



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 11:11 PM UTC

PDB ID : 2DY4 / pdb_00002dy4
Title : Crystal structure of RB69 GP43 in complex with DNA containing Thymine Glycol
Authors : Aller, P.; Rould, M.A.; Hogg, M.; Wallace, S.S.; Doublie, S.
Deposited on : 2006-09-06
Resolution : 2.65 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

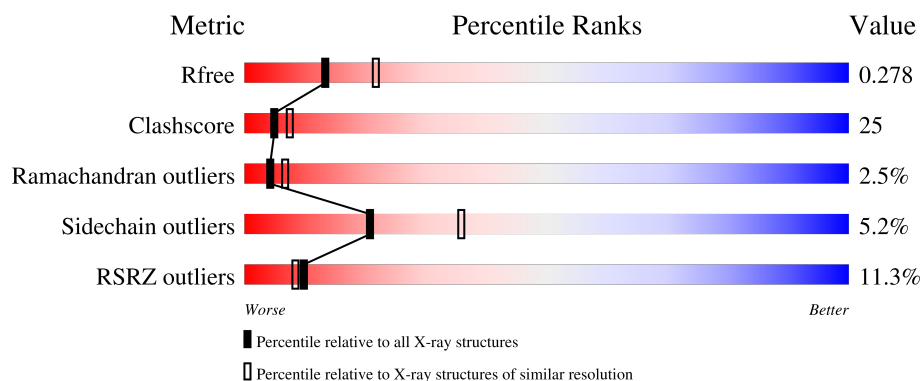
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1110 (2.66-2.66)
Clashscore	190562	1141 (2.66-2.66)
Ramachandran outliers	187476	1126 (2.66-2.66)
Sidechain outliers	187428	1126 (2.66-2.66)
RSRZ outliers	180081	1110 (2.66-2.66)

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	E	18	28% 33% 61% 6%
1	G	18	22% 28% 50%
1	I	18	6% 33% 61%
1	K	18	28% 17% 83%
2	F	15	40% 7% 7% 80% 7%

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Mol	Chain	Length	Quality of chain
2	H	15	13% 47% 40%
2	J	15	40% 60%
2	L	15	40% 20% 80%
3	A	903	7% 57% 38% .
3	B	903	5% 61% 32% 5% .
3	C	903	4% 63% 33% .
3	D	903	26% 45% 45% 8% .

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 31943 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 DNA chain called 5'-D(*CP*GP*(CTG)P*GP*GP*AP*AP*TP*GP*A*CP*AP*GP*CP*CP*GP*CP*G)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	17	Total	C	N	O	P	0	0	0
			348	165	69	99	15			
1	G	18	Total	C	N	O	P	0	0	0
			372	175	74	106	17			
1	I	18	Total	C	N	O	P	0	0	0
			372	175	74	106	17			
1	K	18	Total	C	N	O	P	0	0	0
			372	175	74	106	17			

- Molecule 2 is a DNA chain called 5'-D(*GP*CP*GP*GP*CP*TP*GP*T*CP*AP*TP*TP*CP*CP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	14	Total	C	N	O	P	0	0	0
			276	133	51	80	12			
2	H	15	Total	C	N	O	P	0	0	0
			299	143	53	89	14			
2	J	15	Total	C	N	O	P	0	0	0
			299	143	53	89	14			
2	L	15	Total	C	N	O	P	0	0	0
			299	143	53	89	14			

- Molecule 3 is a protein called DNA polymerase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	A	902	Total	C	N	O	S	Se	0	0	0
			7302	4689	1213	1367	8	25			
3	B	888	Total	C	N	O	S	Se	0	0	0
			7175	4608	1193	1341	8	25			
3	C	900	Total	C	N	O	S	Se	0	0	0
			7300	4683	1214	1370	8	25			

