



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 06:00 PM GMT

PDB ID : 4K4H
Title : Ternary crystal structures of a human DNA POLYMERASE LAMBDA IN COMPLEX WITH DNA AND (-)3TC-TP.
Authors : Vyas, R.; Suo, Z.
Deposited on : 2013-04-12
Resolution : 2.10 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
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

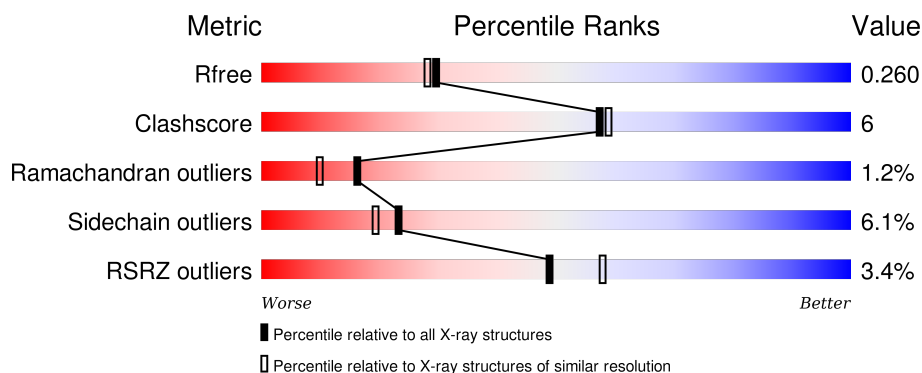
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	91344	3939 (2.10-2.10)
Clashscore	102246	4460 (2.10-2.10)
Ramachandran outliers	100387	4413 (2.10-2.10)
Sidechain outliers	100360	4414 (2.10-2.10)
RSRZ outliers	91569	3948 (2.10-2.10)

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 on the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria. 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	340	<div> <div>3%</div> <div>81%13% . .</div> </div>
1	E	340	<div> <div>4%</div> <div>78%14% . .</div> </div>
1	I	340	<div> <div>5%</div> <div>81%15% . .</div> </div>
1	M	340	<div> <div>2%</div> <div>76%16% . .</div> </div>
2	B	11	<div> <div>73%27%</div> </div>

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Mol	Chain	Length	Quality of chain
2	F	11	
2	J	11	
2	N	11	
3	C	6	
3	G	6	
3	K	6	
3	O	6	
4	D	4	
4	H	4	
4	L	4	
4	P	4	

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
6	CA	A	607	-	-	-	X
6	CA	E	603	-	-	-	X
7	ACT	I	606	-	-	-	X
7	ACT	M	607	-	-	-	X
7	ACT	M	608	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 12678 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 DNA polymerase lambda.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	327	Total	C	N	O	S	0	0	0
			2578	1621	473	473	11			
1	E	326	Total	C	N	O	S	0	0	0
			2563	1612	470	469	12			
1	I	332	Total	C	N	O	S	0	1	0
			2623	1647	483	481	12			
1	M	325	Total	C	N	O	S	0	1	0
			2564	1614	467	471	12			

