



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 25, 2026 – 01:40 PM EDT

PDB ID : 6IS7 / pdb_00006is7
Title : Structure of 9N-I DNA polymerase incorporation with dA in the active site
Authors : Linwu, S.W.; Maestre-Reyna, M.; Tsai, M.D.; Tu, Y.H.; Chang, W.H.
Deposited on : 2018-11-15
Resolution : 2.80 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:

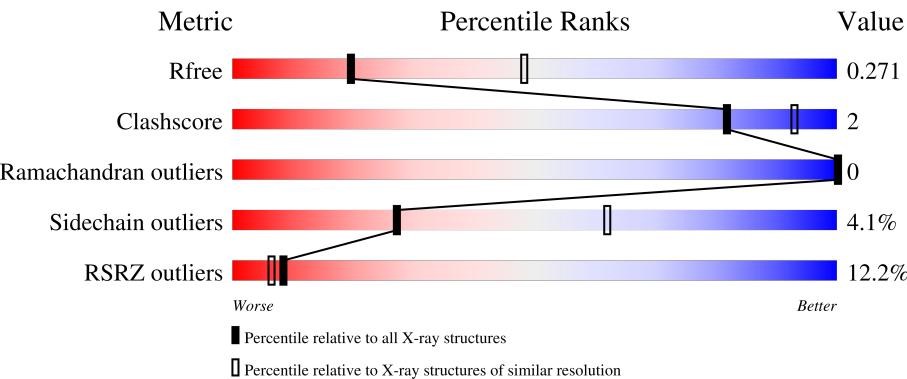
MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
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 2.80 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	3866 (2.80-2.80)
Clashscore	190562	4276 (2.80-2.80)
Ramachandran outliers	187476	4196 (2.80-2.80)
Sidechain outliers	187428	4198 (2.80-2.80)
RSRZ outliers	180081	3869 (2.80-2.80)

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	783	
1	B	783	
2	C	15	
2	E	15	
2	K	15	

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Mol	Chain	Length	Quality of chain
2	L	15	27% 73%
3	D	18	28% 94% 6%
3	F	18	11% 94% 6%
3	I	18	11% 11% 78%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 13390 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.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	757	Total	C	N	O	S	0	0	0
			5883	3812	997	1059	15			
1	B	756	Total	C	N	O	S	0	0	0
			5723	3711	955	1042	15			

There are 22 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	141	ALA	ASP	engineered mutation	UNP Q56366
A	143	ALA	GLU	engineered mutation	UNP Q56366
A	485	LEU	ALA	engineered mutation	UNP Q56366
A	776	LEU	-	expression tag	UNP Q56366
A	777	GLU	-	expression tag	UNP Q56366
A	778	HIS	-	expression tag	UNP Q56366
A	779	HIS	-	expression tag	UNP Q56366
A	780	HIS	-	expression tag	UNP Q56366
A	781	HIS	-	expression tag	UNP Q56366
A	782	HIS	-	expression tag	UNP Q56366
A	783	HIS	-	expression tag	UNP Q56366
B	141	ALA	ASP	engineered mutation	UNP Q56366
B	143	ALA	GLU	engineered mutation	UNP Q56366
B	485	LEU	ALA	engineered mutation	UNP Q56366
B	776	LEU	-	expression tag	UNP Q56366
B	777	GLU	-	expression tag	UNP Q56366
B	778	HIS	-	expression tag	UNP Q56366
B	779	HIS	-	expression tag	UNP Q56366
B	780	HIS	-	expression tag	UNP Q56366
B	781	HIS	-	expression tag	UNP Q56366
B	782	HIS	-	expression tag	UNP Q56366
B	783	HIS	-	expression tag	UNP Q56366

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	15	Total	C	N	O	P	0	0	0
			303	145	56	88	14			
2	E	15	Total	C	N	O	P	0	0	0
			302	145	56	87	14			
2	K	3	Total	C	N	O	P	0	0	0
			59	29	7	20	3			
2	L	4	Total	C	N	O	P	0	0	0
			81	39	12	26	4			