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Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	D	890	Total	C	N	O	S	Se	0	0	0
			6923	4449	1130	1313	8	23			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	222	ALA	ASP	engineered mutation	UNP Q38087
A	327	ALA	ASP	engineered mutation	UNP Q38087
B	222	ALA	ASP	engineered mutation	UNP Q38087
B	327	ALA	ASP	engineered mutation	UNP Q38087
C	222	ALA	ASP	engineered mutation	UNP Q38087
C	327	ALA	ASP	engineered mutation	UNP Q38087
D	222	ALA	ASP	engineered mutation	UNP Q38087
D	327	ALA	ASP	engineered mutation	UNP Q38087

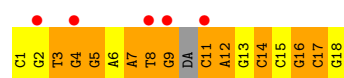
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	9	Total	O	0	0
			9	9		
4	F	5	Total	O	0	0
			5	5		
4	G	18	Total	O	0	0
			18	18		
4	H	9	Total	O	0	0
			9	9		
4	I	17	Total	O	0	0
			17	17		
4	J	4	Total	O	0	0
			4	4		
4	K	5	Total	O	0	0
			5	5		
4	L	2	Total	O	0	0
			2	2		
4	A	117	Total	O	0	0
			117	117		
4	B	205	Total	O	0	0
			205	205		
4	C	160	Total	O	0	0
			160	160		
4	D	55	Total	O	0	0
			55	55		

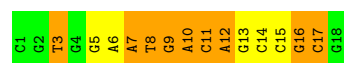
3 Residue-property plots [i](#)

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: 5'-D(*CP*GP*(CTG)P*GP*GP*AP*AP*TP*GP*A*CP*AP*GP*CP*CP*GP*CP*G)-3'



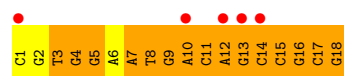
- Molecule 1: 5'-D(*CP*GP*(CTG)P*GP*GP*AP*AP*TP*GP*A*CP*AP*GP*CP*CP*GP*CP*G)-3'



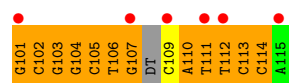
- Molecule 1: 5'-D(*CP*GP*(CTG)P*GP*GP*AP*AP*TP*GP*A*CP*AP*GP*CP*CP*GP*CP*G)-3'



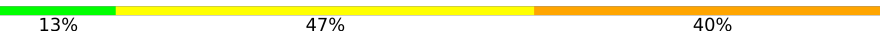
- Molecule 1: 5'-D(*CP*GP*(CTG)P*GP*GP*AP*AP*TP*GP*A*CP*AP*GP*CP*CP*GP*CP*G)-3'



- Molecule 2: 5'-D(*GP*CP*GP*GP*CP*TP*GP*T*CP*AP*TP*TP*CP*CP*A)-3'



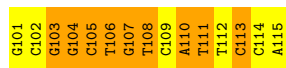
- Molecule 2: 5'-D(*GP*CP*GP*GP*CP*TP*GP*T*CP*AP*TP*TP*CP*CP*A)-3'

Chain H: 



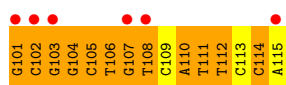
- Molecule 2: 5'-D(*GP*CP*GP*GP*CP*TP*GP*T*CP*AP*TP*TP*CP*CP*A)-3'

Chain J: 



