



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 07:41 AM UTC

PDB ID : 4N3D / pdb_00004n3d
Title : Crystal structure of the dimeric variant EGFP-K162Q in P61 space group
Authors : Pletneva, N.V.; Pletnev, V.Z.; Pletnev, S.V.
Deposited on : 2013-10-07
Resolution : 1.34 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

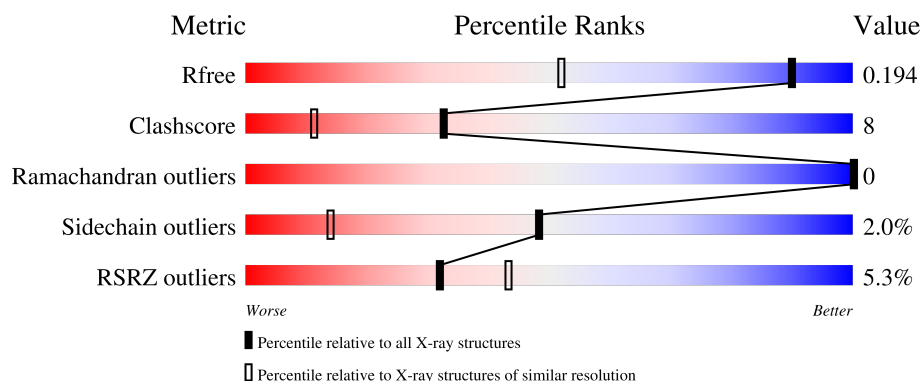
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

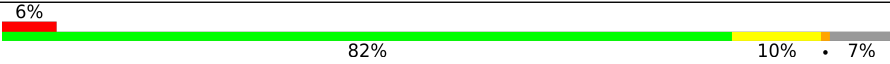
The reported resolution of this entry is 1.34 Å.

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	2194 (1.36-1.32)
Clashscore	190562	2222 (1.36-1.32)
Ramachandran outliers	187476	2197 (1.36-1.32)
Sidechain outliers	187428	2197 (1.36-1.32)
RSRZ outliers	180081	2193 (1.36-1.32)

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	242	
1	B	242	

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	GOL	A	308	-	X	-	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 4368 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	226	Total	C	N	O	S	0	15	0
			1904	1215	318	364	7			
1	B	226	Total	C	N	O	S	0	13	0
			1884	1205	311	361	7			

There are 34 discrepancies between the modelled and reference sequences:

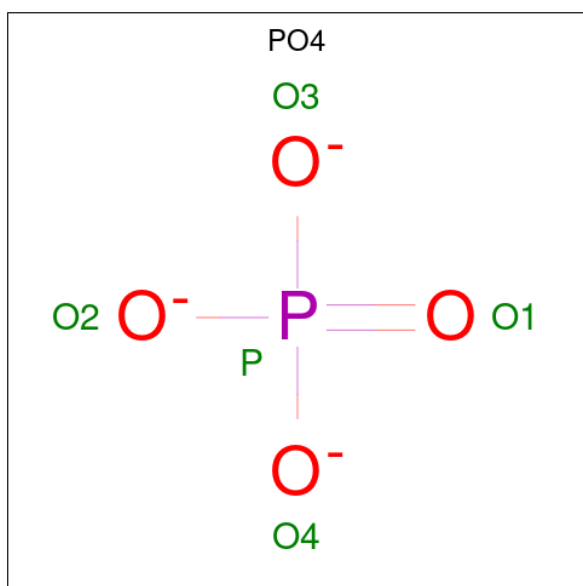
Chain	Residue	Modelled	Actual	Comment	Reference
A	-10	ARG	-	expression tag	UNP P42212
A	-9	GLY	-	expression tag	UNP P42212
A	-8	SER	-	expression tag	UNP P42212
A	-7	HIS	-	expression tag	UNP P42212
A	-6	HIS	-	expression tag	UNP P42212
A	-5	HIS	-	expression tag	UNP P42212
A	-4	HIS	-	expression tag	UNP P42212
A	-3	HIS	-	expression tag	UNP P42212
A	-2	HIS	-	expression tag	UNP P42212
A	-1	GLY	-	expression tag	UNP P42212
A	0	SER	-	expression tag	UNP P42212
A	1	VAL	-	expression tag	UNP P42212
A	65	CRO	SER	chromophore	UNP P42212
A	65	CRO	TYR	chromophore	UNP P42212
A	65	CRO	GLY	chromophore	UNP P42212
A	162	GLN	LYS	engineered mutation	UNP P42212
A	231	LEU	HIS	engineered mutation	UNP P42212
B	-10	ARG	-	expression tag	UNP P42212
B	-9	GLY	-	expression tag	UNP P42212
B	-8	SER	-	expression tag	UNP P42212
B	-7	HIS	-	expression tag	UNP P42212
B	-6	HIS	-	expression tag	UNP P42212
B	-5	HIS	-	expression tag	UNP P42212
B	-4	HIS	-	expression tag	UNP P42212
B	-3	HIS	-	expression tag	UNP P42212

