



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 13, 2024 – 06:20 AM EDT

PDB ID : 4K50  
Title : Rhinovirus 16 polymerase elongation complex (r1\_form)  
Authors : Gong, P.; Peersen, O.B.  
Deposited on : 2013-04-12  
Resolution : 2.93 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](mailto: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>.

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

MolProbity : 4.02b-467  
Mogul : 2022.3.0, CSD as543be (2022)  
Xtriage (Phenix) : 1.20.1  
EDS : 2.36.2  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.36.2

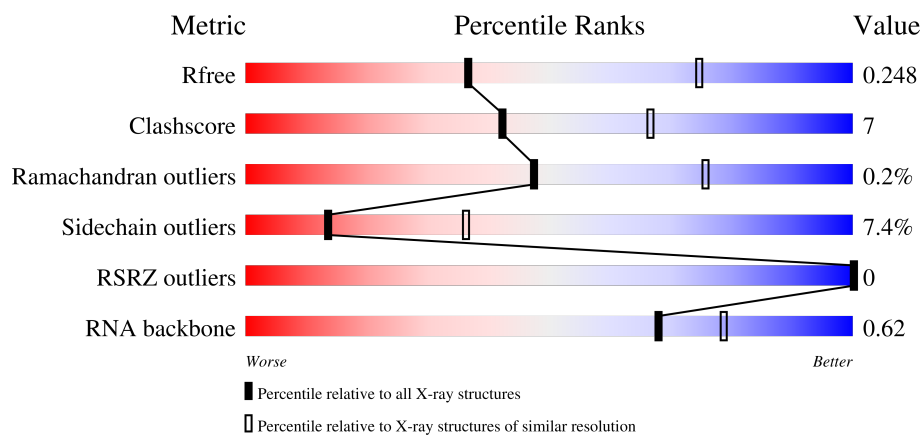
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.93 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.










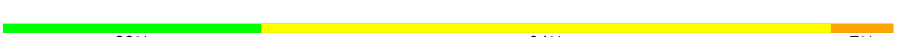
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
$R_{free}$	130704	2969 (2.98-2.90)
Clashscore	141614	3218 (2.98-2.90)
Ramachandran outliers	138981	3122 (2.98-2.90)
Sidechain outliers	138945	3124 (2.98-2.90)
RSRZ outliers	127900	2902 (2.98-2.90)
RNA backbone	3102	1060 (3.20-2.68)

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  $\geq 3$ , 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	460	<div> <div style="width: 79%; background-color: green;"></div> <div style="width: 19%; background-color: yellow;"></div> <div style="width: 2%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> </div> <div>79% 19% .</div>
1	E	460	<div> <div style="width: 77%; background-color: green;"></div> <div style="width: 20%; background-color: yellow;"></div> <div style="width: 3%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> </div> <div>77% 20% .</div>
1	I	460	<div> <div style="width: 81%; background-color: green;"></div> <div style="width: 16%; background-color: yellow;"></div> <div style="width: 3%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> </div> <div>81% 16% .</div>
1	M	460	<div> <div style="width: 77%; background-color: green;"></div> <div style="width: 20%; background-color: yellow;"></div> <div style="width: 3%; background-color: orange;"></div> <div style="width: 2%; background-color: red;"></div> </div> <div>77% 20% .</div>

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Mol	Chain	Length	Quality of chain
2	B	35	
2	F	35	
2	J	35	
2	N	35	
3	C	14	
3	G	14	
3	K	14	
3	O	14	

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
5	ACT	A	506	-	-	X	-
5	ACT	E	502	-	-	X	-

## 2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 19187 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 polymerase 3D-POL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	460	Total	C	N	O	S	0	0	0
			3685	2383	599	686	17			
1	E	460	Total	C	N	O	S	0	0	0
			3685	2383	599	686	17			
1	I	460	Total	C	N	O	S	0	0	0
			3685	2383	599	686	17			
1	M	460	Total	C	N	O	S	0	0	0
			3685	2383	599	686	17			

- Molecule 2 is a RNA chain called RNA (33-MER).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	33	Total	C	N	O	P	0	0	0
			688	305	123	227	33			
2	F	31	Total	C	N	O	P	0	0	0
			662	295	118	218	31			
2	J	33	Total	C	N	O	P	0	0	0
			688	305	123	227	33			
2	N	32	Total	C	N	O	P	0	0	0
			666	295	118	221	32			

- Molecule 3 is a RNA chain called RNA (5'-R(P\*GP\*CP\*CP\*CP\*GP\*GP\*AP\*CP\*GP\*AP\*GP\*AP\*GP\*A)-3').