There are 36 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	244	MET	-	EXPRESSION TAG	UNP Q9UGP5
A	576	LEU	-	EXPRESSION TAG	UNP Q9UGP5
A	577	GLU	-	EXPRESSION TAG	UNP Q9UGP5
A	578	HIS	-	EXPRESSION TAG	UNP Q9UGP5
A	579	HIS	-	EXPRESSION TAG	UNP Q9UGP5
A	580	HIS	-	EXPRESSION TAG	UNP Q9UGP5
A	581	HIS	-	EXPRESSION TAG	UNP Q9UGP5
A	582	HIS	-	EXPRESSION TAG	UNP Q9UGP5
A	583	HIS	-	EXPRESSION TAG	UNP Q9UGP5
E	244	MET	-	EXPRESSION TAG	UNP Q9UGP5
E	576	LEU	-	EXPRESSION TAG	UNP Q9UGP5
E	577	GLU	-	EXPRESSION TAG	UNP Q9UGP5
E	578	HIS	-	EXPRESSION TAG	UNP Q9UGP5
E	579	HIS	-	EXPRESSION TAG	UNP Q9UGP5
E	580	HIS	-	EXPRESSION TAG	UNP Q9UGP5
E	581	HIS	-	EXPRESSION TAG	UNP Q9UGP5
E	582	HIS	-	EXPRESSION TAG	UNP Q9UGP5
E	583	HIS	-	EXPRESSION TAG	UNP Q9UGP5
I	244	MET	-	EXPRESSION TAG	UNP Q9UGP5
I	576	LEU	-	EXPRESSION TAG	UNP Q9UGP5
I	577	GLU	-	EXPRESSION TAG	UNP Q9UGP5

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Chain	Residue	Modelled	Actual	Comment	Reference
I	578	HIS	-	EXPRESSION TAG	UNP Q9UGP5
I	579	HIS	-	EXPRESSION TAG	UNP Q9UGP5
I	580	HIS	-	EXPRESSION TAG	UNP Q9UGP5
I	581	HIS	-	EXPRESSION TAG	UNP Q9UGP5
I	582	HIS	-	EXPRESSION TAG	UNP Q9UGP5
I	583	HIS	-	EXPRESSION TAG	UNP Q9UGP5
M	244	MET	-	EXPRESSION TAG	UNP Q9UGP5
M	576	LEU	-	EXPRESSION TAG	UNP Q9UGP5
M	577	GLU	-	EXPRESSION TAG	UNP Q9UGP5
M	578	HIS	-	EXPRESSION TAG	UNP Q9UGP5
M	579	HIS	-	EXPRESSION TAG	UNP Q9UGP5
M	580	HIS	-	EXPRESSION TAG	UNP Q9UGP5
M	581	HIS	-	EXPRESSION TAG	UNP Q9UGP5
M	582	HIS	-	EXPRESSION TAG	UNP Q9UGP5
M	583	HIS	-	EXPRESSION TAG	UNP Q9UGP5

- Molecule 2 is a DNA chain called DNA (5'-D(*CP*GP*GP*CP*GP*GP*TP*AP*CP*TP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	11	Total	C	N	O	P	0	0	0
			225	107	43	65	10			
2	F	11	Total	C	N	O	P	0	0	0
			225	107	43	65	10			
2	J	11	Total	C	N	O	P	0	0	0
			225	107	43	65	10			
2	N	11	Total	C	N	O	P	0	0	0
			225	107	43	65	10			

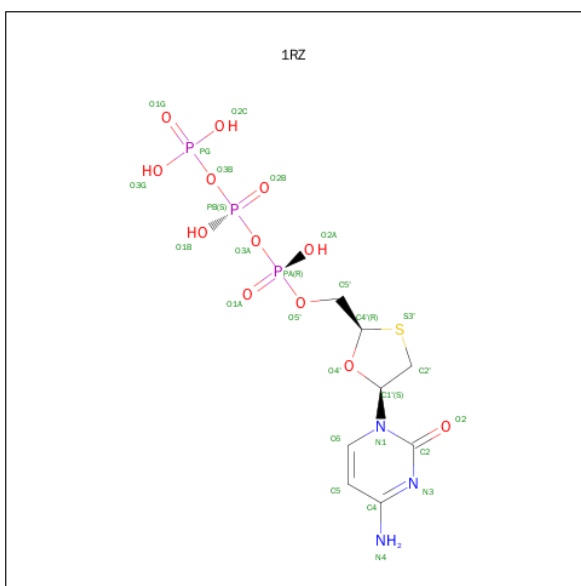
- Molecule 3 is a DNA chain called DNA (5'-D(*CP*AP*GP*TP*AP*C)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	6	Total	C	N	O	P	0	0	0
			119	58	23	33	5			
3	G	6	Total	C	N	O	P	0	0	0
			119	58	23	33	5			
3	K	6	Total	C	N	O	P	0	0	0
			119	58	23	33	5			
3	O	6	Total	C	N	O	P	0	0	0
			119	58	23	33	5			

- Molecule 4 is a DNA chain called DNA (5'-D(P*GP*CP*CP*G)-3').

