



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 6, 2026 – 07:50 PM UTC

PDB ID : 1XXI / pdb_00001xxi
Title : ADP Bound E. coli Clamp Loader Complex
Authors : Kazmirski, S.L.; Podobnik, M.; Weitze, T.F.; O'Donnell, M.; Kuriyan, J.
Deposited on : 2004-11-05
Resolution : 4.10 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

<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
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
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

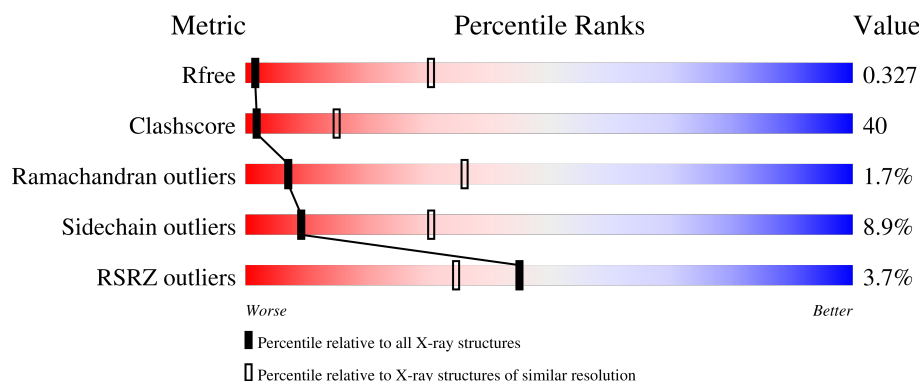
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.10 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}	180053	1243 (4.40-3.80)
Clashscore	190562	1293 (4.40-3.80)
Ramachandran outliers	187476	1206 (4.40-3.80)
Sidechain outliers	187428	1193 (4.40-3.80)
RSRZ outliers	180081	1240 (4.40-3.80)

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	343	4% 46% 37% 13% ..
1	F	343	2% 41% 41% 14% ..
2	B	368	8% 58% 32% 8% ..
2	C	368	2% 52% 41% 6% ..
2	D	368	5% 57% 33% 8% ..

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Mol	Chain	Length	Quality of chain
2	G	368	
2	H	368	
2	I	368	
3	E	334	
3	J	334	

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	ADP	I	803	-	-	X	-
6	PO4	C	1300	-	-	X	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 27688 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 III, delta subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	338	Total	C	N	O	S	0	0	0
			2687	1702	488	487	10			
1	F	338	Total	C	N	O	S	0	0	0
			2687	1702	488	487	10			

- Molecule 2 is a protein called DNA polymerase III subunit gamma.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	364	Total	C	N	O	S	0	0	0
			2829	1779	511	523	16			
2	C	366	Total	C	N	O	S	0	0	0
			2850	1793	514	527	16			
2	D	364	Total	C	N	O	S	0	0	0
			2829	1779	511	523	16			
2	G	364	Total	C	N	O	S	0	0	0
			2829	1779	511	523	16			
2	H	366	Total	C	N	O	S	0	0	0
			2850	1793	514	527	16			
2	I	364	Total	C	N	O	S	0	0	0
			2829	1779	511	523	16			

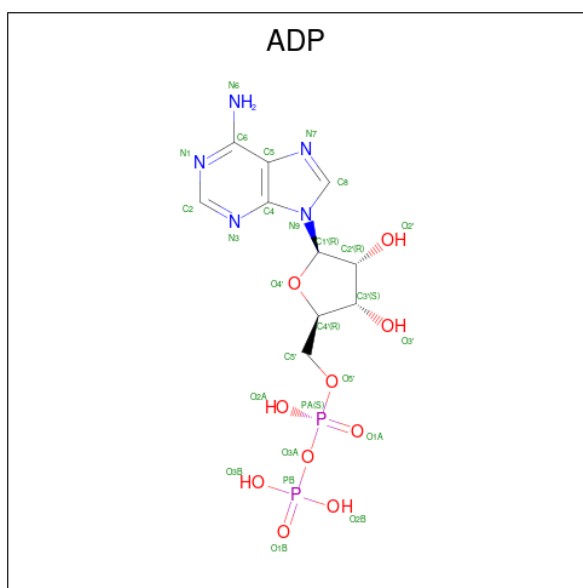
- Molecule 3 is a protein called DNA polymerase III, delta prime subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	334	Total	C	N	O	S	0	0	0
			2602	1655	468	466	13			
3	J	334	Total	C	N	O	S	0	0	0
			2602	1655	468	466	13			

- Molecule 4 is ZINC ION (CCD ID: ZN) (formula: Zn).

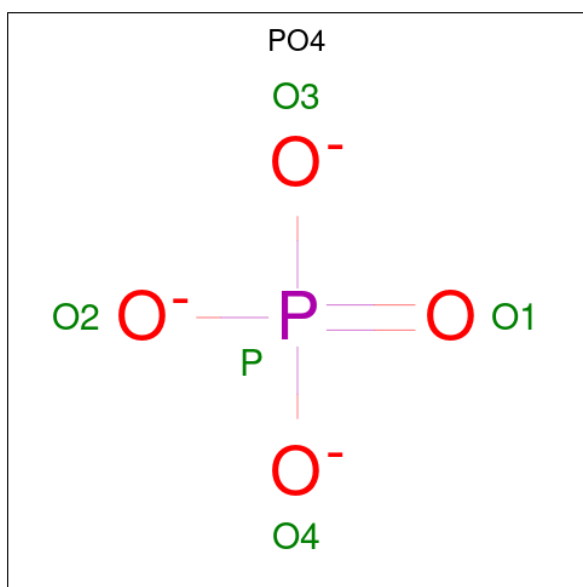
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	Zn	0	0
			1	1		
4	C	1	Total	Zn	0	0
			1	1		
4	D	1	Total	Zn	0	0
			1	1		
4	E	1	Total	Zn	0	0
			1	1		
4	G	1	Total	Zn	0	0
			1	1		
4	H	1	Total	Zn	0	0
			1	1		
4	I	1	Total	Zn	0	0
			1	1		
4	J	1	Total	Zn	0	0
			1	1		

- Molecule 5 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
5	D	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
5	I	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 6 is PHOSPHATE ION (CCD ID: PO4) (formula: O_4P).

