



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 12, 2026 – 08:44 PM UTC

PDB ID : 3T35 / pdb_00003t35
Title : Arabidopsis thaliana dynamin-related protein 1A in postfission state
Authors : Yan, L.M.; Ma, Y.Y.; Sun, Y.N.; Lou, Z.Y.
Deposited on : 2011-07-24
Resolution : 3.59 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

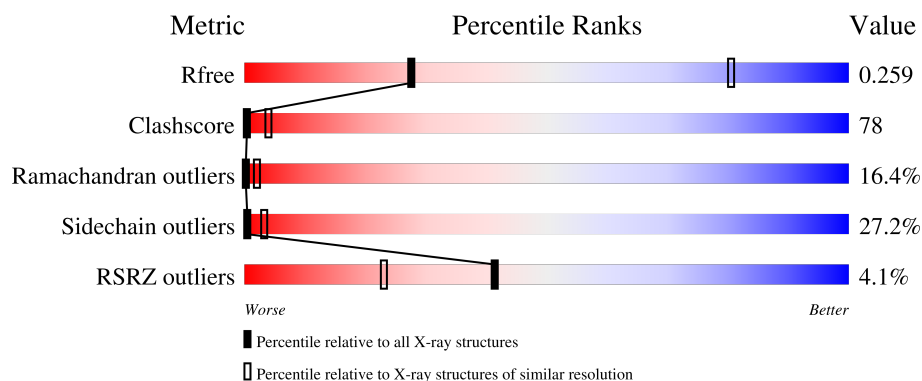
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.59 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	1747 (3.70-3.50)
Clashscore	190562	1827 (3.70-3.50)
Ramachandran outliers	187476	1773 (3.70-3.50)
Sidechain outliers	187428	1772 (3.70-3.50)
RSRZ outliers	180081	1745 (3.70-3.50)

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	360	4% 16% 45% 29% 6%
1	B	360	4% 16% 46% 27% 5% 6%
1	C	360	4% 19% 41% 29% 6% 6%
1	D	360	4% 16% 47% 27% 6% 6%

2 Entry composition [i](#)

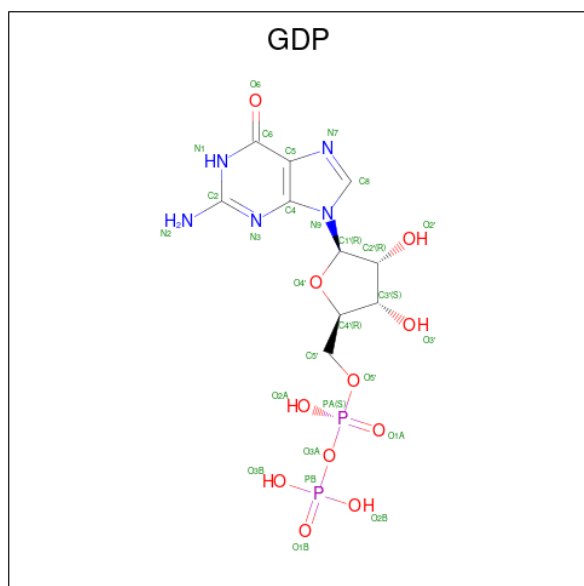
There are 3 unique types of molecules in this entry. The entry contains 11037 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Dynamin-related protein 1A, LINKER, Dynamin-related protein 1A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	339	Total	C	N	O	S	0	0	0
			2636	1649	472	508	7			
1	B	339	Total	C	N	O	S	0	0	0
			2636	1649	472	508	7			
1	C	339	Total	C	N	O	S	0	0	0
			2636	1649	472	508	7			
1	D	339	Total	C	N	O	S	0	0	0
			2636	1649	472	508	7			

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (CCD ID: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
2	B	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	C	1	Total	C	N	O	P	0	0
			28	10	5	11	2		
2	D	1	Total	C	N	O	P	0	0
			28	10	5	11	2		