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	expression tag	UNP P42212
B	-1	GLY	-	expression tag	UNP P42212
B	0	SER	-	expression tag	UNP P42212
B	1	VAL	-	expression tag	UNP P42212
B	65	CRO	SER	chromophore	UNP P42212
B	65	CRO	TYR	chromophore	UNP P42212
B	65	CRO	GLY	chromophore	UNP P42212
B	162	GLN	LYS	engineered mutation	UNP P42212
B	231	LEU	HIS	engineered mutation	UNP P42212

- Molecule 2 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).



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

- Molecule 3 is POTASSIUM ION (CCD ID: K) (formula: K).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	3	Total	K	0	0
			3	3		

- Molecule 4 is GLYCEROL (CCD ID: 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		

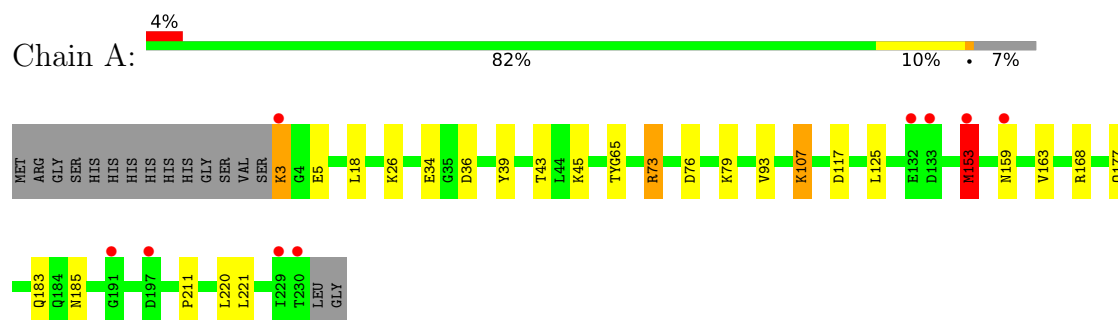
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	278	Total	O	0	0
			278	278		
5	B	271	Total	O	0	0
			271	271		

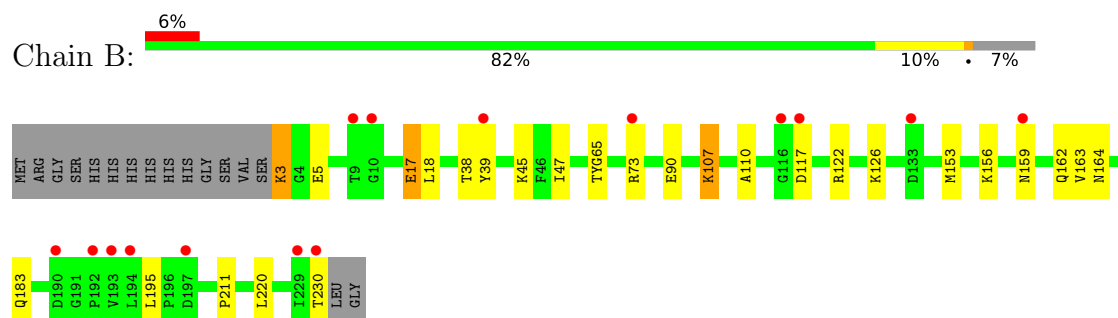
3 Residue-property plots [i](#)