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

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	D	18	Total	C	N	O	P	0	0	0
			368	175	71	105	17			
3	F	18	Total	C	N	O	P	0	0	0
			368	175	71	105	17			
3	I	4	Total	C	N	O	P	0	0	0
			83	39	18	22	4			

- Molecule 4 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	2	Total	Ca	0	0
			2	2		
4	B	5	Total	Ca	0	0
			5	5		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	93	Total	O	0	0
			93	93		
5	B	76	Total	O	0	1
			77	77		
5	C	8	Total	O	0	0
			8	8		
5	D	8	Total	O	0	0
			8	8		
5	E	7	Total	O	0	0
			7	7		
5	F	8	Total	O	0	0
			8	8		

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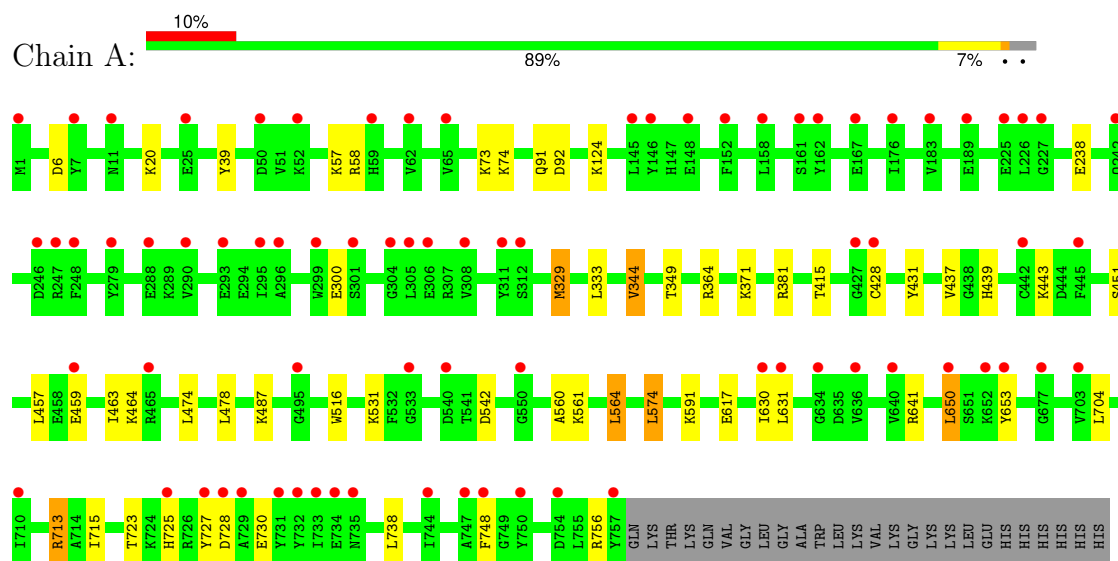
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	I	3	Total 3	O 3	0	0
5	K	3	Total 3	O 3	0	0
5	L	6	Total 6	O 6	0	0