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			
4	H	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			
4	L	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			
4	P	4	Total	C	N	O	P	0	0	0
			83	38	16	25	4			

- Molecule 5 is [[(2R,5S)-5-(4-AZANYL-2-OXIDANYLIDENE-PYRIMIDIN-1-YL)-1,3-OXATHIOLAN-2-YL]METHOXY-OXIDANYL-PHOSPHORYL] PHOSPHONO HYDROGEN PHOSPHATE (three-letter code: 1RZ) (formula: C₈H₁₄N₃O₁₂P₃S).



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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	E	4	Total 4	Ca 4	0	0
6	B	1	Total 1	Ca 1	0	0
6	I	4	Total 4	Ca 4	0	0
6	A	6	Total 6	Ca 6	0	0
6	N	1	Total 1	Ca 1	0	0
6	F	1	Total 1	Ca 1	0	0
6	M	5	Total 5	Ca 5	0	0

- Molecule 7 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	A	1	Total 4	C 2	O 2	0	0
7	I	1	Total 4	C 2	O 2	0	0
7	F	1	Total 4	C 2	O 2	0	0
7	M	1	Total 4	C 2	O 2	0	0

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

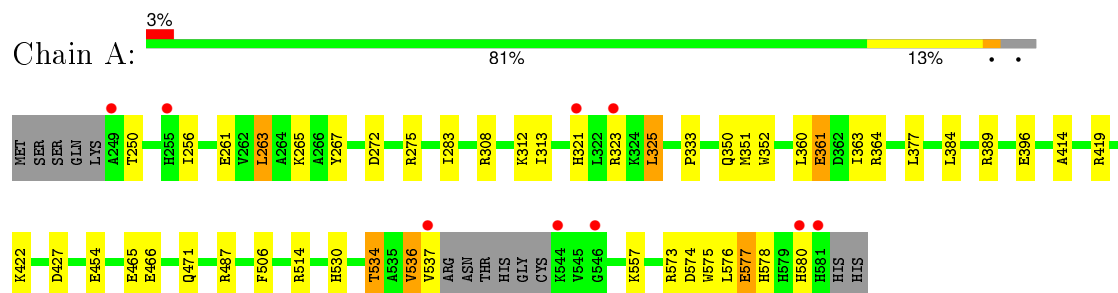
- Molecule 8 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	120	Total	O		0	0
			120	120			
8	B	19	Total	O		0	0
			19	19			
8	C	11	Total	O		0	0
			11	11			
8	D	1	Total	O		0	0
			1	1			
8	E	82	Total	O		0	0
			82	82			
8	F	7	Total	O		0	0
			7	7			
8	G	2	Total	O		0	0
			2	2			
8	H	2	Total	O		0	0
			2	2			
8	I	81	Total	O		0	0
			81	81			
8	J	6	Total	O		0	0
			6	6			
8	K	5	Total	O		0	0
			5	5			
8	M	143	Total	O		0	0
			143	143			
8	N	6	Total	O		0	0
			6	6			
8	O	5	Total	O		0	0
			5	5			
8	P	1	Total	O		0	0
			1	1			