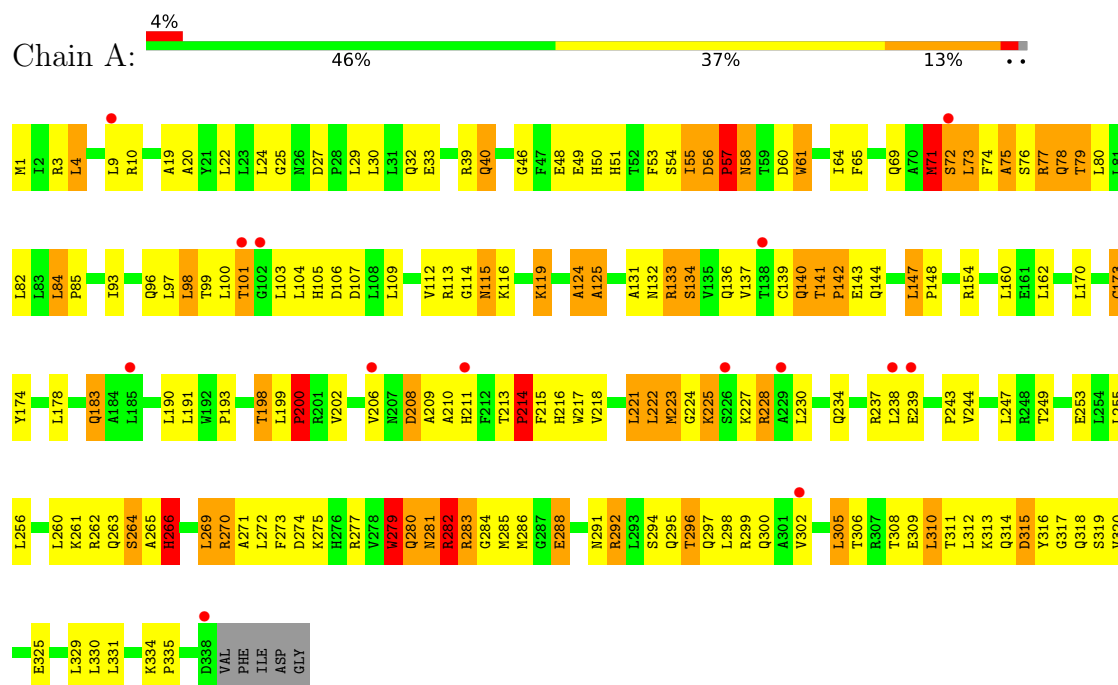


Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	C	1	Total	O	P	0	0
			5	4	1		

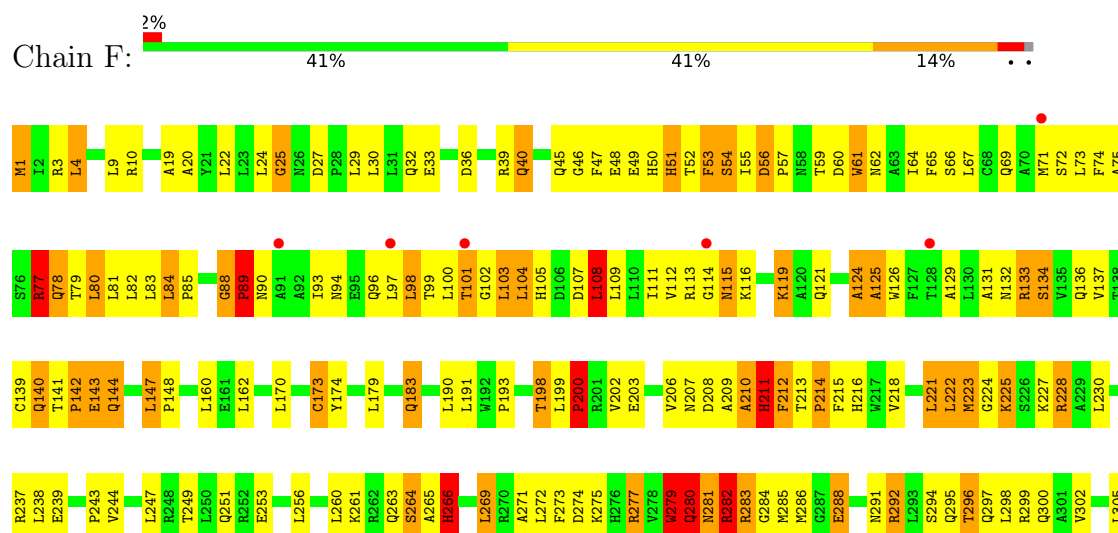
3 Residue-property plots

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 III, delta subunit

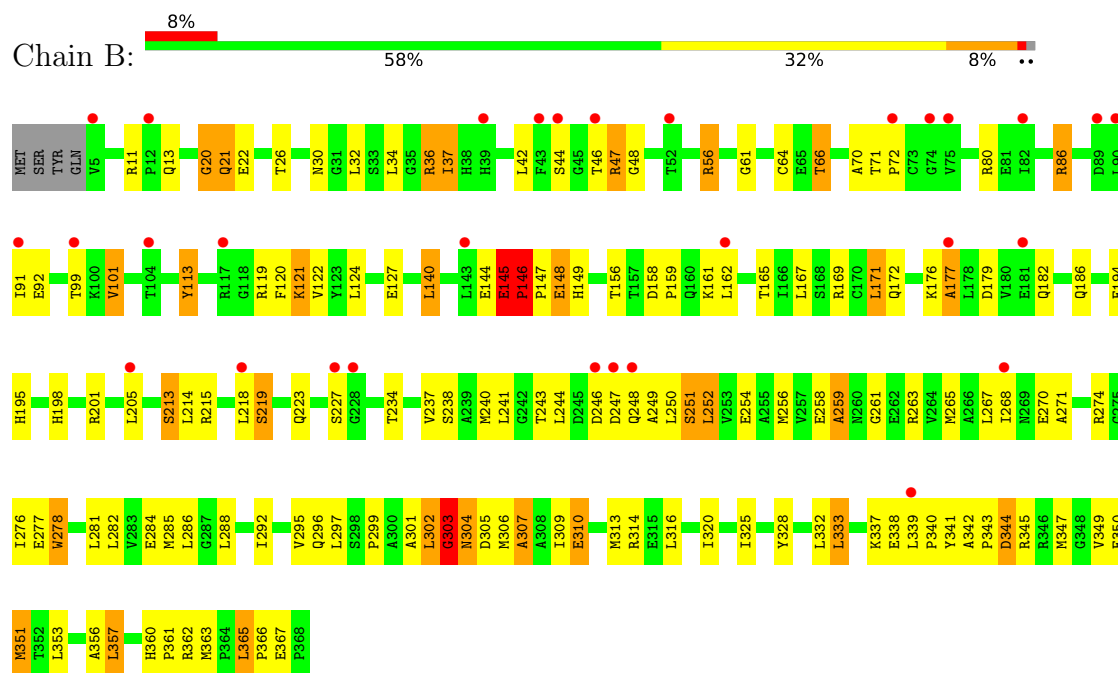


• Molecule 1: DNA polymerase III, delta subunit

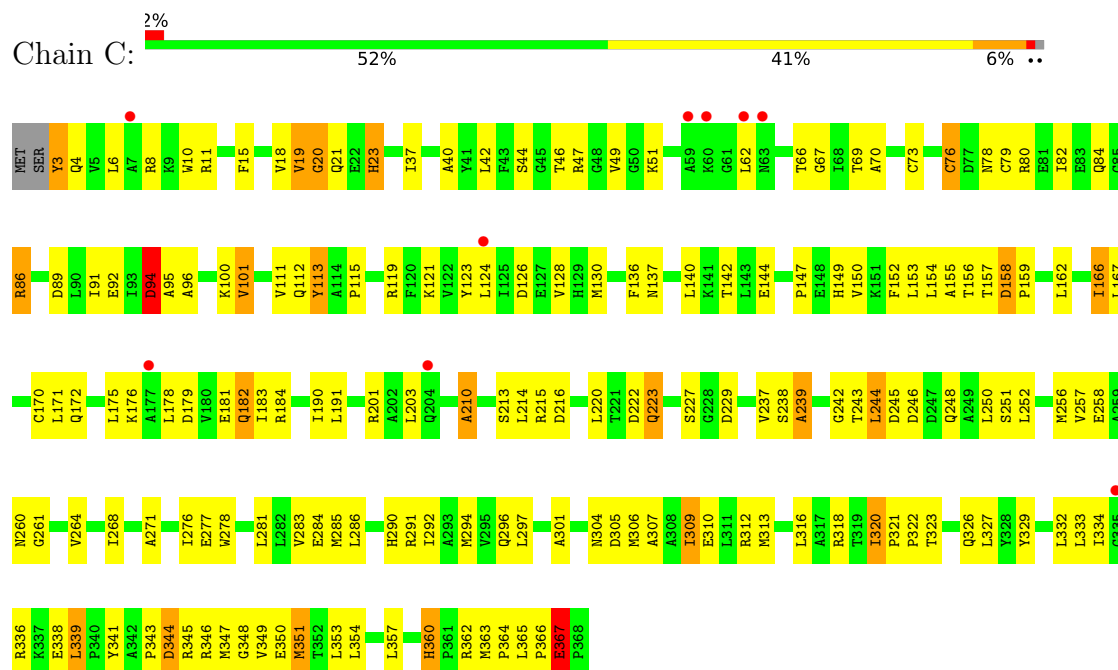




• Molecule 2: DNA polymerase III subunit gamma

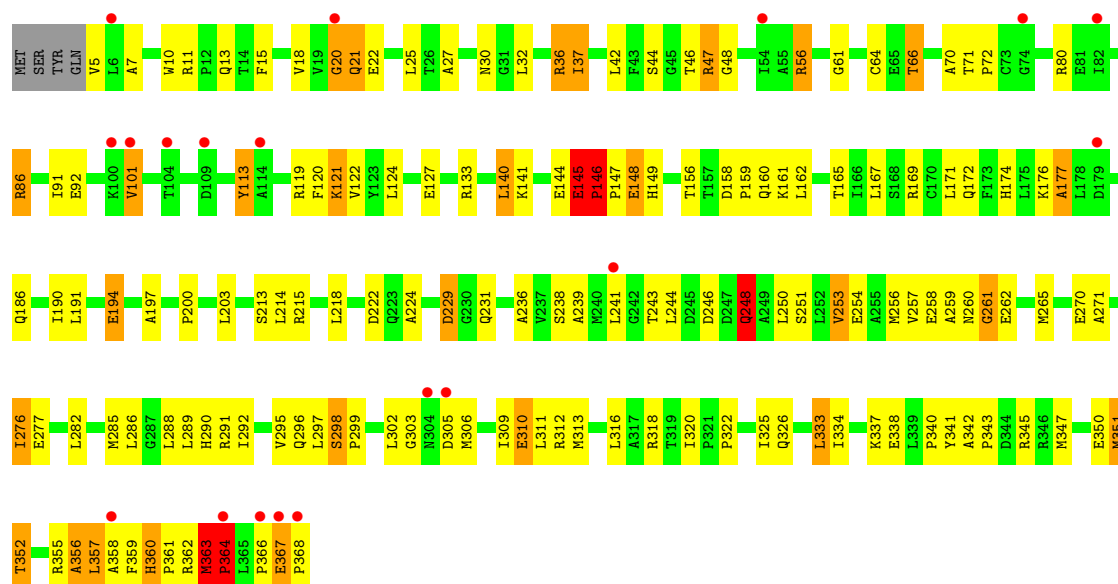


• Molecule 2: DNA polymerase III subunit gamma

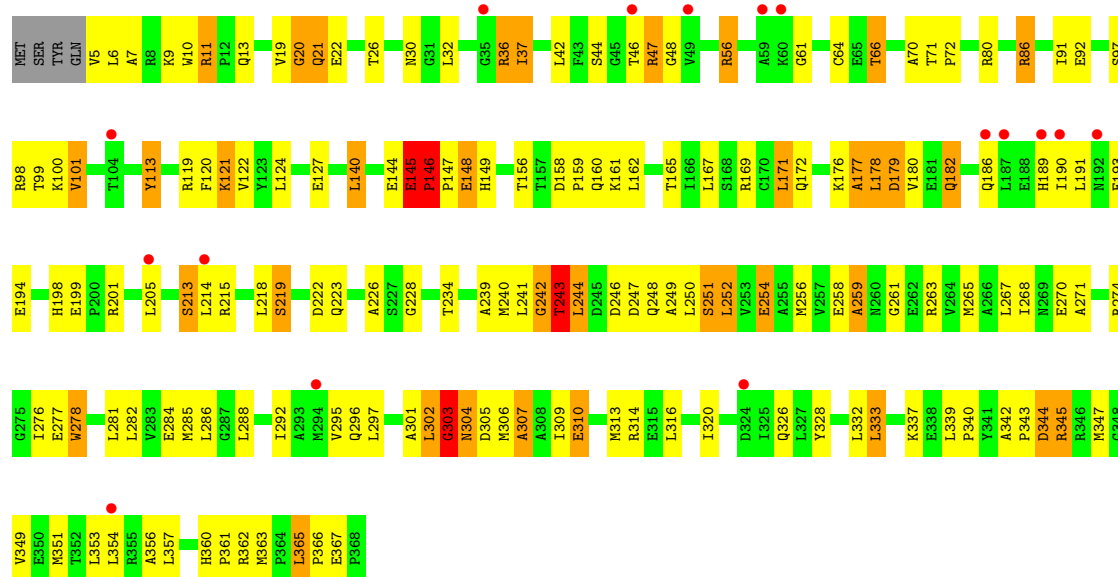


• Molecule 2: DNA polymerase III subunit gamma

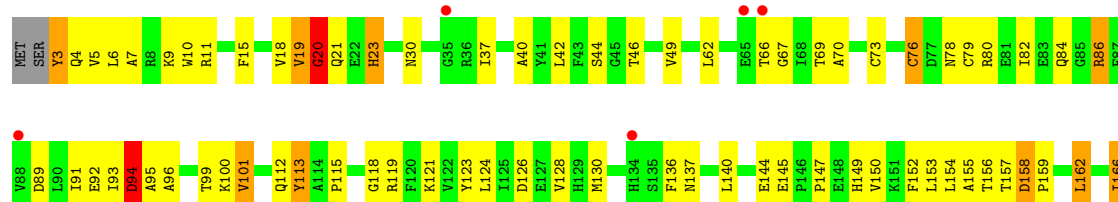


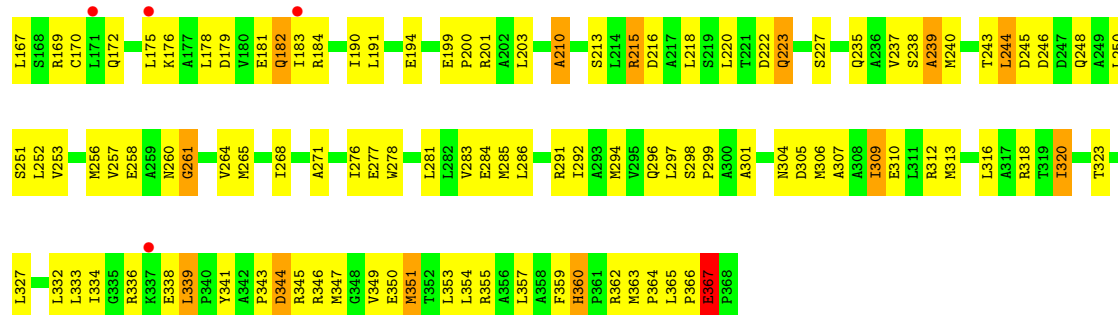


• Molecule 2: DNA polymerase III subunit gamma

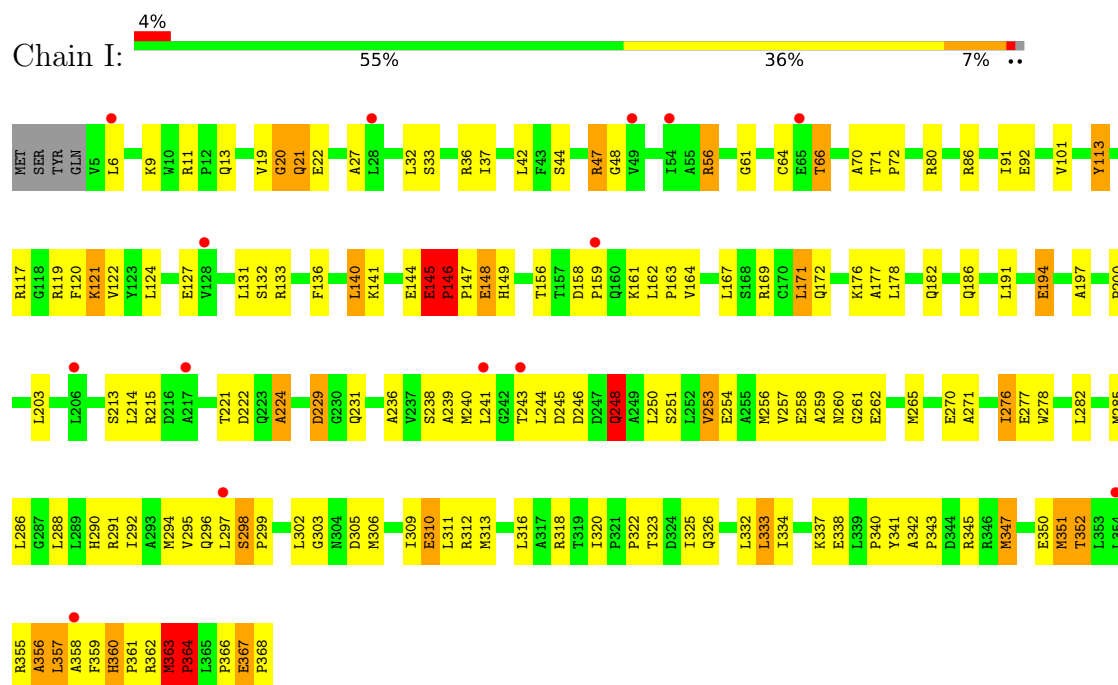


• Molecule 2: DNA polymerase III subunit gamma

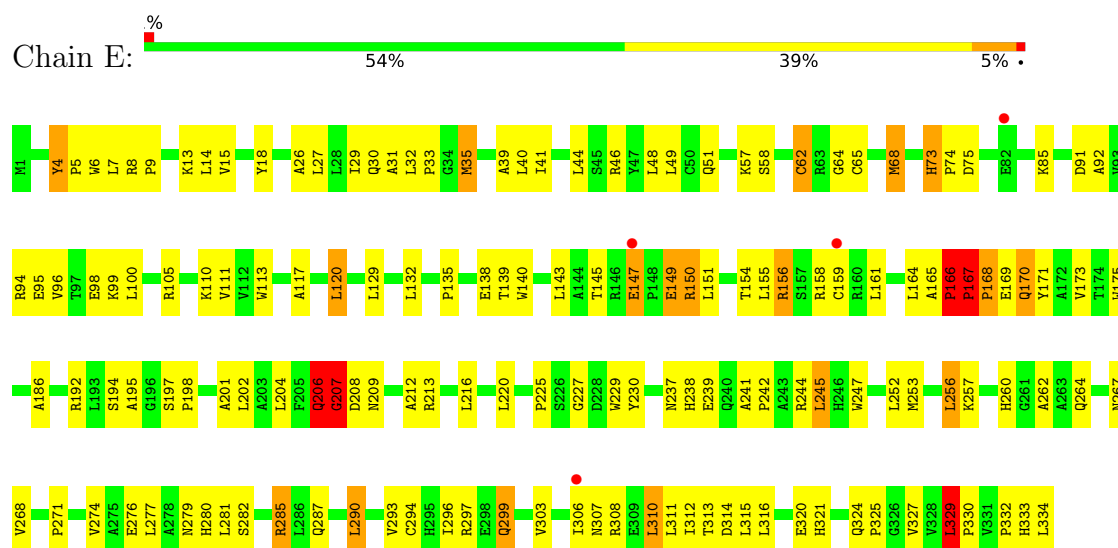




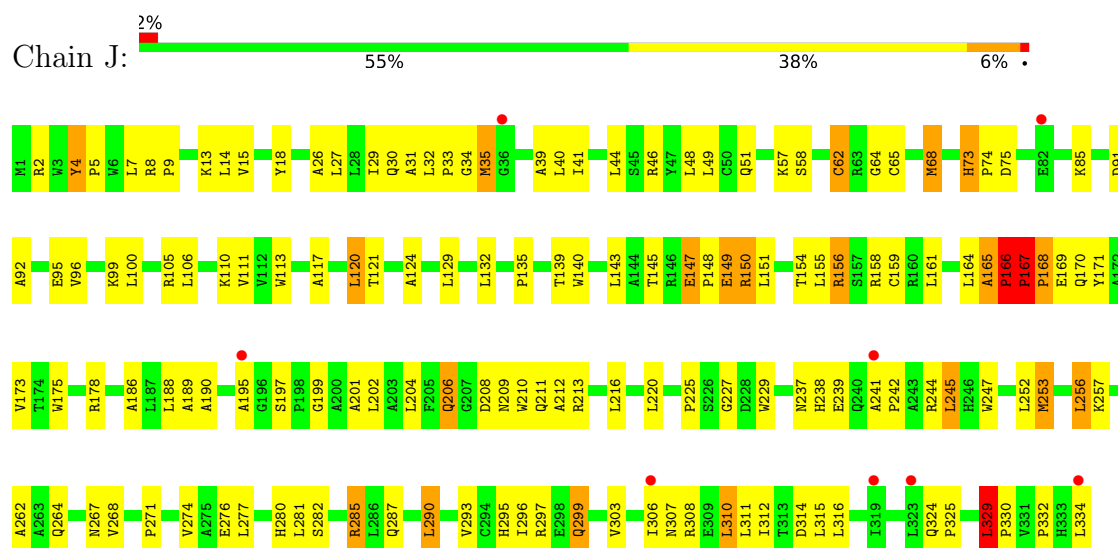
• Molecule 2: DNA polymerase III subunit gamma



• Molecule 3: DNA polymerase III, delta prime subunit



• Molecule 3: DNA polymerase III, delta prime subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	98.21Å 106.57Å 535.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 4.10 20.00 – 4.