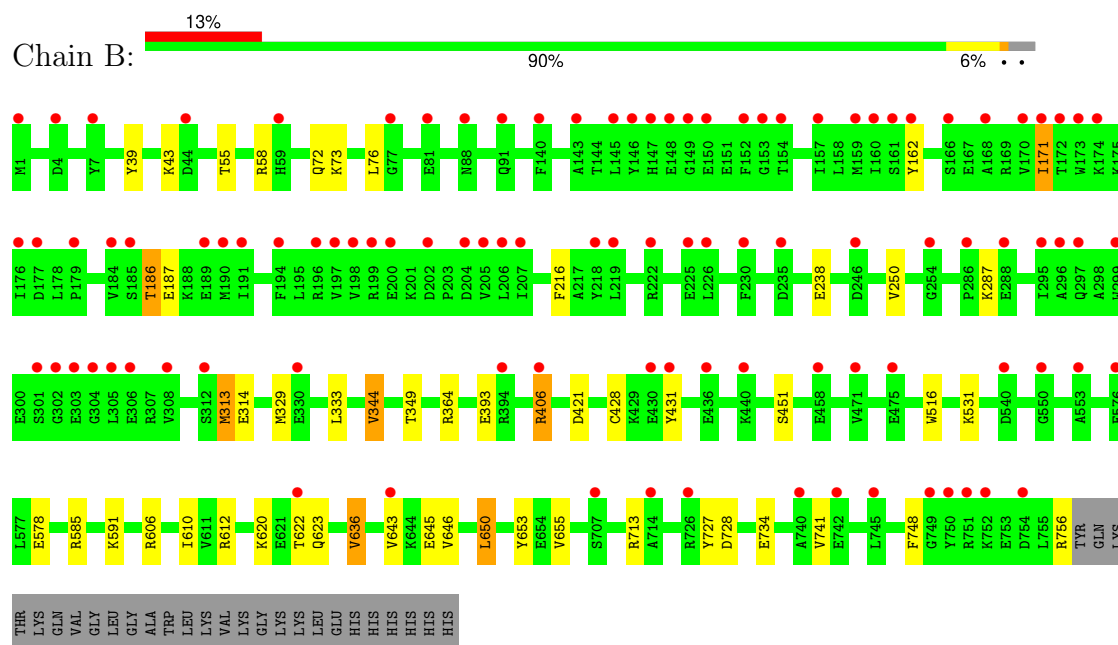
3 Residue-property plots

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: DNA polymerase

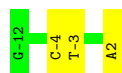


• Molecule 1: DNA polymerase



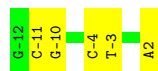
- Molecule 2: DNA (5'-D(P*GP*CP*GP*GP*AP*CP*TP*GP*CP*TP*TP*AP*CP*CP*A)-3')

Chain C:  80% 20%



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

Chain E:  67% 33%



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

Chain K:  20% 20% 80%

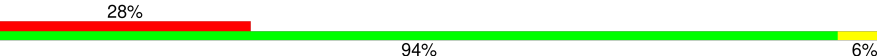


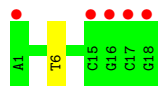
- Molecule 2: DNA (5'-D(P*GP*CP*GP*GP*AP*CP*TP*GP*CP*TP*TP*AP*CP*CP*A)-3')

Chain L:  27% 27% 73%

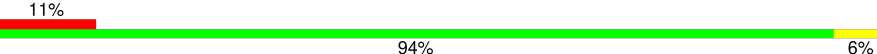


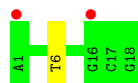
- Molecule 3: DNA (5'-D(*AP*CP*TP*GP*GP*TP*AP*AP*GP*CP*AP*GP*TP*CP*CP*GP*CP*G)-3')

Chain D:  28% 94% 6%



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

Chain F:  11% 94% 6%



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	92.95Å 106.77Å 255.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.29 – 2.80 46.29 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (46.29-2.80) 99.4 (46.29-2.80)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.28 (at 2.81Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, R_{free}	0.225 , 0.276 0.225 , 0.271	Depositor DCC
R_{free} test set	3139 reflections (3.54%)	wwPDB-VP
Wilson B-factor (Å ²)	58.1	Xtriage
Anisotropy	0.272	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 70.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	13390	wwPDB-VP
Average B, all atoms (Å ²)	91.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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: CA

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	1.01	0/6022	1.45	2/8171 (0.0%)
1	B	1.01	0/5854	1.47	2/7959 (0.0%)
2	C	0.41	0/339	0.85	0/521
2	E	0.42	0/338	0.90	0/520
2	K	0.30	0/64	0.64	0/96
2	L	0.28	0/89	0.62	0/135
3	D	0.36	0/413	0.73	0/636
3	F	0.38	0/413	0.76	0/636
3	I	0.30	0/93	0.60	0/141
All	All	0.95	0/13625	1.38	4/18815 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	B	585	ARG	CA-C-N	5.14	125.15	121.65
1	B	585	ARG	C-N-CA	5.14	125.15	121.65
1	A	381	ARG	CA-C-N	5.01	124.73	119.92
1	A	381	ARG	C-N-CA	5.01	124.73	119.92