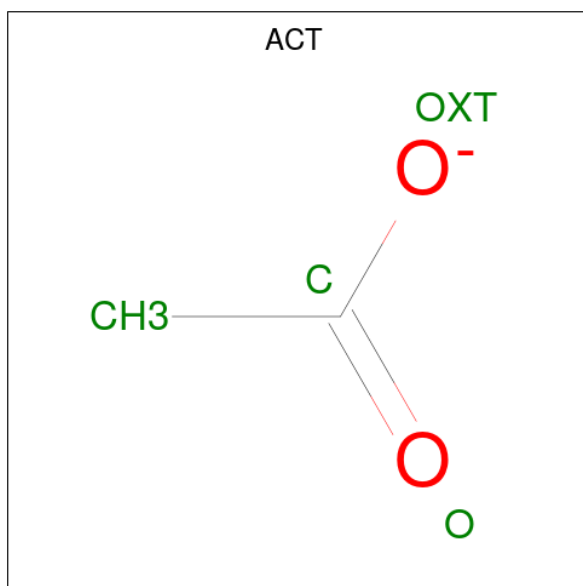
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	14	Total	C	N	O	P	0	0	0
			306	136	62	94	14			
3	G	14	Total	C	N	O	P	0	0	0
			306	136	62	94	14			
3	K	14	Total	C	N	O	P	0	0	0
			306	136	62	94	14			
3	O	14	Total	C	N	O	P	0	0	0
			306	136	62	94	14			

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



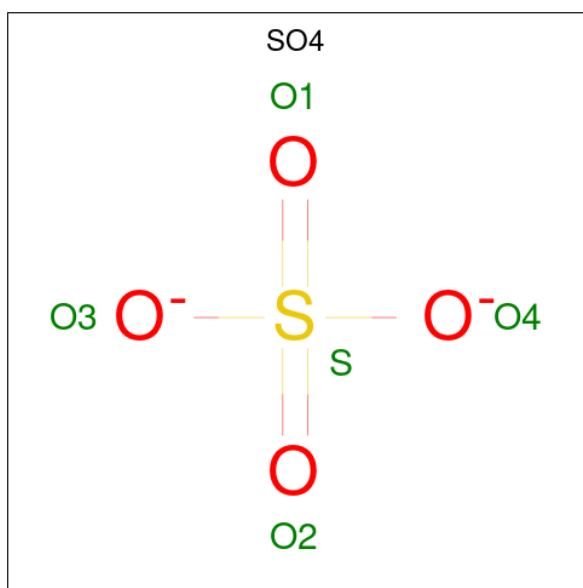
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		
4	I	1	Total	C	O	0	0
			6	3	3		

- 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 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	A	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	B	1	Total C O 4 2 2	0	0
5	E	1	Total C O 4 2 2	0	0
5	E	1	Total C O 4 2 2	0	0
5	E	1	Total C O 4 2 2	0	0
5	E	1	Total C O 4 2 2	0	0
5	F	1	Total C O 4 2 2	0	0
5	F	1	Total C O 4 2 2	0	0
5	I	1	Total C O 4 2 2	0	0
5	I	1	Total C O 4 2 2	0	0
5	I	1	Total C O 4 2 2	0	0
5	I	1	Total C O 4 2 2	0	0
5	I	1	Total C O 4 2 2	0	0
5	J	1	Total C O 4 2 2	0	0
5	K	1	Total C O 4 2 2	0	0
5	M	1	Total C O 4 2 2	0	0
5	M	1	Total C O 4 2 2	0	0
5	M	1	Total C O 4 2 2	0	0

- Molecule 6 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



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

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	97	Total	O	0	0
			97	97		
7	B	33	Total	O	0	0
			33	33		
7	C	8	Total	O	0	0
			8	8		
7	E	55	Total	O	0	0
			55	55		
7	F	10	Total	O	0	0
			10	10		
7	G	2	Total	O	0	0
			2	2		
7	I	90	Total	O	0	0
			90	90		
7	J	25	Total	O	0	0
			25	25		
7	K	9	Total	O	0	0
			9	9		
7	M	61	Total	O	0	0
			61	61		