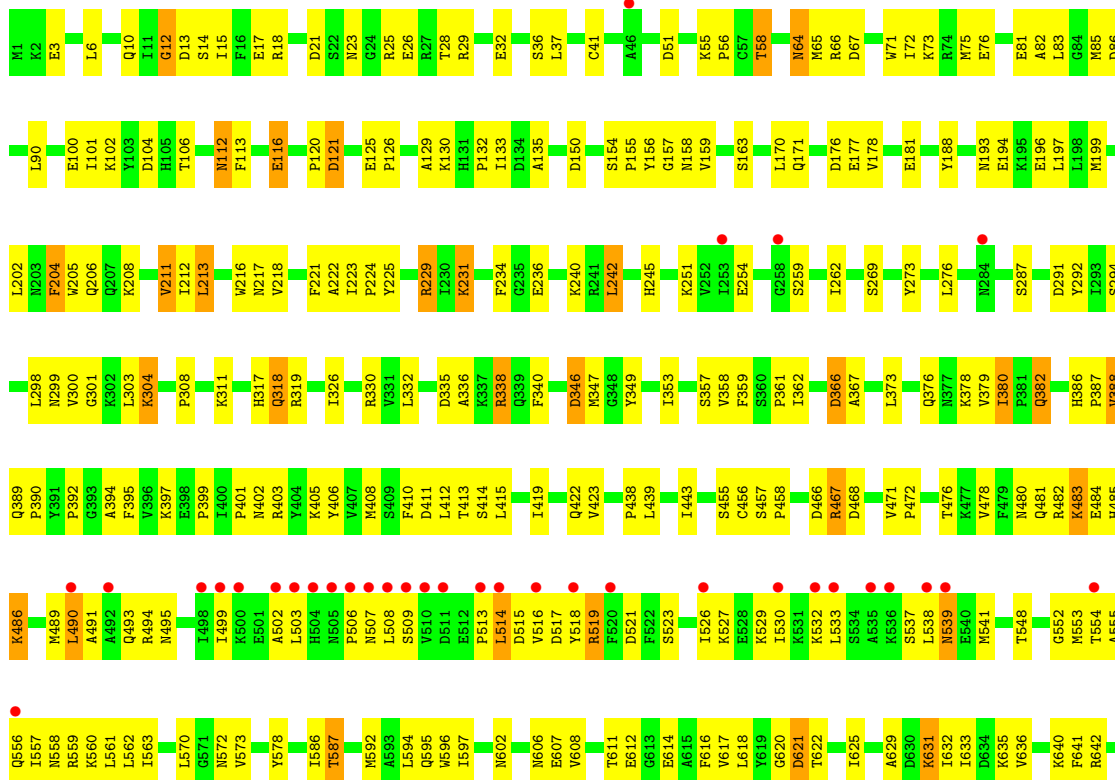
- Molecule 2: 5'-D(*GP*CP*GP*GP*CP*TP*GP*T*CP*AP*TP*TP*CP*CP*A)-3'

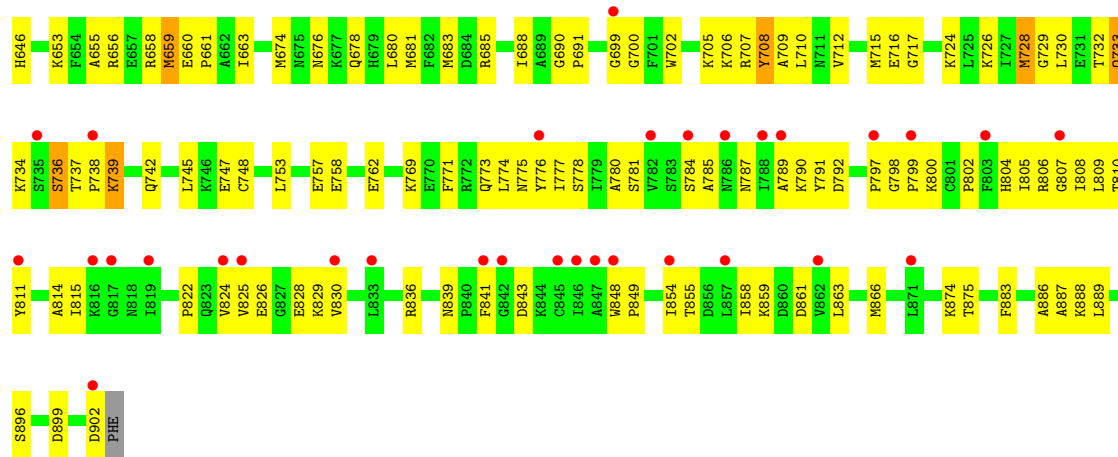
Chain L: 