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	5883	0	5613	29	0
1	B	5723	0	5342	27	0
2	C	303	0	170	3	0
2	E	302	0	167	4	0
2	K	59	0	36	0	0
2	L	81	0	47	0	0
3	D	368	0	203	1	0
3	F	368	0	203	1	0
3	I	83	0	45	1	0
4	A	2	0	0	0	0
4	B	5	0	0	0	0
5	A	93	0	0	2	0
5	B	77	0	0	0	0
5	C	8	0	0	0	0
5	D	8	0	0	0	0
5	E	7	0	0	0	0
5	F	8	0	0	0	0
5	I	3	0	0	0	0
5	K	3	0	0	0	0
5	L	6	0	0	0	0
All	All	13390	0	11826	62	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 2.

All (62) 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:B:610:ILE:HG13	1:B:623:GLN:HE21	1.44	0.82
1:B:636:VAL:HG21	1:B:748:PHE:CD2	2.20	0.76
1:B:643:VAL:HG21	1:B:741:VAL:HG21	1.70	0.73
1:A:730:GLU:OE2	1:A:756:ARG:NH2	2.21	0.73
1:B:364:ARG:NH2	1:B:451:SER:OG	2.22	0.73
1:B:713:ARG:NH1	1:B:728:ASP:OD2	2.24	0.70
1:A:437:VAL:CG1	1:A:439:HIS:CD2	2.75	0.69
1:A:713:ARG:NH1	1:A:728:ASP:OD2	2.25	0.69
1:A:437:VAL:HG12	1:A:439:HIS:CD2	2.31	0.66
1:A:58:ARG:NH1	1:A:92:ASP:OD1	2.31	0.64
1:A:459:GLU:O	1:A:463:ILE:HG13	2.00	0.62
1:A:574:LEU:H	1:A:574:LEU:HD23	1.66	0.61
1:A:437:VAL:HG11	1:A:439:HIS:CD2	2.37	0.59
1:A:574:LEU:HD23	1:A:574:LEU:N	2.19	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:591:LYS:HD3	3:D:6:DT:H5''	1.89	0.55
2:C:-4:DC:H2''	2:C:-3:DT:H5''	1.90	0.54
1:B:636:VAL:HG21	1:B:748:PHE:HD2	1.69	0.54
1:B:643:VAL:CG2	1:B:741:VAL:HG21	2.37	0.54
1:B:734:GLU:OE2	1:B:756:ARG:NH1	2.40	0.54
2:E:-4:DC:H2''	2:E:-3:DT:H5''	1.90	0.52
1:A:333:LEU:HD23	1:A:344:VAL:HG13	1.93	0.51
1:B:622:THR:HG21	1:B:646:VAL:HG11	1.92	0.51
1:B:333:LEU:HD23	1:B:344:VAL:HG13	1.93	0.51
1:B:650:LEU:HD13	1:B:655:VAL:HG21	1.92	0.51
1:B:591:LYS:HD3	3:F:6:DT:H5''	1.95	0.49
1:A:39:TYR:CZ	1:A:73:LYS:HE3	2.48	0.49
1:A:364:ARG:NH2	1:A:451:SER:OG	2.43	0.48
1:A:329:MET:HE2	1:A:329:MET:C	2.39	0.48
1:A:738:LEU:HD11	1:A:756:ARG:HG3	1.95	0.48
1:A:58:ARG:HD2	1:A:91:GLN:HB3	1.96	0.48
1:A:371:LYS:NZ	5:A:901:HOH:O	2.47	0.47
1:A:630:ILE:HD13	1:A:748:PHE:HE2	1.79	0.47
2:E:-11:DC:H2'	2:E:-10:DG:C8	2.49	0.47
1:B:428:CYS:HB2	1:B:431:TYR:CE1	2.51	0.46
1:A:428:CYS:HB2	1:A:431:TYR:CE1	2.50	0.46
1:A:653:TYR:HA	1:A:727:TYR:OH	2.15	0.46
1:B:186:THR:OG1	1:B:187:GLU:N	2.48	0.46
1:B:39:TYR:CZ	1:B:73:LYS:HE3	2.52	0.45
3:I:0:DA:H2''	3:I:1:DA:H5''	1.99	0.45
1:B:76:LEU:C	1:B:421:ASP:HB3	2.42	0.44
1:B:313:MET:HG3	1:B:314:GLU:N	2.33	0.44
1:A:560:ALA:O	1:A:564:LEU:HD22	2.18	0.44
1:B:653:TYR:HA	1:B:727:TYR:OH	2.17	0.44
1:B:406:ARG:NH2	1:B:578:GLU:OE2	2.50	0.44
1:B:643:VAL:O	1:B:646:VAL:HG12	2.19	0.43
1:A:704:LEU:HD22	1:A:725:HIS:HB3	2.01	0.43
1:B:612:ARG:O	1:B:620:LYS:HD3	2.20	0.42
1:A:542:ASP:OD1	2:C:2:DA:O3'	2.37	0.42
1:A:437:VAL:CG1	1:A:439:HIS:NE2	2.82	0.42
1:B:606:ARG:HD2	2:E:2:DA:OP2	2.20	0.42
1:B:636:VAL:CG2	1:B:748:PHE:CD2	2.99	0.42
1:A:415:THR:O	1:A:443:LYS:NZ	2.53	0.42
1:B:610:ILE:HG13	1:B:623:GLN:NE2	2.24	0.42
1:A:631:LEU:HD23	1:A:631:LEU:HA	1.90	0.41
1:B:162:TYR:CE2	1:B:171:ILE:HD11	2.55	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:636:VAL:HG21	1:B:748:PHE:CE2	2.54	0.41
1:A:650:LEU:HD12	1:A:650:LEU:HA	1.87	0.41
1:B:216:PHE:HB2	1:B:250:VAL:HG21	2.03	0.40
2:E:-4:DC:H2''	2:E:-3:DT:C5'	2.52	0.40
2:C:-4:DC:H2''	2:C:-3:DT:C5'	2.51	0.40
1:A:725:HIS:HA	5:A:955:HOH:O	2.20	0.40
1:A:6:ASP:C	1:A:6:ASP:OD1	2.65	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	755/783 (96%)	736 (98%)	19 (2%)	0	100	100
1	B	754/783 (96%)	735 (98%)	19 (2%)	0	100	100
All	All	1509/1566 (96%)	1471 (98%)	38 (2%)	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	550/675 (82%)	525 (96%)	25 (4%)	24	58