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



- Molecule 1: Green fluorescent protein



4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	121.86Å 121.86Å 64.89Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	22.21 – 1.34 22.21 – 1.34	Depositor EDS
% Data completeness (in resolution range)	99.9 (22.21-1.34) 99.9 (22.21-1.34)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.61 (at 1.34Å)	Xtriage
Refinement program	REFMAC	Depositor
R, R_{free}	0.181 , 0.194 0.180 , 0.194	Depositor DCC
R_{free} test set	1231 reflections (1.01%)	wwPDB-VP
Wilson B-factor (Å ²)	13.9	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	0.026 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	4368	wwPDB-VP
Average B, all atoms (Å ²)	18.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.16% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: K, CRO, GOL, PO4

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	1.30	3/1949 (0.2%)	1.02	4/2629 (0.2%)
1	B	1.32	7/1929 (0.4%)	1.08	0/2605
All	All	1.31	10/3878 (0.3%)	1.05	4/5234 (0.1%)

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	1

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	117	ASP	C-O	-6.21	1.15	1.24
1	B	159	ASN	C-N	-6.09	1.24	1.33
1	B	159	ASN	CA-C	5.84	1.60	1.52
1	A	177	GLN	CA-CB	-5.49	1.45	1.53
1	A	34	GLU	C-O	-5.41	1.17	1.23
1	B	17[A]	GLU	C-O	-5.16	1.18	1.23
1	B	17[B]	GLU	C-O	-5.16	1.18	1.23
1	A	45	LYS	CD-CE	-5.15	1.37	1.52
1	B	107[A]	LYS	C-O	-5.05	1.18	1.24
1	B	107[B]	LYS	C-O	-5.05	1.18	1.24

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	159	ASN	CA-C-N	5.14	128.23	122.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	159	ASN	C-N-CA	5.14	128.23	122.42
1	A	153[A]	MET	CB-CA-C	-5.10	99.02	109.38
1	A	153[B]	MET	CB-CA-C	-5.10	99.02	109.38

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	73[A]	ARG	Sidechain

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	1904	0	1878	40	0
1	B	1884	0	1858	23	0
2	A	10	0	0	0	0
3	A	3	0	0	0	0
4	A	18	0	18	4	0
5	A	278	0	0	9	0
5	B	271	0	0	5	0
All	All	4368	0	3754	60	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 8.

All (60) 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:3[B]:LYS:CE	1:A:5:GLU:HB3	1.64	1.28
1:B:107[B]:LYS:HE3	5:B:508:HOH:O	1.38	1.24
1:A:3[B]:LYS:N	1:A:3[B]:LYS:HD3	1.45	1.15
1:A:3[B]:LYS:HE2	1:A:5:GLU:HB3	1.18	1.07
4:A:308:GOL:H32	5:A:471:HOH:O	1.60	0.98
1:A:153[A]:MET:SD	5:A:508:HOH:O	2.22	0.97