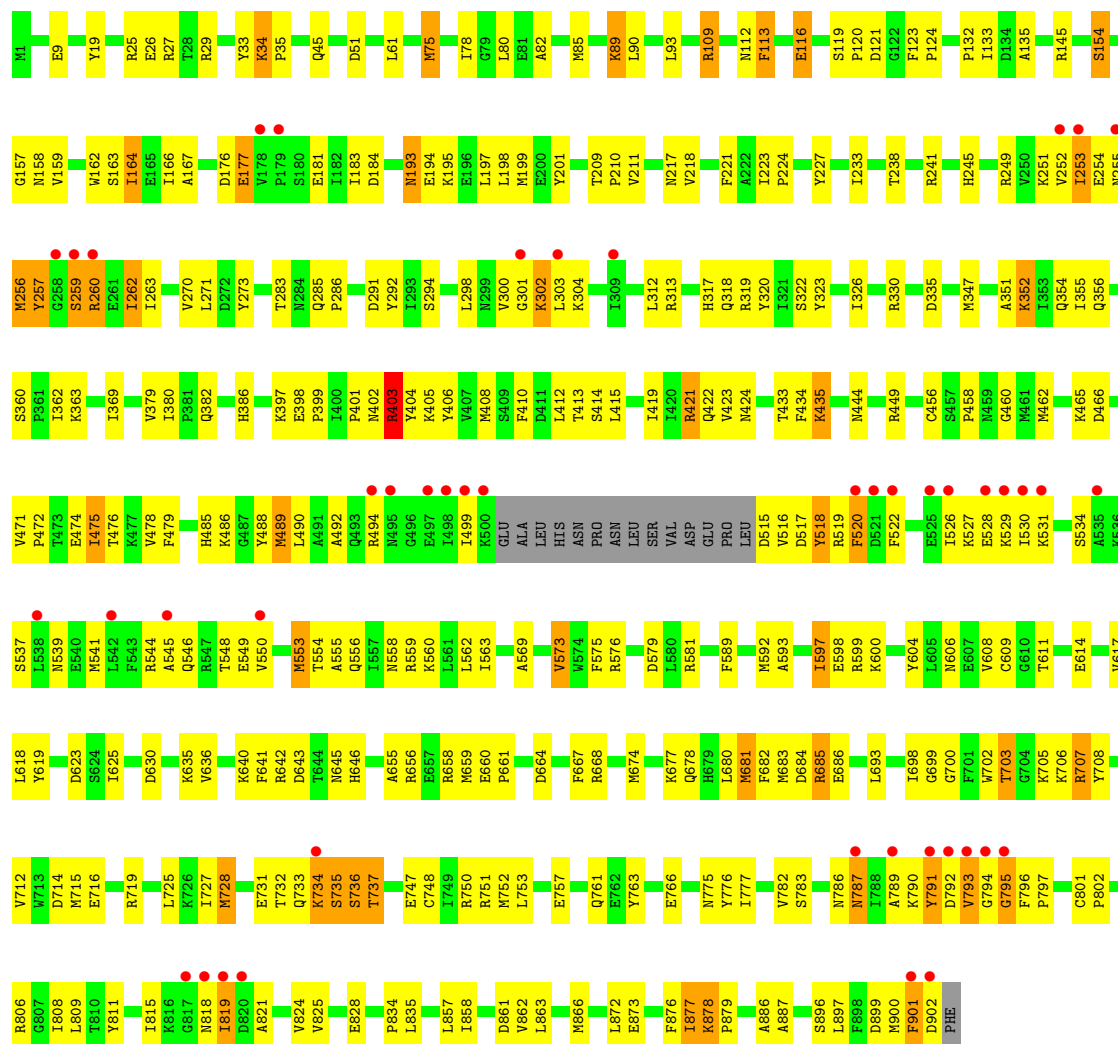
- Molecule 3: DNA polymerase

Chain A: 