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	515/675 (76%)	496 (96%)	19 (4%)	30	65
All	All	1065/1350 (79%)	1021 (96%)	44 (4%)	27	62

All (44) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	20	LYS
1	A	57	LYS
1	A	74	LYS
1	A	124	LYS
1	A	238	GLU
1	A	300	GLU
1	A	329	MET
1	A	344	VAL
1	A	349	THR
1	A	457	LEU
1	A	464	LYS
1	A	474	LEU
1	A	478	LEU
1	A	487	LYS
1	A	516	TRP
1	A	531	LYS
1	A	561	LYS
1	A	564	LEU
1	A	574	LEU
1	A	617	GLU
1	A	641	ARG
1	A	650	LEU
1	A	713	ARG
1	A	715	ILE
1	A	723	THR
1	B	43	LYS
1	B	55	THR
1	B	58	ARG
1	B	72	GLN
1	B	171	ILE
1	B	186	THR
1	B	238	GLU
1	B	287	LYS
1	B	313	MET
1	B	329	MET
1	B	344	VAL

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Mol	Chain	Res	Type
1	B	349	THR
1	B	393	GLU
1	B	406	ARG
1	B	516	TRP
1	B	531	LYS
1	B	636	VAL
1	B	645	GLU
1	B	650	LEU

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	351	ASN
1	A	461	GLN
1	A	679	HIS
1	B	351	ASN
1	B	491	ASN
1	B	623	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 7 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

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

There are no such residues in this entry.