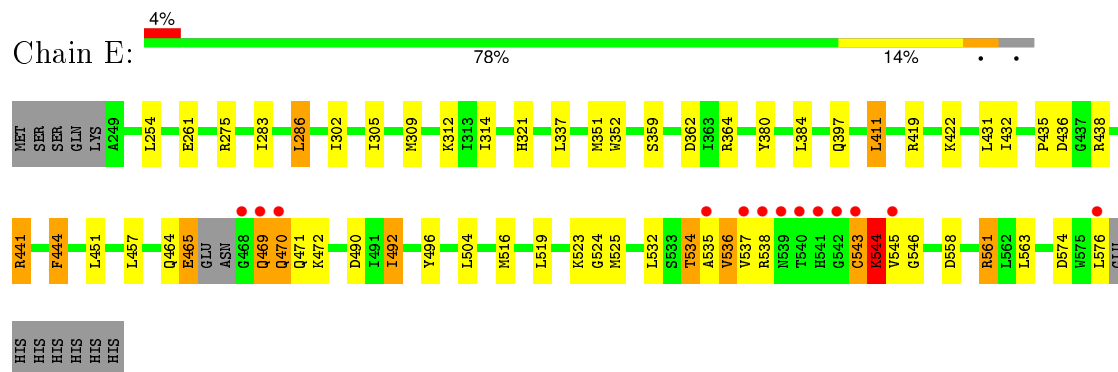
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

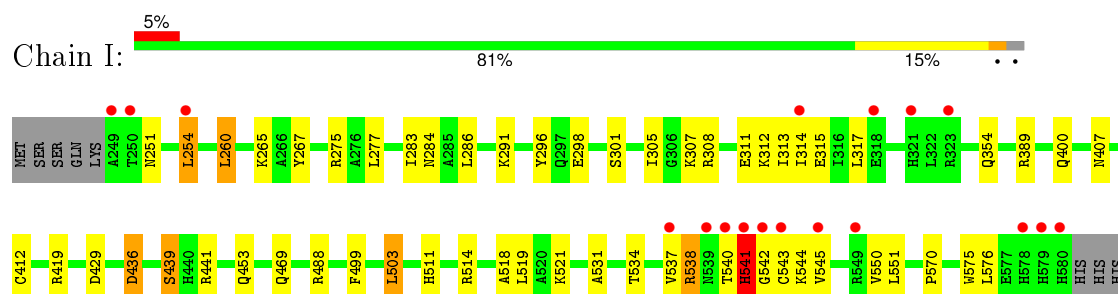
- Molecule 1: DNA polymerase lambda



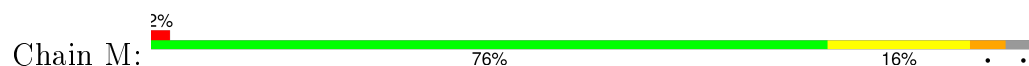
- Molecule 1: DNA polymerase lambda

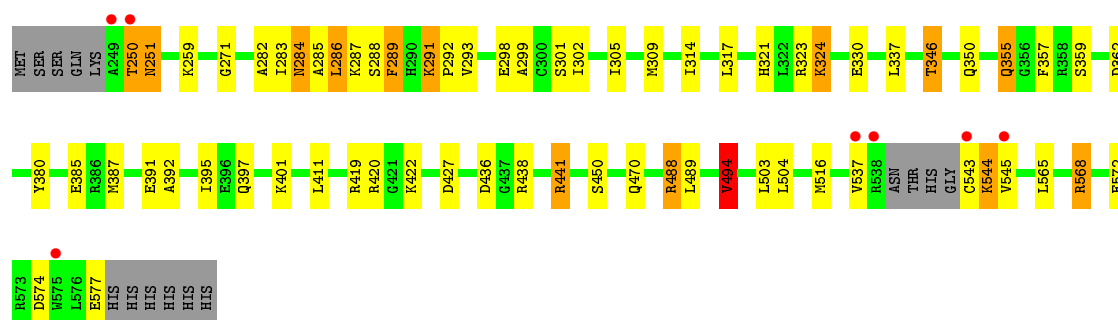


- Molecule 1: DNA polymerase lambda

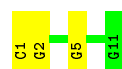


- Molecule 1: DNA polymerase lambda





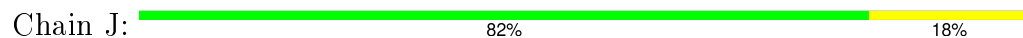
- Molecule 2: DNA (5'-D(*CP*GP*GP*CP*GP*GP*TP*AP*CP*TP*G)-3')