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-4.10) 87.0 (20.00-4.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.21 (at 4.14Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.366 , 0.369 0.334 , 0.327	Depositor DCC
R_{free} test set	4301 reflections (10.10%)	wwPDB-VP
Wilson B-factor (Å ²)	122.7	Xtriage
Anisotropy	0.504	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 39.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.84	EDS
Total number of atoms	27688	wwPDB-VP
Average B, all atoms (Å ²)	147.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.94% 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: ZN, PO4, ADP

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	9/2735 (0.3%)	1.54	47/3716 (1.3%)
1	F	1.16	26/2735 (1.0%)	1.54	52/3716 (1.4%)
2	B	0.65	4/2876 (0.1%)	1.19	28/3900 (0.7%)
2	C	0.67	3/2898 (0.1%)	1.19	32/3930 (0.8%)
2	D	0.92	10/2876 (0.3%)	1.31	38/3900 (1.0%)
2	G	0.65	6/2876 (0.2%)	1.34	46/3900 (1.2%)
2	H	0.65	3/2898 (0.1%)	1.19	32/3930 (0.8%)
2	I	0.93	12/2876 (0.4%)	1.28	43/3900 (1.1%)
3	E	0.71	0/2667	1.22	22/3639 (0.6%)
3	J	0.70	0/2667	1.23	22/3639 (0.6%)
All	All	0.82	73/28104 (0.3%)	1.31	362/38170 (0.9%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	F	0	4
2	C	0	1
2	H	0	1
All	All	0	10