5.8 Polymer linkage issues

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	757/783 (96%)	0.90	77 (10%) 12 9	55, 89, 135, 161	3 (0%)
1	B	756/783 (96%)	0.90	101 (13%) 7 5	55, 89, 162, 232	1 (0%)
2	C	15/15 (100%)	0.49	0 100 100	60, 71, 88, 88	0
2	E	15/15 (100%)	-0.01	0 100 100	51, 62, 75, 78	0
2	K	3/15 (20%)	5.38	3 (100%) 0 0	58, 58, 59, 164	2 (66%)
2	L	4/15 (26%)	3.76	4 (100%) 0 0	56, 57, 57, 156	3 (75%)
3	D	18/18 (100%)	1.39	5 (27%) 1 1	56, 71, 112, 119	1 (5%)
3	F	18/18 (100%)	0.48	2 (11%) 10 7	57, 72, 106, 121	0
3	I	4/18 (22%)	2.63	2 (50%) 0 0	58, 154, 156, 158	1 (25%)
All	All	1590/1680 (94%)	0.91	194 (12%) 8 6	51, 88, 146, 232	11 (0%)

All (194) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	D	18	DG	11.8
2	K	2	DT	6.3
2	K	3	DT	5.3
3	I	3	DC	5.2
1	B	714	ALA	4.6
2	K	1	DC	4.6
2	L	5	DT	4.6
1	A	301	SER	4.5
1	A	735	ASN	4.4
2	L	2	DT	4.4
1	A	428	CYS	4.3
1	B	152	PHE	4.3
1	B	177	ASP	4.2
1	B	157	ILE	4.2
1	B	162	TYR	4.1