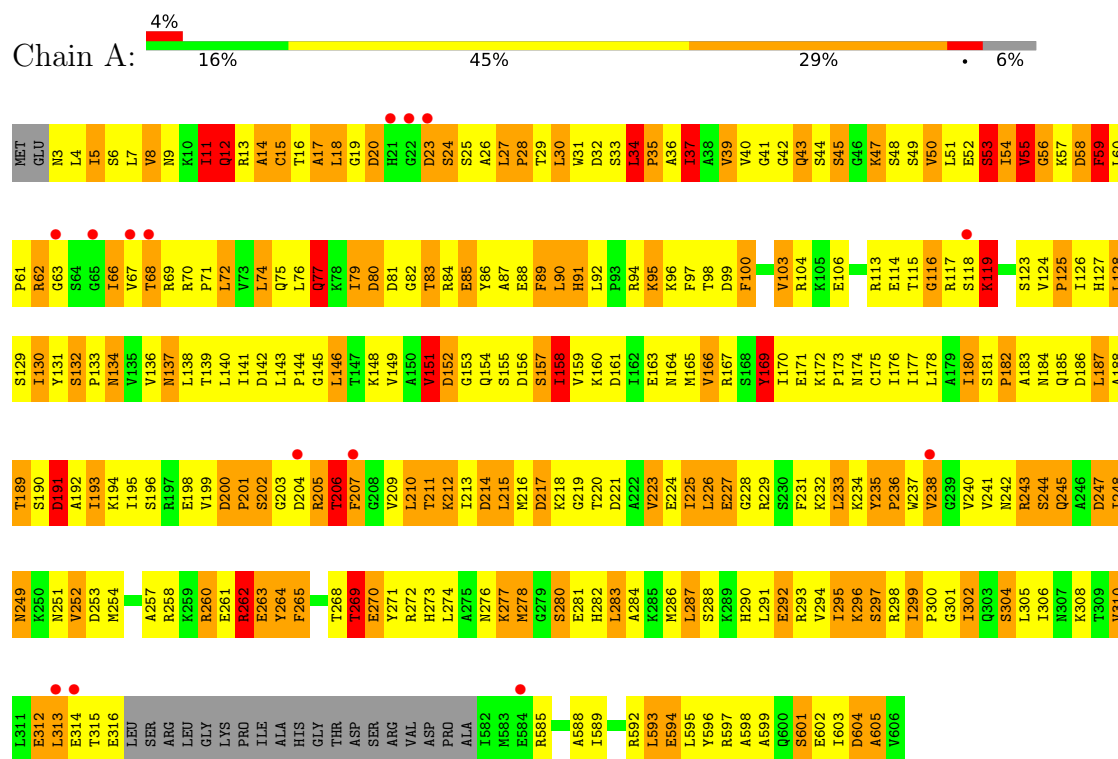
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	87	Total	O	0	0
			87	87		
3	B	121	Total	O	0	0
			121	121		
3	C	93	Total	O	0	0
			93	93		
3	D	80	Total	O	0	0
			80	80		