The worst 5 of 73 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	315	ASP	CB-CG	24.34	2.12	1.52
1	F	315	ASP	CB-CG	24.31	2.12	1.52
2	D	363	MET	SD-CE	19.34	2.27	1.79
2	I	363	MET	SD-CE	19.27	2.27	1.79

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	360	HIS	ND1-CE1	11.54	1.44	1.32

The worst 5 of 362 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	315	ASP	CA-CB-CG	-22.82	89.78	112.60
1	F	315	ASP	CA-CB-CG	-22.81	89.79	112.60
2	G	242	GLY	CA-C-N	-20.20	80.90	121.91
2	G	242	GLY	C-N-CA	-20.20	80.90	121.91
1	A	214	PRO	CA-N-CD	-16.06	89.52	112.00

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	280	GLN	Peptide
1	A	281	ASN	Mainchain
1	A	282	ARG	Mainchain
1	A	319	SER	Mainchain
2	C	94	ASP	Mainchain

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	2687	0	2743	342	4
1	F	2687	0	2735	398	10
2	B	2829	0	2877	201	6
2	C	2850	0	2896	215	0
2	D	2829	0	2878	279	4
2	G	2829	0	2871	278	0
2	H	2850	0	2894	274	0
2	I	2829	0	2878	337	6
3	E	2602	0	2603	159	6
3	J	2602	0	2603	175	4
4	B	1	0	0	0	0
4	C	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
4	I	1	0	0	0	0
4	J	1	0	0	0	0
5	B	27	0	12	8	0
5	D	27	0	12	5	0
5	I	27	0	12	28	0
6	C	5	0	0	3	0
All	All	27688	0	28014	2210	20

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 40.

The worst 5 of 2210 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:D:277:GLU:HB3	3:E:149:GLU:CG	1.26	1.66