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Mol	Chain	Res	Type	RSRZ
1	A	295	ILE	4.0
1	B	176	ILE	4.0
1	B	305	LEU	4.0
1	B	196	ARG	3.9
1	A	734	GLU	3.9
1	B	199	ARG	3.9
1	A	306	GLU	3.8
1	B	185	SER	3.7
1	B	246	ASP	3.7
1	A	465	ARG	3.7
1	B	299	TRP	3.7
1	B	173	TRP	3.6
1	B	148	GLU	3.6
1	A	246	ASP	3.5
2	L	3	DG	3.5
1	A	427	GLY	3.4
1	A	279	TYR	3.4
1	B	172	THR	3.4
1	A	152	PHE	3.4
1	A	727	TYR	3.4
1	A	145	LEU	3.3
1	A	227	GLY	3.3
1	A	754	ASP	3.3
1	B	750	TYR	3.3
3	D	15	DC	3.3
1	A	146	TYR	3.2
3	D	1	DA	3.2
1	A	732	TYR	3.2
1	A	729	ALA	3.2
1	B	140	PHE	3.2
1	B	225	GLU	3.2
1	B	296	ALA	3.1
1	A	725	HIS	3.1
3	D	17	DC	3.1
1	A	640	VAL	3.1
1	B	301	SER	3.0
1	B	91	GLN	3.0
1	B	550	GLY	3.0
1	B	200	GLU	3.0
1	A	59	HIS	3.0
1	B	4	ASP	3.0
1	A	631	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	293	GLU	3.0
1	A	308	VAL	3.0
3	F	1	DA	3.0
1	A	65	VAL	3.0
1	A	630	ILE	3.0
1	A	533	GLY	3.0
1	B	306	GLU	2.9
1	B	147	HIS	2.9
1	B	88	ASN	2.9
1	A	652	LYS	2.9
1	B	295	ILE	2.9
1	A	750	TYR	2.9
1	A	247	ARG	2.9
1	B	154	THR	2.9
1	B	394	ARG	2.9
1	B	308	VAL	2.9
1	A	161	SER	2.9
1	A	445	PHE	2.9
1	B	312	SER	2.9
1	A	703	VAL	2.8
1	A	710	ILE	2.8
1	A	442	CYS	2.8
1	A	733	ILE	2.8
1	B	304	GLY	2.8
1	B	749	GLY	2.8
1	A	290	VAL	2.8
1	A	242	GLN	2.7
1	B	222	ARG	2.7
1	B	288	GLU	2.7
1	A	62	VAL	2.7
1	B	7	TYR	2.7
1	A	312	SER	2.7
1	B	194	PHE	2.7
3	D	16	DG	2.7
1	B	174	LYS	2.7
1	B	406	ARG	2.7
1	A	636	VAL	2.7
1	B	205	VAL	2.7
1	A	305	LEU	2.7
1	A	728	ASP	2.6
1	B	146	TYR	2.6
2	L	4	DC	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	471	VAL	2.6
3	F	16	DG	2.6
1	A	176	ILE	2.6
1	A	744	ILE	2.6
1	B	170	VAL	2.6
1	B	150	GLU	2.6
1	A	747	ALA	2.6
1	B	143	ALA	2.6
1	B	59	HIS	2.6
1	A	731	TYR	2.6
1	A	650	LEU	2.6
1	B	206	LEU	2.6
1	A	148	GLU	2.6
1	A	757	TYR	2.5
1	B	145	LEU	2.5
1	B	226	LEU	2.5
1	B	171	ILE	2.5
1	B	436	GLU	2.5
1	A	550	GLY	2.5
1	B	219	LEU	2.5
1	A	225	GLU	2.5
1	A	167	GLU	2.5
1	B	303	GLU	2.5
1	B	726	ARG	2.4
1	B	160	ILE	2.4
1	B	77	GLY	2.4
1	B	230	PHE	2.4
1	B	159	MET	2.4
1	B	149	GLY	2.4
1	B	302	GLY	2.4
1	B	81	GLU	2.4
1	B	475	GLU	2.4
1	A	748	PHE	2.3
1	B	204	ASP	2.3
1	B	430	GLU	2.3
1	A	1	MET	2.3
1	A	162	TYR	2.3
1	B	197	VAL	2.3
1	A	11	ASN	2.3
1	A	296	ALA	2.3
1	B	153	GLY	2.3
1	A	248	PHE	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	754	ASP	2.3
3	I	1	DA	2.3
1	B	553	ALA	2.3
1	A	50	ASP	2.3
1	B	44	ASP	2.3
1	A	52	LYS	2.3
1	B	207	ILE	2.3
1	A	299	TRP	2.3
1	B	286	PRO	2.3
1	B	254	GLY	2.3
1	B	1	MET	2.2
1	B	189	GLU	2.2
1	B	191	ILE	2.2
1	B	235	ASP	2.2
1	A	7	TYR	2.2
1	B	707	SER	2.2
1	A	495	GLY	2.2
1	A	311	TYR	2.2
1	B	168	ALA	2.2
1	B	297	GLN	2.2
1	B	643	VAL	2.2
1	B	431	TYR	2.2
1	B	166	SER	2.2
1	A	459	GLU	2.2
1	B	184	VAL	2.1
1	B	440	LYS	2.1
1	B	745	LEU	2.1
1	A	25	GLU	2.1
1	B	218	TYR	2.1
1	A	540	ASP	2.1
1	B	202	ASP	2.1
1	B	622	THR	2.1
1	A	189	GLU	2.1
1	B	458	GLU	2.1
1	B	161	SER	2.1
1	B	752	LYS	2.1
1	A	226	LEU	2.1
1	A	634	GLY	2.1
1	A	653	TYR	2.1
1	B	190	MET	2.0
1	B	179	PRO	2.0
1	A	304	GLY	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	677	GLY	2.0
1	B	540	ASP	2.0
1	A	288	GLU	2.0
1	A	183	VAL	2.0
1	B	198	VAL	2.0
1	A	158	LEU	2.0
1	B	751	ARG	2.0
1	B	740	ALA	2.0
1	B	330	GLU	2.0
1	B	576	GLU	2.0
1	B	742	GLU	2.0

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 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(Å ²)	Q<0.9
4	CA	B	801	1/1	0.87	0.20	109,109,109,109	0
4	CA	B	805	1/1	0.87	0.26	102,102,102,102	0
4	CA	B	804	1/1	0.91	0.10	117,117,117,117	0
4	CA	B	802	1/1	0.91	0.11	126,126,126,126	0
4	CA	A	801	1/1	0.92	0.15	109,109,109,109	0
4	CA	A	802	1/1	0.93	0.13	107,107,107,107	0
4	CA	B	803	1/1	0.97	0.06	77,77,77,77	0

6.5 Other polymers [i](#)

There are no such residues in this entry.