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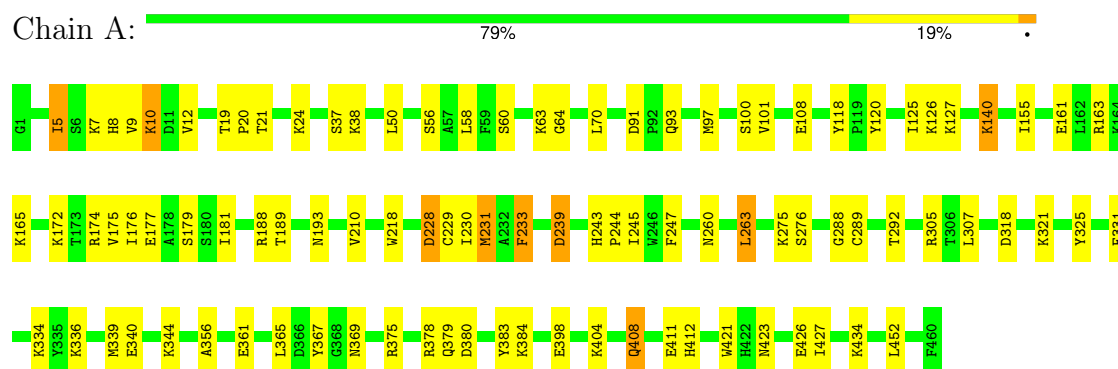
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	N	14	Total	O	0	0
			14	14		
7	O	4	Total	O	0	0
			4	4		



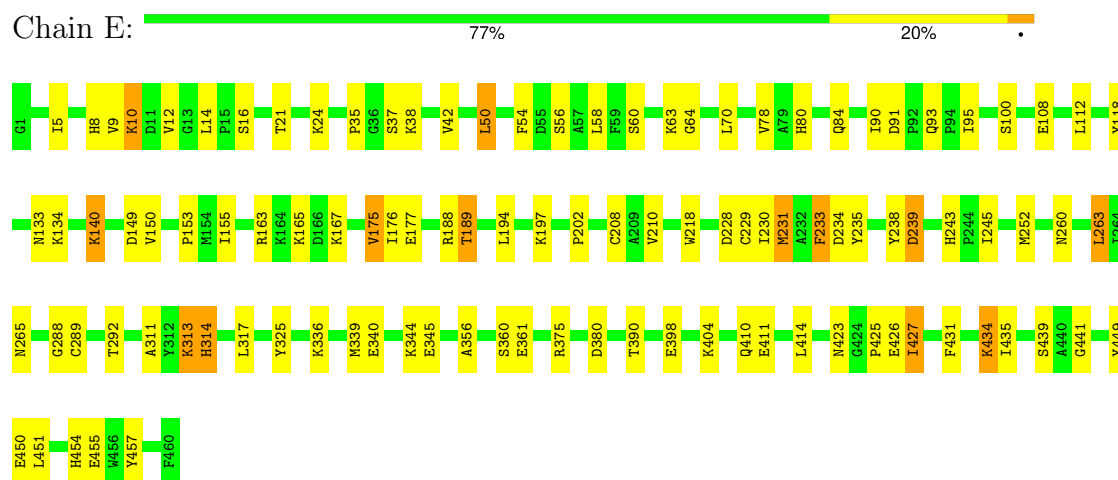
### 3 Residue-property plots

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.