- Molecule 2: DNA (5'-D(*CP*GP*GP*CP*GP*GP*TP*AP*CP*TP*G)-3')



- Molecule 2: DNA (5'-D(*CP*GP*GP*CP*GP*GP*TP*AP*CP*TP*G)-3')



- Molecule 2: DNA (5'-D(*CP*GP*GP*CP*GP*GP*TP*AP*CP*TP*G)-3')

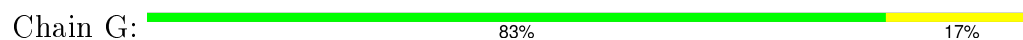


- Molecule 3: DNA (5'-D(*CP*AP*GP*TP*AP*C)-3')



There are no outlier residues recorded for this chain.

- Molecule 3: DNA (5'-D(*CP*AP*GP*TP*AP*C)-3')




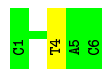
- Molecule 3: DNA (5'-D(*CP*AP*GP*TP*AP*C)-3')

Chain K:  100%

There are no outlier residues recorded for this chain.

- Molecule 3: DNA (5'-D(*CP*AP*GP*TP*AP*C)-3')

Chain O:  83% 17%



- Molecule 4: DNA (5'-D(P*GP*CP*CP*G)-3')

Chain D:  50% 25% 25%



- Molecule 4: DNA (5'-D(P*GP*CP*CP*G)-3')

Chain H:  25% 50% 25%



- Molecule 4: DNA (5'-D(P*GP*CP*CP*G)-3')

Chain L:  50% 50%



- Molecule 4: DNA (5'-D(P*GP*CP*CP*G)-3')

Chain P:  75% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 2 ₁ 2 ₁ 2	Depositor
Cell constants a, b, c, α , β , γ	194.95Å 97.44Å 105.17Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	40.88 – 2.10 40.88 – 2.10	Depositor EDS
% Data completeness (in resolution range)	95.1 (40.88-2.10) 95.2 (40.88-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.64 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.7.0029	Depositor
R, R_{free}	0.204 , 0.260 0.209 , 0.260	Depositor DCC
R_{free} test set	5588 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	32.9	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 42.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 111724 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12678	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.87% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: CA, 1RZ, ACT

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	0.95	2/2633 (0.1%)	0.97	9/3554 (0.3%)
1	E	0.86	1/2615 (0.0%)	0.92	6/3528 (0.2%)
1	I	0.83	1/2682 (0.0%)	0.93	5/3621 (0.1%)
1	M	0.92	1/2618 (0.0%)	1.11	11/3532 (0.3%)
2	B	0.78	0/252	1.02	0/388
2	F	0.58	0/252	1.05	2/388 (0.5%)
2	J	0.76	1/252 (0.4%)	1.19	1/388 (0.3%)
2	N	0.71	0/252	1.01	3/388 (0.8%)
3	C	0.84	0/133	0.95	0/203
3	G	0.76	1/133 (0.8%)	0.80	0/203
3	K	0.83	0/133	0.97	0/203
3	O	0.68	0/133	0.97	1/203 (0.5%)
4	D	1.27	1/92 (1.1%)	1.07	2/138 (1.4%)
4	H	1.31	1/92 (1.1%)	0.78	0/138
4	L	1.26	1/92 (1.1%)	0.87	0/138
4	P	1.13	1/92 (1.1%)	0.96	1/138 (0.7%)
All	All	0.89	11/12456 (0.1%)	0.99	41/17151 (0.2%)