2:G:10:TRP:HZ2	2:G:193:GLU:CB	0.98	1.59
1:A:29:LEU:CD2	1:A:154:ARG:HH12	1.08	1.58
1:F:71:MET:HB3	1:F:108:LEU:CD1	1.23	1.58
1:A:65:PHE:CE1	1:A:99:THR:HG21	1.06	1.58

The worst 5 of 20 symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:227:LYS:NZ	2:D:368:PRO:CG[4_455]	0.40	1.80
2:B:299:PRO:CG	3:E:279:ASN:ND2[4_455]	1.13	1.07
1:F:119:LYS:CB	2:I:117:ARG:NH2[1_455]	1.25	0.95
1:A:227:LYS:NZ	2:D:368:PRO:CD[4_455]	1.29	0.91
1:A:227:LYS:CE	2:D:368:PRO:CG[4_455]	1.51	0.69

5.3 Torsion angles

5.3.1 Protein backbone

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	336/343 (98%)	302 (90%)	24 (7%)	10 (3%)	3	25
1	F	336/343 (98%)	294 (88%)	32 (10%)	10 (3%)	3	25
2	B	362/368 (98%)	340 (94%)	16 (4%)	6 (2%)	7	36
2	C	364/368 (99%)	336 (92%)	24 (7%)	4 (1%)	11	44
2	D	362/368 (98%)	335 (92%)	19 (5%)	8 (2%)	5	31
2	G	362/368 (98%)	338 (93%)	18 (5%)	6 (2%)	7	36
2	H	364/368 (99%)	336 (92%)	24 (7%)	4 (1%)	11	44
2	I	362/368 (98%)	335 (92%)	22 (6%)	5 (1%)	9	39
3	E	332/334 (99%)	301 (91%)	28 (8%)	3 (1%)	14	49
3	J	332/334 (99%)	300 (90%)	30 (9%)	2 (1%)	21	58
All	All	3512/3562 (99%)	3217 (92%)	237 (7%)	58 (2%)	7	36

5 of 58 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	279	TRP
2	B	310	GLU
2	C	20	GLY
2	C	364	PRO
2	D	261	GLY