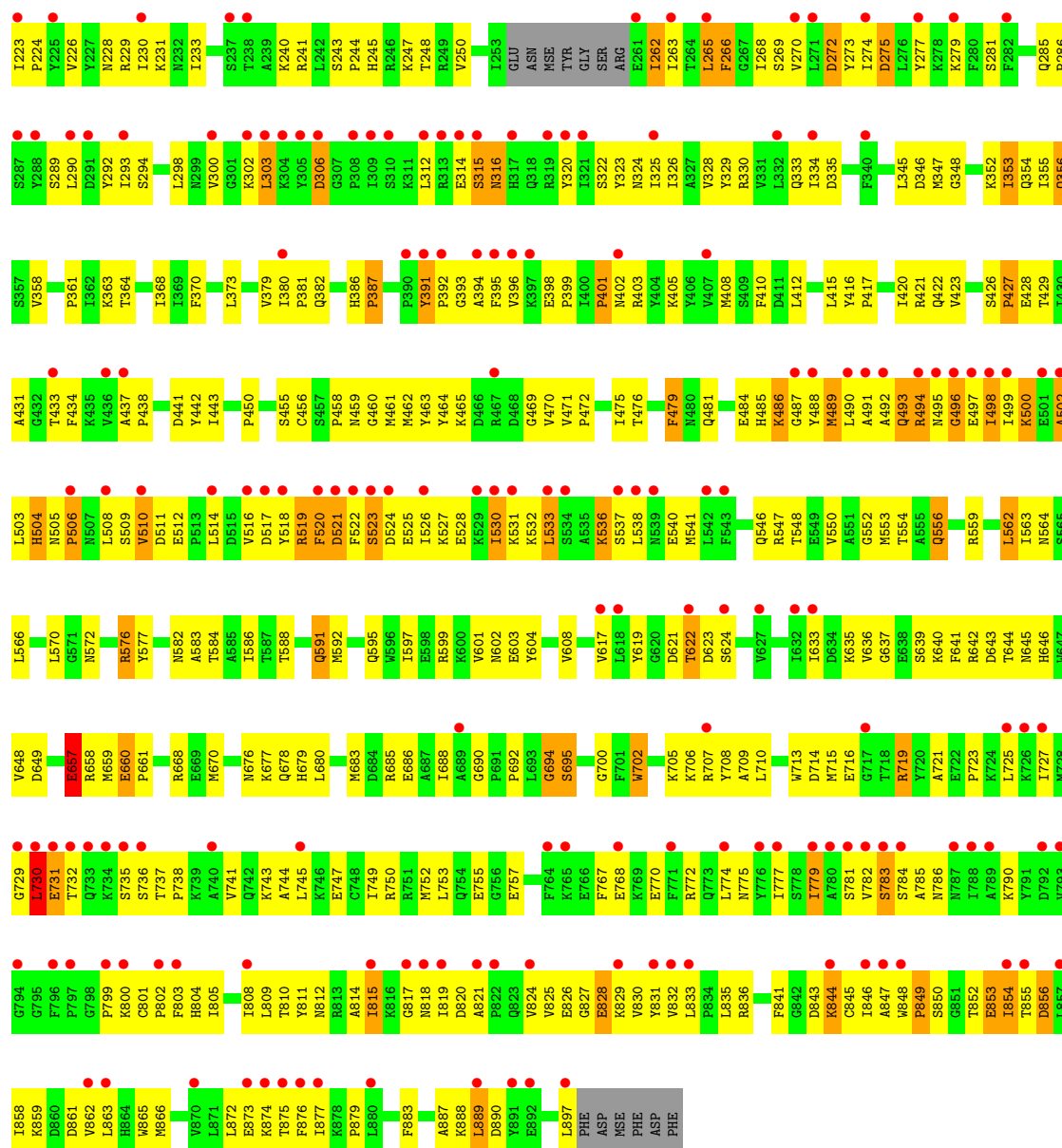


• Molecule 3: DNA polymerase



• Molecule 3: DNA polymerase





4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	132.61Å 122.63Å 168.69Å 90.00° 96.31° 90.00°	Depositor
Resolution (Å)	50.00 – 2.65 50.00 – 2.65	Depositor EDS
% Data completeness (in resolution range)	88.3 (50.00-2.65) 92.1 (50.00-2.65)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.54 (at 2.61Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.229 , 0.281 0.226 , 0.278	Depositor DCC
R_{free} test set	28873 reflections (9.49%)	wwPDB-VP
Wilson B-factor (Å ²)	47.3	Xtriage
Anisotropy	0.252	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 57.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	31943	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.13% 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: CTG