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	E	0	1

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	H	1	DG	OP3-P	-10.90	1.48	1.61
4	L	1	DG	OP3-P	-10.41	1.48	1.61

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	1	DG	OP3-P	-10.20	1.49	1.61
4	P	1	DG	OP3-P	-9.43	1.49	1.61
1	I	429	ASP	CB-CG	6.44	1.65	1.51

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	M	488	ARG	NE-CZ-NH2	-20.73	109.94	120.30
1	M	488	ARG	NE-CZ-NH1	16.06	128.33	120.30
2	J	9	DC	O5'-P-OP1	-12.46	94.49	105.70
1	M	441	ARG	NE-CZ-NH2	-10.22	115.19	120.30
1	M	427	ASP	CB-CG-OD1	9.84	127.16	118.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	E	469	GLN	Peptide

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	2578	0	2564	25	0
1	E	2563	0	2570	43	0
1	I	2623	0	2617	31	0
1	M	2564	0	2575	37	0
2	B	225	0	125	2	0
2	F	225	0	125	7	0
2	J	225	0	125	0	0
2	N	225	0	125	2	0
3	C	119	0	68	0	0
3	G	119	0	69	0	0
3	K	119	0	69	0	0
3	O	119	0	69	0	0
4	D	83	0	45	1	0
4	H	83	0	45	3	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	L	83	0	45	1	0
4	P	83	0	45	0	0
5	A	27	0	12	0	0
5	E	27	0	11	0	0
5	I	27	0	12	0	0
5	M	27	0	11	0	0
6	A	6	0	0	0	0
6	B	1	0	0	0	0
6	E	4	0	0	0	0
6	F	1	0	0	0	0
6	I	4	0	0	0	0
6	J	1	0	0	0	0
6	M	5	0	0	0	0
6	N	1	0	0	0	0
7	A	4	0	3	0	0
7	F	4	0	3	0	0
7	I	4	0	3	0	0
7	M	8	0	6	0	0
8	A	120	0	0	6	0
8	B	19	0	0	0	0
8	C	11	0	0	0	0
8	D	1	0	0	0	0
8	E	82	0	0	3	0
8	F	7	0	0	1	0
8	G	2	0	0	0	0
8	H	2	0	0	0	0
8	I	81	0	0	2	0
8	J	6	0	0	0	0
8	K	5	0	0	0	0
8	M	143	0	0	4	0
8	N	6	0	0	1	0
8	O	5	0	0	0	0
8	P	1	0	0	0	0
All	All	12678	0	11342	142	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 6.

The worst 5 of 142 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:F:8:DA:OP2	8:F:201:HOH:O	1.89	0.89
1:M:321:HIS:ND1	8:M:760:HOH:O	2.13	0.81
1:A:333:PRO:O	8:A:721:HOH:O	2.00	0.80
1:M:387:MET:HE1	1:M:395:ILE:HD12	1.64	0.79
1:E:464:GLN:HG3	2:F:8:DA:O3'	1.82	0.78

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	323/340 (95%)	309 (96%)	12 (4%)	2 (1%)	30	24
1	E	322/340 (95%)	304 (94%)	12 (4%)	6 (2%)	10	4
1	I	331/340 (97%)	316 (96%)	13 (4%)	2 (1%)	30	24
1	M	322/340 (95%)	304 (94%)	13 (4%)	5 (2%)	12	6
All	All	1298/1360 (95%)	1233 (95%)	50 (4%)	15 (1%)	16	10

5 of 15 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	470	GLN
1	I	538	ARG
1	I	541	HIS
1	M	251	ASN
1	A	250	THR

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	274/287 (96%)	260 (95%)	14 (5%)	29	26
1	E	273/287 (95%)	259 (95%)	14 (5%)	29	26
1	I	280/287 (98%)	263 (94%)	17 (6%)	23	19
1	M	274/287 (96%)	252 (92%)	22 (8%)	15	11
All	All	1101/1148 (96%)	1034 (94%)	67 (6%)	23	19