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	
1	A	287/291 (99%)	251 (88%)	36 (12%)	4	19
1	F	287/291 (99%)	253 (88%)	34 (12%)	5	21
2	B	301/305 (99%)	280 (93%)	21 (7%)	14	38
2	C	303/305 (99%)	286 (94%)	17 (6%)	19	43
2	D	301/305 (99%)	279 (93%)	22 (7%)	13	36
2	G	301/305 (99%)	278 (92%)	23 (8%)	12	35
2	H	303/305 (99%)	285 (94%)	18 (6%)	18	42
2	I	301/305 (99%)	279 (93%)	22 (7%)	13	36
3	E	270/270 (100%)	237 (88%)	33 (12%)	5	20
3	J	270/270 (100%)	237 (88%)	33 (12%)	5	20
All	All	2924/2952 (99%)	2665 (91%)	259 (9%)	9	30

5 of 259 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	J	110	LYS
3	J	166	PRO
3	E	15	VAL
2	D	357	LEU
3	J	202	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 92 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	297	GLN
2	H	149	HIS
1	F	318	GLN
2	G	189	HIS
2	H	360	HIS

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 12 ligands modelled in this entry, 8 are monoatomic - leaving 4 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	ADP	I	803	-	28,29,29	1.50	6 (21%)	43,45,45	1.21	6 (13%)
6	PO4	C	1300	-	4,4,4	1.43	1 (25%)	6,6,6	0.90	0
5	ADP	D	801	-	28,29,29	1.50	7 (25%)	43,45,45	1.21	6 (13%)
5	ADP	B	802	-	28,29,29	1.49	6 (21%)	43,45,45	1.21	6 (13%)

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	ADP	I	803	-	-	3/16/32/32	0/3/3/3
5	ADP	D	801	-	-	3/16/32/32	0/3/3/3
5	ADP	B	802	-	-	3/16/32/32	0/3/3/3

The worst 5 of 20 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	803	ADP	C2-N1	2.95	1.39	1.33
5	B	802	ADP	C2-N1	2.93	1.39	1.33
5	D	801	ADP	C2-N1	2.86	1.39	1.33
5	D	801	ADP	C5-C4	2.83	1.44	1.39
5	I	803	ADP	C5-C4	2.78	1.44	1.39

The worst 5 of 18 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	I	803	ADP	C4-N9-C1'	3.48	134.77	126.63
5	B	802	ADP	C4-N9-C1'	3.47	134.74	126.63
5	D	801	ADP	C4-N9-C1'	3.45	134.69	126.63
5	I	803	ADP	C4-N9-C8	-2.36	103.26	105.74
5	B	802	ADP	C4-N9-C8	-2.34	103.28	105.74

There are no chirality outliers.

5 of 9 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	B	802	ADP	C5'-O5'-PA-O3A
5	D	801	ADP	C5'-O5'-PA-O1A
5	D	801	ADP	C5'-O5'-PA-O2A
5	D	801	ADP	C5'-O5'-PA-O3A
5	I	803	ADP	C5'-O5'-PA-O3A

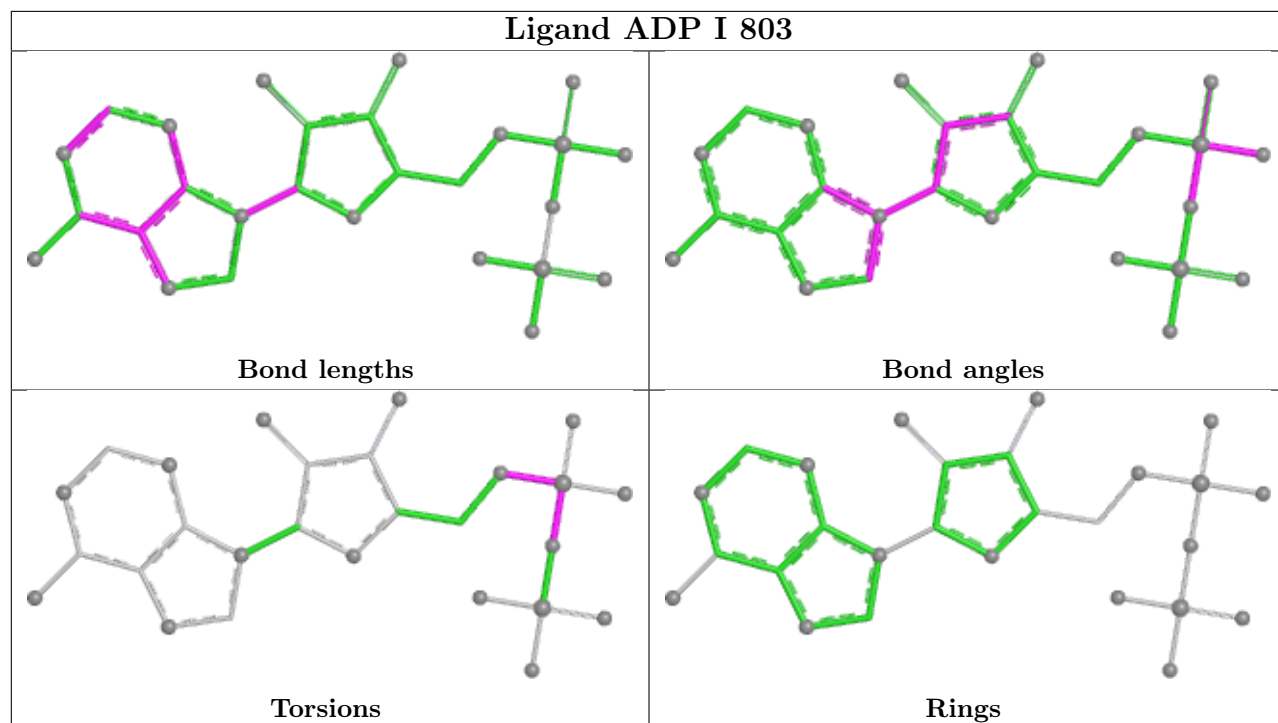
There are no ring outliers.

4 monomers are involved in 44 short contacts:

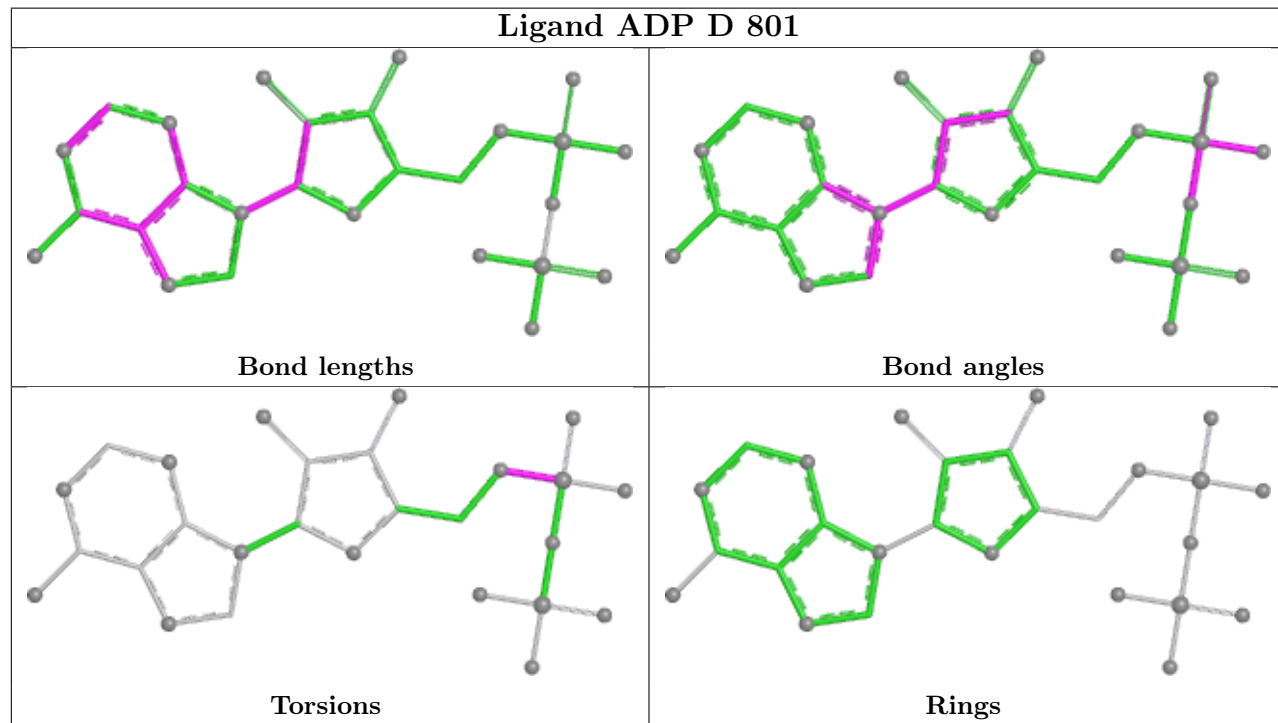
Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	I	803	ADP	28	0
6	C	1300	PO4	3	0
5	D	801	ADP	5	0
5	B	802	ADP	8	0

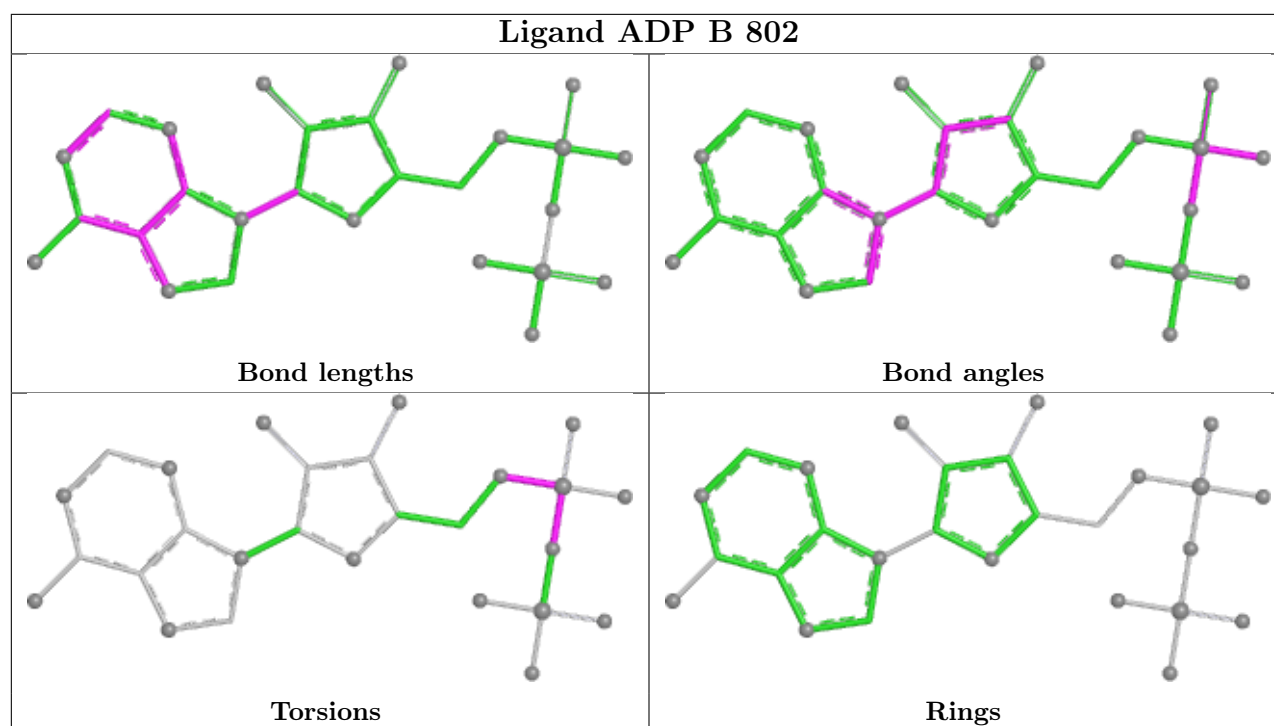
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand ADP I 803



Ligand ADP D 801





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	338/343 (98%)	0.65	14 (4%) 41 33	78, 150, 164, 164	0
1	F	338/343 (98%)	0.50	7 (2%) 63 48	149, 189, 201, 201	0
2	B	364/368 (98%)	0.71	30 (8%) 17 19	41, 130, 151, 151	0
2	C	366/368 (99%)	0.43	9 (2%) 58 44	21, 41, 132, 132	0
2	D	364/368 (98%)	0.62	19 (5%) 33 28	36, 43, 73, 73	0
2	G	364/368 (98%)	0.51	16 (4%) 39 31	176, 263, 290, 290	0
2	H	366/368 (99%)	0.43	9 (2%) 58 44	180, 199, 272, 272	0
2	I	364/368 (98%)	0.40	14 (3%) 44 34	198, 201, 205, 205	0
3	E	334/334 (100%)	0.36	4 (1%) 76 60	37, 55, 98, 98	0
3	J	334/334 (100%)	0.33	8 (2%) 59 45	138, 169, 221, 221	0
All	All	3532/3562 (99%)	0.50	130 (3%) 45 35	21, 150, 272, 290	0

The worst 5 of 130 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	246	ASP	6.3
2	D	104	THR	5.7
2	G	59	ALA	5.5
1	F	338	ASP	5.1
2	B	177	ALA	4.7

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 [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