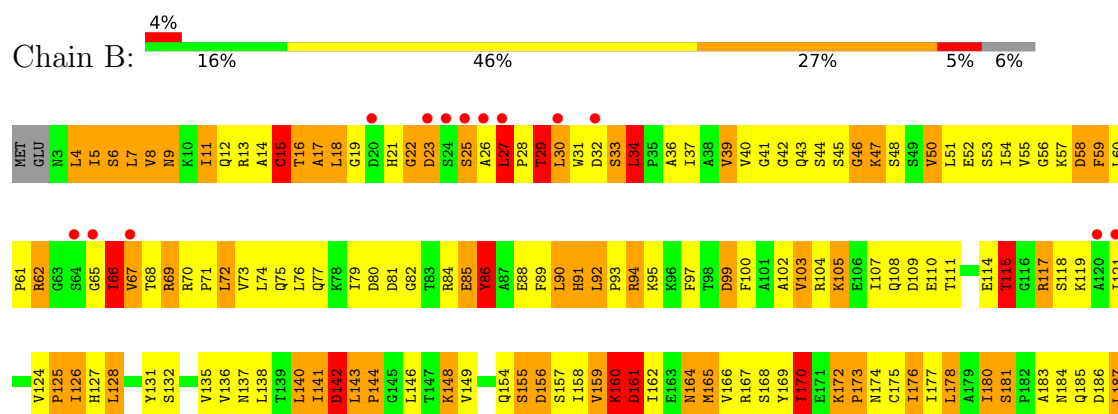
3 Residue-property plots

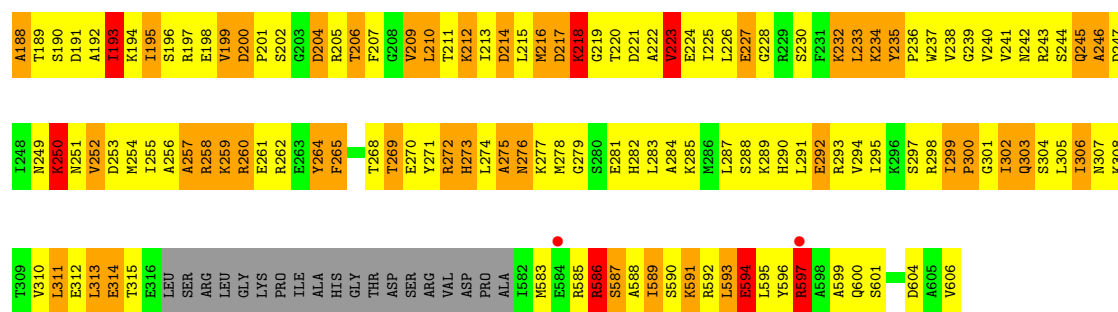
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Dynamin-related protein 1A, LINKER, Dynamin-related protein 1A