5 of 67 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	I	265	LYS
1	I	469	GLN
1	M	494	VAL
1	I	277	LEU
1	I	436	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 12 such sidechains are listed below:

Mol	Chain	Res	Type
1	I	270	GLN
1	I	372	GLN
1	I	511	HIS
1	E	290	HIS
1	I	453	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry

Of 32 ligands modelled in this entry, 23 are monoatomic - leaving 9 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
5	1RZ	A	601	6	20,28,28	1.08	2 (10%)	30,43,43	1.25	3 (10%)
7	ACT	A	608	-	1,3,3	1.58	0	0,3,3	0.00	-
5	1RZ	E	601	6	20,28,28	0.97	1 (5%)	30,43,43	1.68	6 (20%)
7	ACT	F	102	-	1,3,3	2.41	1 (100%)	0,3,3	0.00	-
5	1RZ	I	601	6	20,28,28	0.74	0	30,43,43	1.70	6 (20%)
7	ACT	I	606	-	1,3,3	1.86	0	0,3,3	0.00	-
5	1RZ	M	601	6	20,28,28	0.91	0	30,43,43	2.46	15 (50%)
7	ACT	M	607	-	1,3,3	2.33	1 (100%)	0,3,3	0.00	-
7	ACT	M	608	-	1,3,3	2.26	1 (100%)	0,3,3	0.00	-

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
5	1RZ	A	601	6	-	0/18/31/31	0/2/2/2
7	ACT	A	608	-	-	0/0/0/0	0/0/0/0
5	1RZ	E	601	6	-	0/18/31/31	0/2/2/2
7	ACT	F	102	-	-	0/0/0/0	0/0/0/0
5	1RZ	I	601	6	-	0/18/31/31	0/2/2/2
7	ACT	I	606	-	-	0/0/0/0	0/0/0/0
5	1RZ	M	601	6	-	0/18/31/31	0/2/2/2
7	ACT	M	607	-	-	0/0/0/0	0/0/0/0
7	ACT	M	608	-	-	0/0/0/0	0/0/0/0

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	601	1RZ	O4'-C1'	-2.33	1.37	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	E	601	1RZ	PG-O3G	-2.18	1.46	1.54
5	A	601	1RZ	C2'-S3'	-2.06	1.75	1.81
7	M	608	ACT	CH3-C	2.26	1.52	1.48
7	M	607	ACT	CH3-C	2.33	1.52	1.48

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	601	1RZ	PB-O3A-PA	-4.63	119.72	132.73
5	M	601	1RZ	C5-C4-N3	-3.67	117.17	121.80
5	A	601	1RZ	O3A-PA-O5'	-3.32	94.12	102.94
5	E	601	1RZ	PB-O3A-PA	-2.79	124.89	132.73
5	M	601	1RZ	O4'-C1'-C2'	-2.79	102.74	109.29

There are no chirality outliers.

There are no torsion outliers.

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

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	327/340 (96%)	-0.12	9 (2%) 56 64	18, 33, 62, 116	0
1	E	326/340 (95%)	-0.02	13 (3%) 42 51	22, 38, 70, 131	0
1	I	332/340 (97%)	-0.00	18 (5%) 29 38	22, 39, 70, 132	0
1	M	325/340 (95%)	-0.15	7 (2%) 65 71	17, 35, 55, 90	0
2	B	11/11 (100%)	-0.26	0 100 100	24, 27, 46, 46	0
2	F	11/11 (100%)	-0.39	0 100 100	37, 43, 52, 68	0
2	J	11/11 (100%)	-0.51	0 100 100	33, 38, 43, 45	0
2	N	11/11 (100%)	-0.55	0 100 100	26, 32, 45, 46	0
3	C	6/6 (100%)	-0.36	0 100 100	21, 26, 39, 42	0
3	G	6/6 (100%)	-0.23	0 100 100	30, 34, 59, 73	0
3	K	6/6 (100%)	-0.24	0 100 100	25, 29, 59, 61	0
3	O	6/6 (100%)	-0.42	0 100 100	28, 31, 50, 55	0
4	D	4/4 (100%)	-0.70	0 100 100	33, 33, 38, 42	0
4	H	4/4 (100%)	-0.69	0 100 100	30, 33, 36, 41	0
4	L	4/4 (100%)	-0.59	0 100 100	38, 42, 45, 46	0
4	P	4/4 (100%)	-0.70	0 100 100	34, 36, 45, 45	0
All	All	1394/1444 (96%)	-0.10	47 (3%) 49 58	17, 36, 64, 132	0