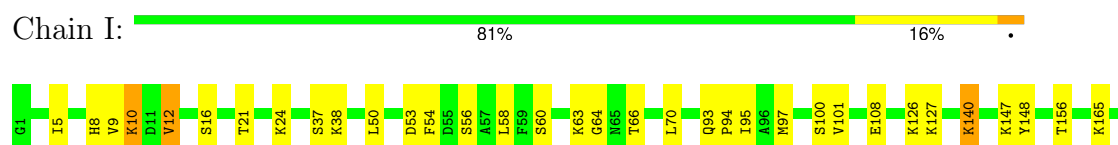
#### • Molecule 1: RNA polymerase 3D-POL

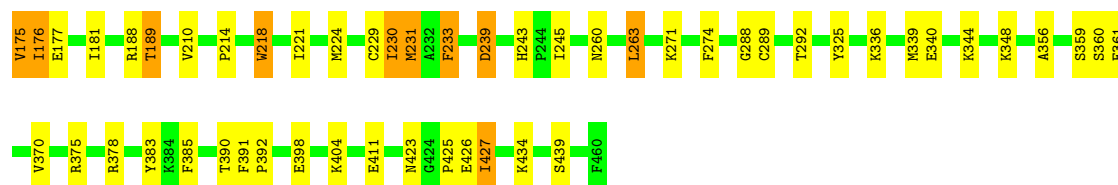


#### • Molecule 1: RNA polymerase 3D-POL

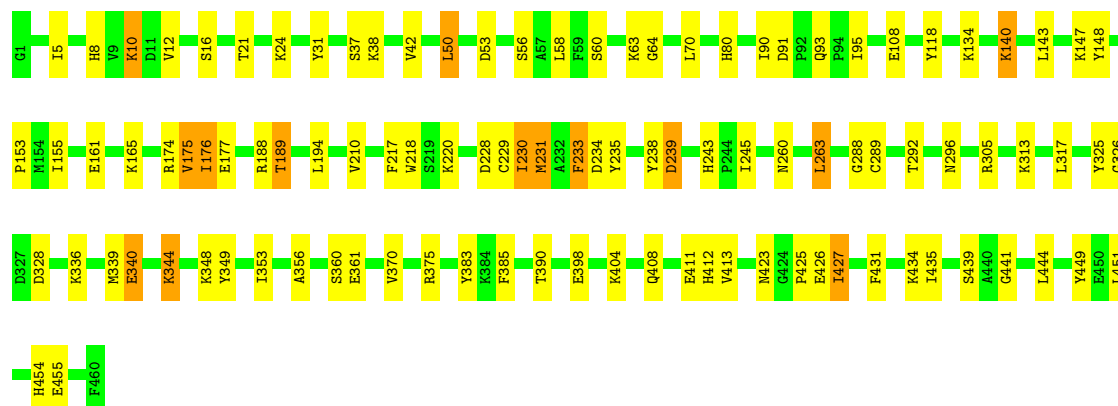
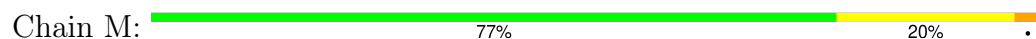


#### • Molecule 1: RNA polymerase 3D-POL

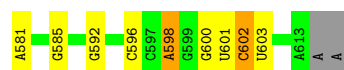




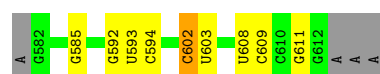
• Molecule 1: RNA polymerase 3D-POL



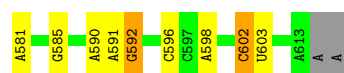
• Molecule 2: RNA (33-MER)



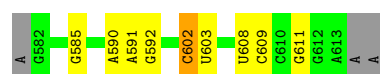
• Molecule 2: RNA (33-MER)



• Molecule 2: RNA (33-MER)



• Molecule 2: RNA (33-MER)



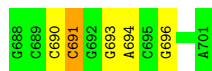
- Molecule 3: RNA (5'-R(P\*GP\*CP\*CP\*CP\*GP\*GP\*AP\*CP\*GP\*AP\*GP\*AP\*GP\*A)-3')

Chain C:  57% 36% 7%



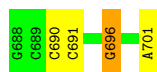
- Molecule 3: RNA (5'-R(P\*GP\*CP\*CP\*CP\*GP\*GP\*AP\*CP\*GP\*AP\*GP\*AP\*GP\*A)-3')

Chain G:  64% 29% 7%



- Molecule 3: RNA (5'-R(P\*GP\*CP\*CP\*CP\*GP\*GP\*AP\*CP\*GP\*AP\*GP\*AP\*GP\*A)-3')

Chain K:  71% 21% 7%



- Molecule 3: RNA (5'-R(P\*GP\*CP\*CP\*CP\*GP\*GP\*AP\*CP\*GP\*AP\*GP\*AP\*GP\*A)-3')