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	E	0.23	0/365	1.46	13/558 (2.3%)
1	G	0.29	0/393	1.37	9/603 (1.5%)
1	I	0.35	0/393	1.38	14/603 (2.3%)
1	K	0.41	0/393	1.43	16/603 (2.7%)
2	F	0.25	0/307	1.40	12/468 (2.6%)
2	H	0.32	0/333	1.38	7/510 (1.4%)
2	J	0.33	0/333	1.39	12/510 (2.4%)
2	L	0.44	0/333	1.47	15/510 (2.9%)
3	A	0.46	0/7457	0.92	21/10050 (0.2%)
3	B	0.49	0/7326	0.94	18/9873 (0.2%)
3	C	0.48	0/7454	0.92	15/10045 (0.1%)
3	D	0.35	0/7072	0.86	18/9590 (0.2%)
All	All	0.44	0/32159	0.97	170/43923 (0.4%)

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	G	1	0
2	H	0	1
All	All	1	1

There are no bond length outliers.

The worst 5 of 170 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	211	VAL	N-CA-C	-13.19	99.08	111.48
1	G	12	DA	C2'-C3'-O3'	10.62	127.44	111.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	211	VAL	N-CA-C	-9.77	102.39	111.67
3	B	255	ASN	N-CA-C	-9.05	95.47	108.96
1	G	12	DA	C4'-C3'-O3'	9.00	123.50	110.00

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	G	12	DA	C3'

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	H	115	DA	Sidechain

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	E	348	0	195	40	0
1	G	372	0	204	26	0
1	I	372	0	204	39	0
1	K	372	0	204	38	0
2	F	276	0	155	22	0
2	H	299	0	165	23	0
2	J	299	0	165	28	0
2	L	299	0	165	26	0
3	A	7302	0	7141	316	0
3	B	7175	0	6995	318	0
3	C	7300	0	7144	260	0
3	D	6923	0	6512	433	0
4	A	117	0	0	28	0
4	B	205	0	0	19	0
4	C	160	0	0	14	0
4	D	55	0	0	27	0
4	E	9	0	0	2	0
4	F	5	0	0	1	0
4	G	18	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	H	9	0	0	2	0
4	I	17	0	0	3	0
4	J	4	0	0	0	0
4	K	5	0	0	1	0
4	L	2	0	0	0	0
All	All	31943	0	29249	1529	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 25.

The worst 5 of 1529 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:I:14:DC:H2''	1:I:15:DC:H5''	1.21	1.17
2:J:111:DT:H2''	2:J:112:DT:H5'	1.16	1.13
3:B:164:ILE:HD12	3:B:164:ILE:H	1.13	1.09
2:L:104:DG:H2''	2:L:105:DC:H5''	1.32	1.07
1:G:11:DC:H2''	1:G:12:DA:H5''	1.34	1.05

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	
3	A	900/903 (100%)	804 (89%)	84 (9%)	12 (1%)	9	16
3	B	884/903 (98%)	802 (91%)	70 (8%)	12 (1%)	9	14
3	C	898/903 (99%)	830 (92%)	56 (6%)	12 (1%)	9	16
3	D	886/903 (98%)	701 (79%)	131 (15%)	54 (6%)	1	1
All	All	3568/3612 (99%)	3137 (88%)	341 (10%)	90 (2%)	4	7

5 of 90 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	A	519	ARG
3	A	611	THR
3	A	621	ASP
3	B	177	GLU
3	C	256	MSE

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	
3	A	785/775 (101%)	744 (95%)	41 (5%)	21	36
3	B	767/775 (99%)	724 (94%)	43 (6%)	19	32
3	C	786/775 (101%)	747 (95%)	39 (5%)	22	37
3	D	711/775 (92%)	675 (95%)	36 (5%)	21	36
All	All	3049/3100 (98%)	2890 (95%)	159 (5%)	21	36