The worst 5 of 47 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	539	ASN	8.8
1	E	540	THR	8.0
1	E	542	GLY	7.4
1	I	542	GLY	7.4
1	I	541	HIS	6.6

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

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates ⓘ

There are no carbohydrates 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(Å ²)	Q<0.9
6	CA	E	603	1/1	0.96	0.14	5.43	39,39,39,39	0
7	ACT	I	606	4/4	0.91	0.24	3.91	44,47,51,56	0
6	CA	A	607	1/1	0.89	0.17	2.99	51,51,51,51	0
7	ACT	M	608	4/4	0.87	0.18	2.89	34,40,45,46	0
7	ACT	M	607	4/4	0.61	0.24	2.39	53,54,58,61	0
6	CA	M	604	1/1	0.96	0.11	1.46	39,39,39,39	0
5	1RZ	I	601	27/27	0.94	0.13	1.39	40,49,68,75	0
7	ACT	A	608	4/4	0.91	0.12	0.95	43,46,47,51	0
5	1RZ	A	601	27/27	0.98	0.11	0.02	18,22,25,26	0
5	1RZ	M	601	27/27	0.94	0.10	-0.25	23,38,51,54	0
5	1RZ	E	601	27/27	0.98	0.11	-0.29	22,28,39,42	0
6	CA	M	605	1/1	0.82	0.08	-1.35	66,66,66,66	0
6	CA	A	605	1/1	0.97	0.07	-1.96	33,33,33,33	0
6	CA	I	605	1/1	0.99	0.04	-3.35	34,34,34,34	0
6	CA	I	602	1/1	0.89	0.10	-	46,46,46,46	0
6	CA	J	101	1/1	0.81	0.08	-	68,68,68,68	0
6	CA	M	603	1/1	0.88	0.06	-	64,64,64,64	0
6	CA	F	101	1/1	0.91	0.11	-	52,52,52,52	0
6	CA	I	603	1/1	0.95	0.05	-	49,49,49,49	0
6	CA	E	602	1/1	0.98	0.10	-	26,26,26,26	0
6	CA	A	602	1/1	1.00	0.09	-	24,24,24,24	0
6	CA	A	603	1/1	0.94	0.06	-	46,46,46,46	0
6	CA	I	604	1/1	0.80	0.13	-	59,59,59,59	0
7	ACT	F	102	4/4	0.93	0.17	-	42,44,45,49	0
6	CA	M	602	1/1	0.84	0.12	-	55,55,55,55	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
6	CA	A	604	1/1	0.96	0.05	-	29,29,29,29	0
6	CA	B	101	1/1	0.85	0.13	-	65,65,65,65	0
6	CA	M	606	1/1	0.96	0.04	-	45,45,45,45	0
6	CA	E	605	1/1	0.92	0.11	-	67,67,67,67	0
6	CA	A	606	1/1	0.86	0.11	-	62,62,62,62	0
6	CA	E	604	1/1	0.71	0.10	-	53,53,53,53	0
6	CA	N	101	1/1	0.80	0.18	-	60,60,60,60	0

6.5 Other polymers [i](#)

There are no such residues in this entry.