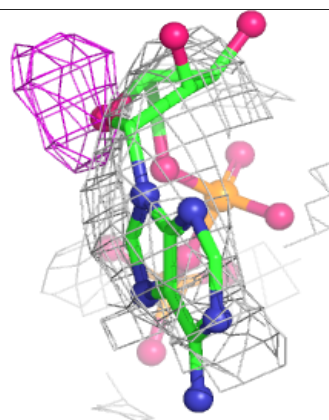
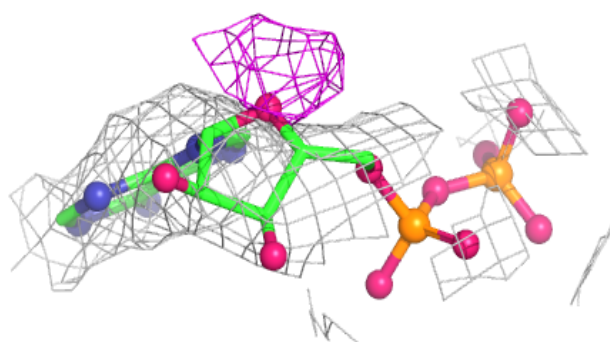
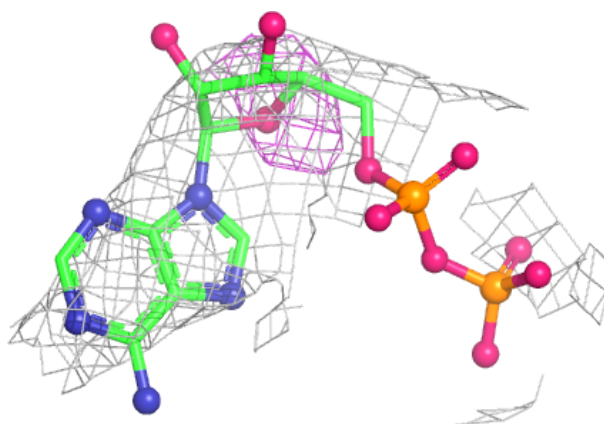
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	ZN	H	405	1/1	0.58	0.19	395,395,395,395	0
4	ZN	J	408	1/1	0.86	0.06	228,228,228,228	0
5	ADP	B	802	27/27	0.87	0.12	68,68,68,68	0
5	ADP	I	803	27/27	0.87	0.12	203,203,203,203	0
4	ZN	I	406	1/1	0.90	0.06	119,119,119,119	0
4	ZN	G	407	1/1	0.90	0.05	350,350,350,350	0
6	PO4	C	1300	5/5	0.90	0.05	58,58,58,58	0
5	ADP	D	801	27/27	0.92	0.12	27,27,27,27	0
4	ZN	E	404	1/1	0.94	0.05	124,124,124,124	0
4	ZN	B	403	1/1	0.95	0.04	138,138,138,138	0
4	ZN	C	401	1/1	0.96	0.04	147,147,147,147	0
4	ZN	D	402	1/1	0.98	0.03	43,43,43,43	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

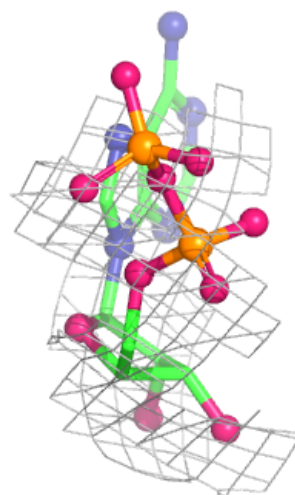
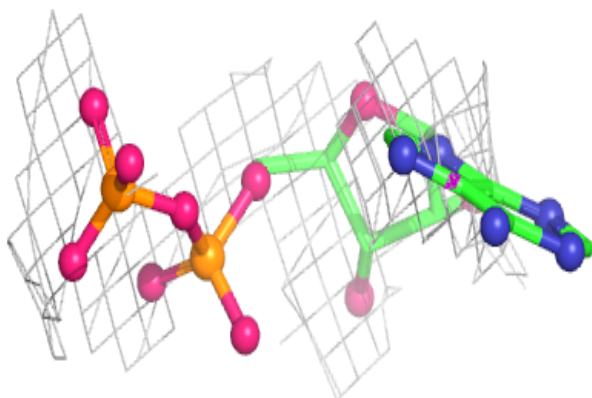
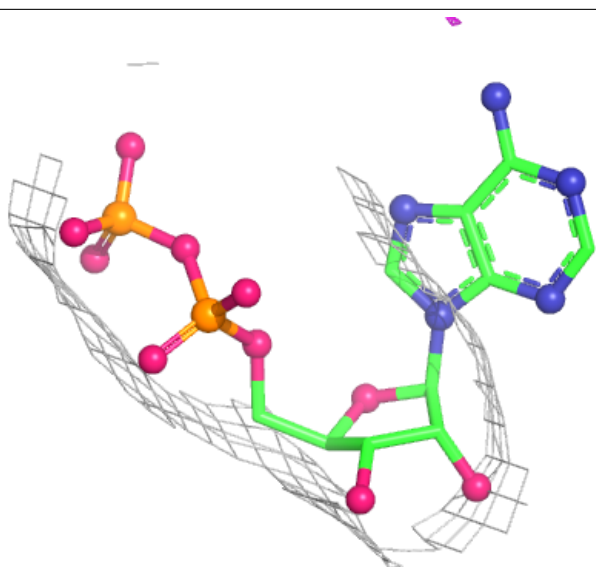
Electron density around ADP B 802:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



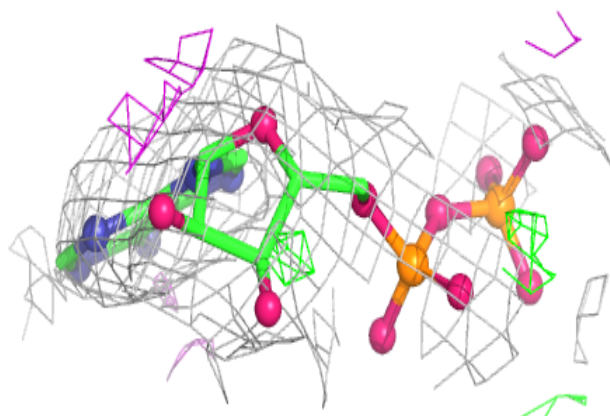
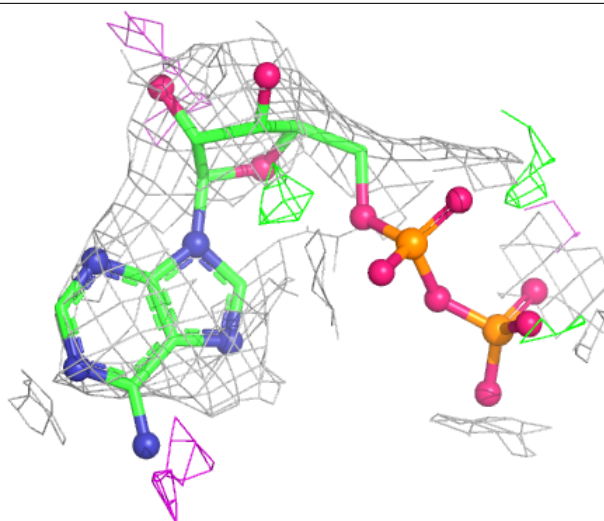
Electron density around ADP I 803:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around ADP D 801:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.5 Other polymers [i](#)

There are no such residues in this entry.