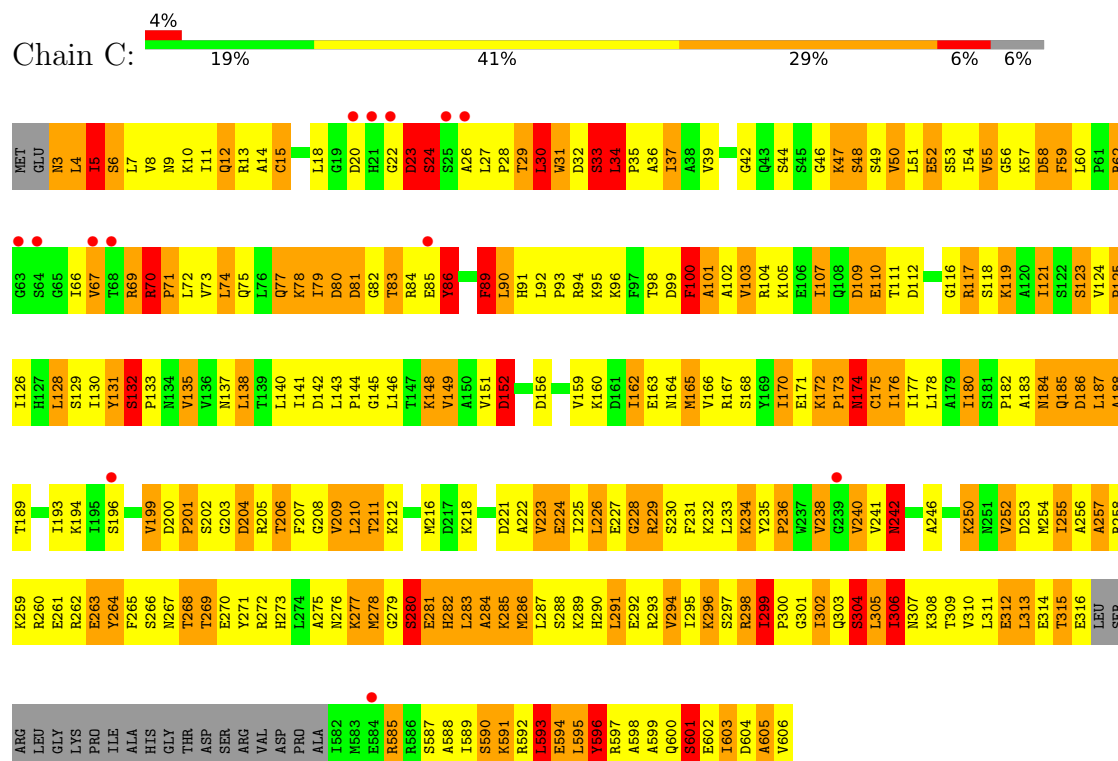


- Molecule 1: Dynamin-related protein 1A, LINKER, Dynamin-related protein 1A

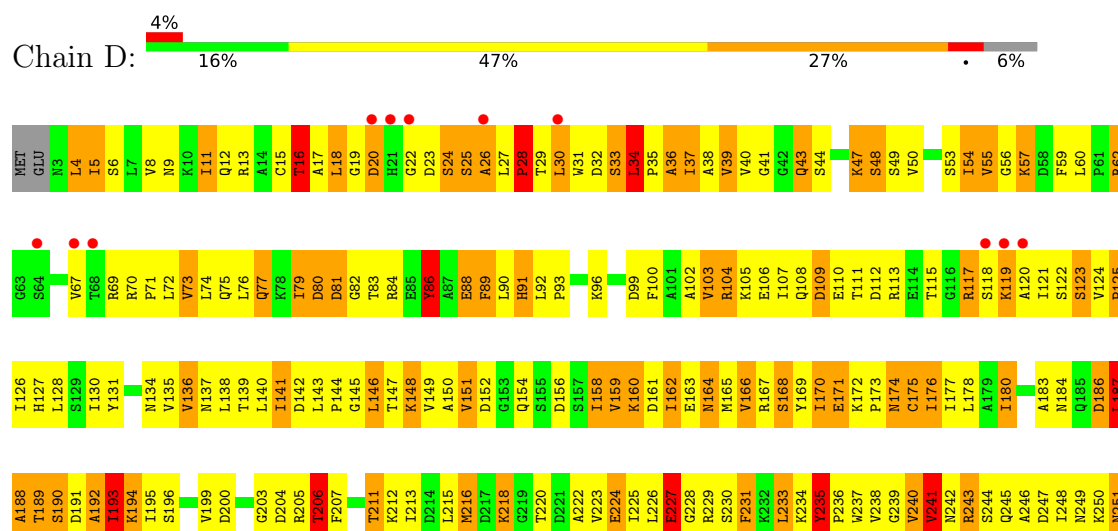




- Molecule 1: Dynamin-related protein 1A, LINKER, Dynamin-related protein 1A



- Molecule 1: Dynamin-related protein 1A, LINKER, Dynamin-related protein 1A



V252	D253	M254	I255	A256	A257	R258	K259	R260	E261	R262	E263	Y264	F265	S266	N267	T268	T269	E270	Y271	R272	H273	L274	A275	N276	K277	G279	S280	E281	H282	L283	A284	K285	M286	L287	S288	K289	H290	L291	E292	R293	V294	I295	K296	R297	R298	I299	P300	G301	I302	Q303	S304	L305	I306	N307	K308	T309	V310	L311
E312	L313	E314	T315	E316	LEU	SER	ARG	LEU	GLY	LYS	PRO	ILE	ALA	HIS	GLY	THR	ASP	SER	ARG	VAL	ASP	PRO	ALA	I582	H583	E584	R585	A588	I589	S590	R591	R592	I593	E594	I595	Y596	R597	A598	A599	D600	S601	E602	I603	D604	A605	Y606												

4 Data and refinement statistics

Property	Value	Source
Space group	P 61	Depositor
Cell constants a, b, c, α , β , γ	146.16Å 146.16Å 204.25Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	43.32 – 3.59 43.32 – 3.59	Depositor EDS
% Data completeness (in resolution range)	87.2 (43.32-3.59) 98.5 (43.32-3.59)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.09 (at 3.57Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.1_357)	Depositor
R, R_{free}	0.238 , 0.291 (Not available) , 0.259	Depositor DCC
R_{free} test set	1464 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	50.3	Xtriage
Anisotropy	0.303	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.23 , 64.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.52$, $\langle L^2 \rangle = 0.35$	Xtriage
Estimated twinning fraction	0.066 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	11037	wwPDB-VP
Average B, all atoms (Å ²)	56.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.60% 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: GDP

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	0.72	1/2671 (0.0%)	1.17	22/3605 (0.6%)
1	B	0.80	3/2671 (0.1%)	1.23	24/3605 (0.7%)
1	C	0.74	0/2671	1.20	31/3605 (0.9%)
1	D	0.67	0/2671	1.15	19/3605 (0.5%)
All	All	0.74	4/10684 (0.0%)	1.19	96/14420 (0.7%)

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	B	0	1
1	D	0	2
All	All	0	3

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	597	ARG	C-N	6.80	1.43	1.33
1	B	193	ILE	CA-CB	-5.42	1.48	1.54
1	B	302	ILE	CA-CB	5.20	1.60	1.54
1	A	37	ILE	CA-CB	-5.09	1.48	1.54

The worst 5 of 96 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	227	GLU	N-CA-C	-11.70	99.49	113.88
1	C	304	SER	N-CA-C	-9.40	101.33	113.17
1	D	235	TYR	CA-C-N	-9.28	108.24	119.84