5 of 159 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	C	859	LYS
3	D	530	ILE
3	C	881	GLU
3	D	209	THR
3	D	660	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 101 such sidechains are listed below:

Mol	Chain	Res	Type
3	C	158	ASN
3	C	595	GLN
3	D	812	ASN
3	C	203	ASN
3	C	481	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

4 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	CTG	E	3	1,2	18,23,24	0.75	0	21,35,38	1.10	2 (9%)
1	CTG	I	3	1,2	18,23,24	0.89	1 (5%)	21,35,38	1.19	3 (14%)
1	CTG	G	3	1,2	18,23,24	0.87	1 (5%)	21,35,38	1.11	1 (4%)
1	CTG	K	3	1	18,23,24	1.04	1 (5%)	21,35,38	1.06	2 (9%)

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	CTG	E	3	1,2	-	2/7/45/46	0/2/2/2
1	CTG	I	3	1,2	-	2/7/45/46	0/2/2/2
1	CTG	G	3	1,2	-	0/7/45/46	0/2/2/2
1	CTG	K	3	1	-	0/7/45/46	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	K	3	CTG	C5-C4	2.82	1.55	1.52
1	I	3	CTG	C1'-N1	2.41	1.48	1.45
1	G	3	CTG	C1'-N1	2.04	1.48	1.45

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	3	CTG	O3'-C3'-C2'	2.85	120.79	110.88
1	E	3	CTG	O3'-C3'-C2'	2.60	119.92	110.88
1	G	3	CTG	N3-C2-N1	-2.47	114.20	116.78
1	K	3	CTG	N3-C2-N1	-2.39	114.28	116.78
1	K	3	CTG	O3'-C3'-C2'	2.32	118.95	110.88

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
1	E	3	CTG	C3'-C4'-C5'-O5'
1	E	3	CTG	O4'-C4'-C5'-O5'
1	I	3	CTG	C3'-C4'-C5'-O5'
1	I	3	CTG	O4'-C4'-C5'-O5'

There are no ring outliers.

4 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	E	3	CTG	2	0
1	I	3	CTG	1	0
1	G	3	CTG	1	0
1	K	3	CTG	3	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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	E	16/18 (88%)	1.90	5 (31%) 1 0	87, 109, 126, 131	0
1	G	17/18 (94%)	-0.35	0 100 100	34, 47, 76, 79	0
1	I	17/18 (94%)	0.22	0 100 100	35, 50, 84, 91	0
1	K	17/18 (94%)	1.73	5 (29%) 1 1	65, 80, 81, 81	0
2	F	14/15 (93%)	2.05	6 (42%) 0 0	106, 125, 133, 135	0
2	H	15/15 (100%)	-0.03	0 100 100	36, 49, 100, 100	0
2	J	15/15 (100%)	0.26	0 100 100	33, 65, 112, 113	0
2	L	15/15 (100%)	1.94	6 (40%) 1 0	78, 80, 82, 82	0
3	A	877/903 (97%)	0.33	66 (7%) 20 15	23, 51, 125, 141	0
3	B	863/903 (95%)	0.05	45 (5%) 33 25	16, 44, 116, 139	0
3	C	875/903 (96%)	0.13	38 (4%) 40 32	17, 47, 114, 142	0
3	D	867/903 (96%)	1.46	236 (27%) 1 1	54, 102, 140, 153	0
All	All	3608/3744 (96%)	0.51	407 (11%) 10 8	16, 58, 131, 153	0

The worst 5 of 407 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	498	ILE	10.3
3	C	526	ILE	6.7
3	A	846	ILE	6.4
3	D	135	ALA	6.1
3	C	498	ILE	5.7

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	CTG	K	3	22/23	0.67	0.16	75,79,85,88	0
1	CTG	E	3	22/23	0.84	0.15	110,111,113,114	0
1	CTG	I	3	22/23	0.94	0.08	58,61,62,63	0
1	CTG	G	3	22/23	0.97	0.07	32,41,42,43	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.