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3[B]:LYS:N	1:A:3[B]:LYS:CD	2.30	0.92
1:A:3[B]:LYS:NZ	1:A:5:GLU:HB3	1.88	0.87
1:A:3[B]:LYS:HE2	1:A:5:GLU:CB	2.03	0.86
1:A:43[B]:THR:HG22	1:A:221:LEU:HG	1.61	0.80
1:B:17[B]:GLU:OE1	1:B:122:ARG:NH1	2.15	0.79
1:B:45:LYS:HE2	1:B:47[A]:ILE:HD11	1.66	0.78
1:A:3[B]:LYS:HZ1	1:A:5:GLU:CD	1.94	0.75
1:B:162:GLN:HE21	1:B:164:ASN:HD21	1.35	0.74
1:A:153[A]:MET:CE	5:A:508:HOH:O	2.37	0.73
1:A:117:ASP:HB2	5:A:646:HOH:O	1.87	0.72
1:A:73[B]:ARG:HE	1:B:211:PRO:HB3	1.56	0.70
1:A:3[B]:LYS:CE	1:A:5:GLU:CB	2.58	0.67
1:B:73:ARG:NH2	5:B:487:HOH:O	2.27	0.67
1:A:3[B]:LYS:NZ	1:A:5:GLU:CD	2.52	0.67
1:A:26:LYS:HE3	5:A:666:HOH:O	2.00	0.62
1:B:38:THR:O	1:B:73:ARG:HD2	1.99	0.62
1:A:36:ASP:OD2	4:A:307:GOL:H12	2.03	0.59
1:A:73[B]:ARG:NE	1:B:211:PRO:HB3	2.17	0.59
1:A:3[B]:LYS:HE2	1:A:5:GLU:H	1.69	0.58
1:A:39:TYR:CE2	4:A:307:GOL:H11	2.39	0.57
1:B:3:LYS:HG2	1:B:5:GLU:HG2	1.86	0.56
1:B:153[B]:MET:HE3	1:B:162:GLN:NE2	2.20	0.56
1:A:3[B]:LYS:HZ3	1:A:5:GLU:HB3	1.68	0.55
1:A:3[B]:LYS:NZ	1:A:5:GLU:CB	2.68	0.53
1:B:38:THR:O	1:B:73:ARG:CD	2.56	0.53
1:A:3[B]:LYS:HE2	1:A:5:GLU:N	2.26	0.51
1:B:107[A]:LYS:HD2	5:B:457:HOH:O	2.09	0.51
1:A:43[B]:THR:HG22	1:A:221:LEU:CG	2.35	0.51
4:A:308:GOL:C3	5:A:471:HOH:O	2.37	0.51
1:A:73[B]:ARG:CZ	1:B:211:PRO:HB3	2.41	0.51
1:A:163:VAL:HB	1:A:183:GLN:HB3	1.95	0.48
1:A:3[B]:LYS:NZ	1:A:5:GLU:OE1	2.33	0.47
1:A:3[B]:LYS:HG2	5:A:494:HOH:O	2.16	0.46
1:B:18[B]:LEU:C	1:B:18[B]:LEU:HD23	2.41	0.45
1:B:110:ALA:HA	1:B:122:ARG:O	2.17	0.45
1:B:162:GLN:HE21	1:B:164:ASN:ND2	2.09	0.45
1:B:73:ARG:NH1	5:B:558:HOH:O	2.44	0.44
1:A:211:PRO:HD2	1:B:39:TYR:CE1	2.52	0.44
1:A:153[A]:MET:HE3	5:A:508:HOH:O	2.14	0.44
1:B:3:LYS:HE3	1:B:5:GLU:OE2	2.17	0.44
1:A:220:LEU:C	1:A:221:LEU:HD12	2.42	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:3[B]:LYS:HZ3	1:A:5:GLU:CG	2.31	0.43
1:A:93:VAL:O	1:A:185:ASN:HA	2.18	0.43
1:A:153[B]:MET:HE3	1:A:153[B]:MET:HB3	1.80	0.43
1:B:90:GLU:HG3	5:B:380:HOH:O	2.20	0.42
1:A:73[B]:ARG:HE	1:B:211:PRO:CB	2.28	0.42
1:B:163:VAL:HB	1:B:183:GLN:HB3	2.02	0.42
1:A:107[A]:LYS:HE3	1:A:107[A]:LYS:HB3	1.28	0.41
1:A:76:ASP:HA	1:A:79:LYS:HE2	2.03	0.41
1:A:3[B]:LYS:HZ3	1:A:5:GLU:CB	2.32	0.41
1:A:125:LEU:HD23	1:A:125:LEU:C	2.47	0.40
1:A:168:ARG:NH1	5:A:606:HOH:O	2.43	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	
1	A	235/242 (97%)	233 (99%)	2 (1%)	0	100	100
1	B	234/242 (97%)	232 (99%)	2 (1%)	0	100	100
All	All	469/484 (97%)	465 (99%)	4 (1%)	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	212/210 (101%)	206 (97%)	6 (3%)	38 7
1	B	210/210 (100%)	205 (98%)	5 (2%)	43 10
All	All	422/420 (100%)	411 (97%)	11 (3%)	48 8

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	3[A]	LYS
1	A	3[B]	LYS
1	A	107[A]	LYS
1	A	107[B]	LYS
1	A	153[A]	MET
1	A	153[B]	MET
1	B	3	LYS
1	B	126	LYS
1	B	156	LYS
1	B	195	LEU
1	B	230	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (6) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	149	ASN
1	A	159	ASN
1	A	162	GLN
1	B	146	ASN
1	B	149	ASN
1	B	162	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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
1	CRO	B	65	1	22,23,24	0.97	1 (4%)	30,32,34	1.38	4 (13%)
1	CRO	A	65	1	22,23,24	0.95	0	30,32,34	1.16	2 (6%)

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	CRO	B	65	1	-	1/12/31/32	0/2/2/2
1	CRO	A	65	1	-	1/12/31/32	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	65	CRO	CB2-CA2	3.29	1.38	1.35