Chain O:  29% 64% 7%



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	53.75Å 113.89Å 122.60Å 90.01° 90.49° 90.00°	Depositor
Resolution (Å)	45.30 – 2.93 45.30 – 2.90	Depositor EDS
% Data completeness (in resolution range)	98.2 (45.30-2.93) 98.1 (45.30-2.90)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.69 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.8.2_1309	Depositor
R, $R_{free}$	0.191 , 0.247 0.192 , 0.248	Depositor DCC
$R_{free}$ test set	3179 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.8	Xtriage
Anisotropy	0.039	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 12.8	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.53$ , $\langle L^2 \rangle = 0.37$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-l 0.429 for -h,k,-l 0.000 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	19187	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	37.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.74% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: GOL, ACT, SO4

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	0.47	0/3776	0.60	0/5110
1	E	0.50	0/3776	0.60	0/5110
1	I	0.49	0/3776	0.61	0/5110
1	M	0.51	0/3776	0.60	0/5110
2	B	0.63	0/768	1.09	2/1196 (0.2%)
2	F	0.69	0/739	1.03	0/1150
2	J	0.62	0/768	1.06	1/1196 (0.1%)
2	N	0.68	0/743	1.05	0/1157
3	C	0.68	0/343	1.21	2/534 (0.4%)
3	G	0.62	0/343	1.08	0/534
3	K	0.67	0/343	1.28	1/534 (0.2%)
3	O	0.63	0/343	1.04	0/534
All	All	0.53	0/19494	0.75	6/27275 (0.0%)

There are no bond length outliers.

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	J	596	C	C6-N1-C2	6.92	123.07	120.30
3	C	696	G	O5'-P-OP2	-6.07	100.24	105.70
3	K	696	G	O5'-P-OP2	-5.66	100.61	105.70
2	B	596	C	C6-N1-C2	5.53	122.51	120.30
2	B	598	A	C8-N9-C4	5.08	107.83	105.80

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	3685	0	3694	53	0
1	E	3685	0	3694	59	0
1	I	3685	0	3694	51	0
1	M	3685	0	3694	54	0
2	B	688	0	345	7	0
2	F	662	0	335	3	0
2	J	688	0	345	6	0
2	N	666	0	334	3	0
3	C	306	0	155	3	0
3	G	306	0	155	2	0
3	K	306	0	155	2	0
3	O	306	0	155	5	0
4	A	6	0	8	1	0
4	I	12	0	16	1	0
5	A	16	0	12	2	0
5	B	8	0	6	0	0
5	E	16	0	12	2	0
5	F	8	0	6	1	0
5	I	20	0	15	1	0
5	J	4	0	3	0	0
5	K	4	0	3	1	0
5	M	12	0	9	0	0
6	A	5	0	0	0	0
7	A	97	0	0	6	0
7	B	33	0	0	0	0
7	C	8	0	0	0	0
7	E	55	0	0	4	0
7	F	10	0	0	1	0
7	G	2	0	0	0	0
7	I	90	0	0	4	0
7	J	25	0	0	0	0
7	K	9	0	0	0	0
7	M	61	0	0	4	0
7	N	14	0	0	0	0
7	O	4	0	0	0	0
All	All	19187	0	16845	244	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 7.

The worst 5 of 244 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:M:288:GLY:H	1:M:292:THR:HG21	1.36	0.89
1:E:288:GLY:H	1:E:292:THR:HG21	1.34	0.89
1:A:8:HIS:HB3	1:A:10:LYS:HE3	1.59	0.85
1:M:8:HIS:HB3	1:M:10:LYS:HE3	1.58	0.85
1:I:288:GLY:H	1:I:292:THR:HG21	1.40	0.84

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	458/460 (100%)	435 (95%)	21 (5%)	2 (0%)	34	64
1	E	458/460 (100%)	435 (95%)	23 (5%)	0	100	100
1	I	458/460 (100%)	437 (95%)	21 (5%)	0	100	100
1	M	458/460 (100%)	432 (94%)	25 (6%)	1 (0%)	47	76
All	All	1832/1840 (100%)	1739 (95%)	90 (5%)	3 (0%)	47	76

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	275	LYS
1	A	367	TYR
1	M	31	TYR

