271 (83%)	220 (97%)	6 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	198/231 (86%)	191 (96%)	7 (4%)	32	22

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LYS
1	A	47	PHE
1	A	125	LYS
1	A	150	ASN
1	A	164	LEU
1	A	193	LYS
1	A	198	LYS

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

Mol	Chain	Res	Type
1	A	205	GLN

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Mol	Chain	Res	Type
1	A	208	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is 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$
1	QYG	A	70	1	24,25,26	2.53	6 (25%)	31,34,36	3.43	14 (45%)

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
1	QYG	A	70	1	-	0/13/32/33	0/2/2/2

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	70	QYG	CB2-CA2	7.10	1.42	1.35
1	A	70	QYG	C1-N2	5.51	1.40	1.32
1	A	70	QYG	C1-N3	4.53	1.44	1.37
1	A	70	QYG	CA3-N3	-3.87	1.40	1.47
1	A	70	QYG	CG2-CB2	-3.03	1.41	1.46
1	A	70	QYG	CD2-CG2	-2.00	1.35	1.39

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	70	QYG	C2-N3-C1	-9.35	103.74	108.07
1	A	70	QYG	CA1-C1-N3	-8.93	113.21	124.84
1	A	70	QYG	O2-C2-CA2	-8.69	125.47	131.02
1	A	70	QYG	CA2-C2-N3	6.80	109.21	103.50
1	A	70	QYG	CA1-C1-N2	3.23	129.88	123.57
1	A	70	QYG	CE1-CD1-CG2	-3.09	117.22	121.22
1	A	70	QYG	CB2-CA2-N2	3.07	132.92	128.76
1	A	70	QYG	CB2-CA2-C2	-2.88	118.87	122.36
1	A	70	QYG	CB1-CG1-CD3	-2.65	103.57	112.55
1	A	70	QYG	N3-C1-N2	2.50	113.45	111.48
1	A	70	QYG	CD1-CE1-CZ	2.12	122.13	119.88
1	A	70	QYG	CD1-CG2-CB2	-2.10	114.00	121.22
1	A	70	QYG	CD1-CG2-CD2	2.06	120.71	117.65
1	A	70	QYG	CD2-CE2-CZ	-2.00	117.76	119.88

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 6 ligands modelled in this entry, 3 are monoatomic - leaving 3 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	$\# Z > 2$
3	GOL	A	304	-	5,5,5	0.75	0	5,5,5	1.46	1 (20%)
4	PO4	A	306	-	4,4,4	0.69	0	6,6,6	2.47	3 (50%)
3	GOL	A	305	-	5,5,5	0.88	0	5,5,5	0.99	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
3	GOL	A	304	-	-	0/4/4/4	-
3	GOL	A	305	-	-	2/4/4/4	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	306	PO4	O3-P-O1	-4.28	95.83	110.95
3	A	304	GOL	C3-C2-C1	-3.08	100.50	111.80
4	A	306	PO4	O2-P-O1	3.01	121.59	110.95
4	A	306	PO4	O4-P-O2	2.02	114.20	107.91

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	305	GOL	C1-C2-C3-O3
3	A	305	GOL	O2-C2-C3-O3

There are no ring outliers.

No monomer is involved in short contacts.

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	229/271 (84%)	0.02	9 (3%)	43 50	13, 26, 47, 63	1 (0%)

All (9) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	191	GLY	4.9
1	A	8	ALA	3.1
1	A	212	PRO	3.1
1	A	193	LYS	3.1
1	A	190	GLY	2.8
1	A	189	VAL	2.7
1	A	131	SER	2.3
1	A	136	LYS	2.1
1	A	236	GLU	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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(Å ²)	Q < 0.9
1	QYG	A	70	24/25	0.97	0.07	18,23,40,47	0

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
3	GOL	A	305	6/6	0.86	0.21	56,68,74,77	0
3	GOL	A	304	6/6	0.94	0.15	36,50,51,55	0
2	CL	A	301	1/1	0.97	0.13	41,41,41,41	0
2	CL	A	302	1/1	0.98	0.10	31,31,31,31	0
2	CL	A	303	1/1	0.99	0.09	30,30,30,30	0
4	PO4	A	306	5/5	0.99	0.08	25,34,38,38	0

6.5 Other polymers [i](#)

There are no such residues in this entry.