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	65	CRO	CA1-C1-N3	-3.34	120.73	124.69
1	B	65	CRO	CA2-N2-C1	3.13	108.25	105.80
1	B	65	CRO	C2-CA2-N2	-2.34	107.27	108.95
1	A	65	CRO	OG1-CB1-CA1	2.26	113.81	109.00
1	A	65	CRO	CA1-C1-N3	-2.25	122.03	124.69
1	B	65	CRO	CD2-CE2-CZ	2.22	122.23	119.88

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	A	65	CRO	N3-C1-CA1-CB1
1	B	65	CRO	N3-C1-CA1-CB1

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 8 ligands modelled in this entry, 3 are monoatomic - leaving 5 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
4	GOL	A	306	-	5,5,5	0.93	0	5,5,5	1.20	1 (20%)
4	GOL	A	308	-	5,5,5	1.48	1 (20%)	5,5,5	1.98	2 (40%)
2	PO4	A	302	-	4,4,4	1.38	0	6,6,6	0.59	0
2	PO4	A	301	-	4,4,4	1.29	1 (25%)	6,6,6	0.63	0
4	GOL	A	307	-	5,5,5	0.38	0	5,5,5	1.27	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
4	GOL	A	308	-	-	4/4/4/4	-
4	GOL	A	306	-	-	0/4/4/4	-
4	GOL	A	307	-	-	2/4/4/4	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	308	GOL	O3-C3	-2.29	1.32	1.42
2	A	301	PO4	P-O3	-2.13	1.48	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	308	GOL	C3-C2-C1	-3.36	99.48	111.80
4	A	308	GOL	O1-C1-C2	2.89	123.37	110.38
4	A	306	GOL	O1-C1-C2	2.10	119.83	110.38

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	308	GOL	O1-C1-C2-O2
4	A	308	GOL	O1-C1-C2-C3
4	A	308	GOL	C1-C2-C3-O3
4	A	308	GOL	O2-C2-C3-O3
4	A	307	GOL	O2-C2-C3-O3
4	A	307	GOL	O1-C1-C2-O2

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	308	GOL	2	0
4	A	307	GOL	2	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	225/242 (92%)	0.19	9 (4%)	42 54	6, 13, 26, 45	24 (10%)
1	B	225/242 (92%)	0.47	15 (6%)	24 33	6, 16, 29, 46	23 (10%)
All	All	450/484 (92%)	0.33	24 (5%)	32 43	6, 15, 28, 46	47 (10%)

All (24) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	230	THR	5.5
1	A	229	ILE	4.5
1	A	3[A]	LYS	4.1
1	B	230	THR	3.8
1	B	133	ASP	3.1
1	B	190	ASP	2.8
1	B	73	ARG	2.8
1	B	197	ASP	2.7
1	B	192	PRO	2.7
1	A	153[A]	MET	2.7
1	B	229	ILE	2.7
1	B	193	VAL	2.5
1	B	194	LEU	2.5
1	B	117	ASP	2.4
1	A	197	ASP	2.3
1	A	159	ASN	2.3
1	B	39	TYR	2.3
1	B	9	THR	2.2
1	B	10	GLY	2.2
1	B	159	ASN	2.2
1	A	133	ASP	2.1
1	B	116	GLY	2.1
1	A	132	GLU	2.1
1	A	191	GLY	2.1

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($\text{\AA}^2$)	Q<0.9
1	CRO	A	65	22/23	0.98	0.04	8,9,11,14	0
1	CRO	B	65	22/23	0.98	0.04	9,10,13,16	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
4	GOL	A	307	6/6	0.73	0.17	16,19,22,25	6
4	GOL	A	306	6/6	0.78	0.20	15,20,26,30	6
4	GOL	A	308	6/6	0.83	0.16	23,27,29,33	6
2	PO4	A	302	5/5	0.89	0.15	26,28,29,32	5
3	K	A	303	1/1	0.95	0.11	20,20,20,20	1
3	K	A	305	1/1	0.96	0.08	9,9,9,9	1
2	PO4	A	301	5/5	0.97	0.09	12,14,18,19	5
3	K	A	304	1/1	0.98	0.04	14,14,14,14	0

6.5 Other polymers [i](#)

There are no such residues in this entry.