### 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	410/410 (100%)	381 (93%)	29 (7%)	14	38
1	E	410/410 (100%)	377 (92%)	33 (8%)	12	32
1	I	410/410 (100%)	381 (93%)	29 (7%)	14	38
1	M	410/410 (100%)	379 (92%)	31 (8%)	13	35
All	All	1640/1640 (100%)	1518 (93%)	122 (7%)	13	36

5 of 122 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	360	SER
1	M	233	PHE
1	I	70	LEU
1	M	231	MET
1	M	408	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	260	ASN
1	A	418	HIS
1	I	8	HIS
1	I	418	HIS

### 5.3.3 RNA [i](#)

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	B	31/35 (88%)	3 (9%)	0
2	F	30/35 (85%)	4 (13%)	0
2	J	31/35 (88%)	3 (9%)	0
2	N	30/35 (85%)	4 (13%)	0
3	C	13/14 (92%)	1 (7%)	0

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
3	G	13/14 (92%)	3 (23%)	0
3	K	13/14 (92%)	1 (7%)	0
3	O	13/14 (92%)	4 (30%)	0
All	All	174/196 (88%)	23 (13%)	0

5 of 23 RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	B	585	G
2	B	592	G
2	B	602	C
3	C	696	G
2	F	585	G

There are no RNA pucker outliers to report.

## 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 monosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

26 ligands 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	$\# Z  > 2$
5	ACT	A	505	-	3,3,3	0.85	0	3,3,3	1.43	0
5	ACT	I	503	-	3,3,3	0.76	0	3,3,3	1.47	0
5	ACT	I	507	-	3,3,3	0.73	0	3,3,3	1.54	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
5	ACT	E	501	-	3,3,3	0.84	0	3,3,3	1.70	2 (66%)
5	ACT	A	503	-	3,3,3	0.78	0	3,3,3	1.35	0
5	ACT	A	502	-	3,3,3	0.86	0	3,3,3	1.33	0
5	ACT	I	506	-	3,3,3	0.65	0	3,3,3	1.54	1 (33%)
5	ACT	M	501	-	3,3,3	0.77	0	3,3,3	1.57	1 (33%)
5	ACT	B	702	-	3,3,3	0.99	0	3,3,3	1.38	0
5	ACT	M	503	-	3,3,3	0.94	0	3,3,3	1.02	0
5	ACT	I	501	-	3,3,3	0.90	0	3,3,3	1.13	0
5	ACT	E	502	-	3,3,3	0.85	0	3,3,3	1.34	0
5	ACT	E	503	-	3,3,3	0.93	0	3,3,3	1.42	0
4	GOL	I	505	-	5,5,5	0.40	0	5,5,5	0.80	0
4	GOL	I	502	-	5,5,5	0.41	0	5,5,5	0.19	0
5	ACT	F	701	-	3,3,3	0.83	0	3,3,3	1.61	1 (33%)
5	ACT	J	701	-	3,3,3	0.71	0	3,3,3	1.60	1 (33%)
5	ACT	E	504	-	3,3,3	0.85	0	3,3,3	1.26	0
5	ACT	M	502	-	3,3,3	1.06	0	3,3,3	1.69	1 (33%)
6	SO4	A	504	-	4,4,4	0.27	0	6,6,6	0.49	0
5	ACT	F	702	-	3,3,3	0.80	0	3,3,3	1.49	0
5	ACT	B	701	-	3,3,3	0.73	0	3,3,3	1.36	0
4	GOL	A	501	-	5,5,5	0.32	0	5,5,5	1.21	0
5	ACT	K	801	-	3,3,3	0.94	0	3,3,3	1.31	0
5	ACT	I	504	-	3,3,3	0.89	0	3,3,3	1.23	0
5	ACT	A	506	-	3,3,3	0.82	0	3,3,3	1.07	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	I	505	-	-	2/4/4/4	-
4	GOL	I	502	-	-	4/4/4/4	-
4	GOL	A	501	-	-	2/4/4/4	-

There are no bond length outliers.

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	M	502	ACT	OXT-C-O	-2.41	113.08	122.03
5	E	501	ACT	OXT-C-O	-2.15	114.05	122.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	J	701	ACT	OXT-C-CH3	2.14	124.04	115.05
5	M	501	ACT	OXT-C-CH3	2.13	123.98	115.05
5	I	506	ACT	OXT-C-CH3	2.12	123.94	115.05

There are no chirality outliers.

5 of 8 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	501	GOL	O1-C1-C2-C3
4	I	502	GOL	O1-C1-C2-C3
4	I	502	GOL	C1-C2-C3-O3
4	I	502	GOL	O2-C2-C3-O3
4	I	505	GOL	O1-C1-C2-O2

There are no ring outliers.

7 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	501	ACT	1	0
5	E	502	ACT	2	0
4	I	502	GOL	1	0
5	F	701	ACT	1	0
4	A	501	GOL	1	0
5	K	801	ACT	1	0
5	A	506	ACT	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 [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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	460/460 (100%)	-0.64	0 100 100	15, 27, 48, 74	0
1	E	460/460 (100%)	-0.48	0 100 100	24, 38, 63, 82	0
1	I	460/460 (100%)	-0.65	0 100 100	15, 27, 48, 75	0
1	M	460/460 (100%)	-0.50	0 100 100	24, 38, 63, 83	0
2	B	33/35 (94%)	-0.59	0 100 100	19, 35, 75, 108	0
2	F	31/35 (88%)	-0.58	0 100 100	30, 47, 66, 97	0
2	J	33/35 (94%)	-0.60	0 100 100	18, 35, 76, 105	0
2	N	32/35 (91%)	-0.63	0 100 100	30, 50, 81, 112	0
3	C	14/14 (100%)	-0.39	0 100 100	22, 35, 93, 104	0
3	G	14/14 (100%)	-0.46	0 100 100	32, 48, 99, 109	0
3	K	14/14 (100%)	-0.36	0 100 100	19, 33, 93, 104	0
3	O	14/14 (100%)	-0.43	0 100 100	30, 48, 99, 107	0
All	All	2025/2036 (99%)	-0.57	0 100 100	15, 33, 61, 112	0

There are no RSRZ outliers to report.

### 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 monosaccharides 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. The B-factors column lists the minimum, median, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
5	ACT	B	702	4/4	0.89	0.22	25,35,35,38	0
5	ACT	K	801	4/4	0.91	0.19	19,32,37,41	0
5	ACT	I	504	4/4	0.92	0.14	33,36,45,46	0
5	ACT	J	701	4/4	0.93	0.17	20,25,28,29	0
5	ACT	E	503	4/4	0.93	0.20	27,35,39,40	0
5	ACT	M	501	4/4	0.94	0.14	27,30,34,38	0
5	ACT	M	502	4/4	0.94	0.16	27,37,38,38	0
4	GOL	A	501	6/6	0.95	0.27	24,30,32,39	0
5	ACT	A	503	4/4	0.95	0.13	39,44,45,46	0
5	ACT	I	501	4/4	0.95	0.12	40,42,49,54	0
5	ACT	B	701	4/4	0.95	0.15	21,24,29,30	0
6	SO4	A	504	5/5	0.95	0.15	38,54,61,66	0
5	ACT	E	501	4/4	0.96	0.11	30,41,43,45	0
5	ACT	I	503	4/4	0.96	0.13	44,46,48,49	0
4	GOL	I	502	6/6	0.96	0.18	33,39,44,59	0
5	ACT	E	504	4/4	0.96	0.11	48,52,53,54	0
5	ACT	A	506	4/4	0.97	0.14	35,38,42,44	0
4	GOL	I	505	6/6	0.97	0.19	18,20,22,24	0
5	ACT	A	505	4/4	0.97	0.12	32,42,44,46	0
5	ACT	M	503	4/4	0.97	0.13	29,40,40,40	0
5	ACT	F	702	4/4	0.97	0.27	36,47,48,49	0
5	ACT	F	701	4/4	0.98	0.14	28,32,34,34	0
5	ACT	A	502	4/4	0.98	0.10	34,35,37,39	0
5	ACT	I	506	4/4	0.98	0.10	28,34,36,37	0
5	ACT	I	507	4/4	0.98	0.09	27,30,35,42	0
5	ACT	E	502	4/4	0.98	0.09	34,40,41,42	0

## 6.5 Other polymers ⓘ

There are no such residues in this entry.