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	235	TYR	C-N-CA	-9.28	108.24	119.84
1	D	34	LEU	CA-C-N	-9.25	108.28	119.84

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	34	LEU	Peptide
1	D	26	ALA	Peptide
1	D	28	PRO	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	2636	0	2705	439	0
1	B	2636	0	2705	401	1
1	C	2636	0	2705	440	0
1	D	2636	0	2705	441	1
2	A	28	0	12	7	0
2	B	28	0	12	7	0
2	C	28	0	12	6	0
2	D	28	0	12	8	0
3	A	87	0	0	12	0
3	B	121	0	0	18	0
3	C	93	0	0	34	0
3	D	80	0	0	32	0
All	All	11037	0	10868	1683	1

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 78.

The worst 5 of 1683 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:A:276:ASN:OD1	1:A:277:LYS:HD3	1.27	1.24

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:25:SER:O	1:B:308:LYS:CE	1.86	1.23
1:D:32:ASP:O	1:D:35:PRO:HD3	1.44	1.15
1:B:29:THR:HA	1:B:32:ASP:HB2	1.26	1.15
1:A:276:ASN:OD1	1:A:277:LYS:CD	1.95	1.14

All (1) 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:B:234:LYS:NZ	1:D:313:LEU:CD1[1_655]	1.86	0.34

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	335/360 (93%)	201 (60%)	80 (24%)	54 (16%)	0	2
1	B	335/360 (93%)	194 (58%)	81 (24%)	60 (18%)	0	1
1	C	335/360 (93%)	205 (61%)	73 (22%)	57 (17%)	0	2
1	D	335/360 (93%)	192 (57%)	94 (28%)	49 (15%)	0	3
All	All	1340/1440 (93%)	792 (59%)	328 (24%)	220 (16%)	0	2

5 of 220 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	11	ILE
1	A	14	ALA
1	A	43	GLN
1	A	58	ASP
1	A	72	LEU

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	294/313 (94%)	214 (73%)	80 (27%)	0	3
1	B	294/313 (94%)	218 (74%)	76 (26%)	0	4
1	C	294/313 (94%)	209 (71%)	85 (29%)	0	2
1	D	294/313 (94%)	215 (73%)	79 (27%)	0	3
All	All	1176/1252 (94%)	856 (73%)	320 (27%)	0	3

5 of 320 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	299	ILE
1	D	233	LEU
1	C	596	TYR
1	D	135	VAL
1	D	278	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 36 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	290	HIS
1	D	600	GLN
1	C	303	GLN
1	D	185	GLN
1	B	43	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](#)

4 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	$\# Z > 2$
2	GDP	B	9001	-	29,30,30	1.12	2 (6%)	45,47,47	1.86	8 (17%)
2	GDP	A	9001	-	29,30,30	1.23	4 (13%)	45,47,47	2.06	13 (28%)
2	GDP	D	9001	-	29,30,30	1.19	4 (13%)	45,47,47	1.93	10 (22%)
2	GDP	C	9001	-	29,30,30	1.23	4 (13%)	45,47,47	1.84	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
2	GDP	B	9001	-	-	2/16/32/32	0/3/3/3
2	GDP	A	9001	-	-	6/16/32/32	0/3/3/3
2	GDP	D	9001	-	-	5/16/32/32	0/3/3/3
2	GDP	C	9001	-	-	0/16/32/32	0/3/3/3

The worst 5 of 14 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	9001	GDP	C5-C4	3.06	1.47	1.38
2	B	9001	GDP	C5-C4	2.97	1.46	1.38
2	A	9001	GDP	C5-C4	2.90	1.46	1.38
2	C	9001	GDP	C6-N1	-2.83	1.33	1.38
2	A	9001	GDP	C6-N1	-2.77	1.33	1.38

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	9001	GDP	C5-C4-N3	-6.56	117.95	128.39
2	A	9001	GDP	C5-C4-N3	-6.52	118.01	128.39
2	B	9001	GDP	C5-C4-N3	-6.19	118.54	128.39
2	D	9001	GDP	C5-C4-N3	-5.48	119.67	128.39
2	A	9001	GDP	C2-N3-C4	5.30	121.43	112.30

There are no chirality outliers.

5 of 13 torsion outliers are listed below:

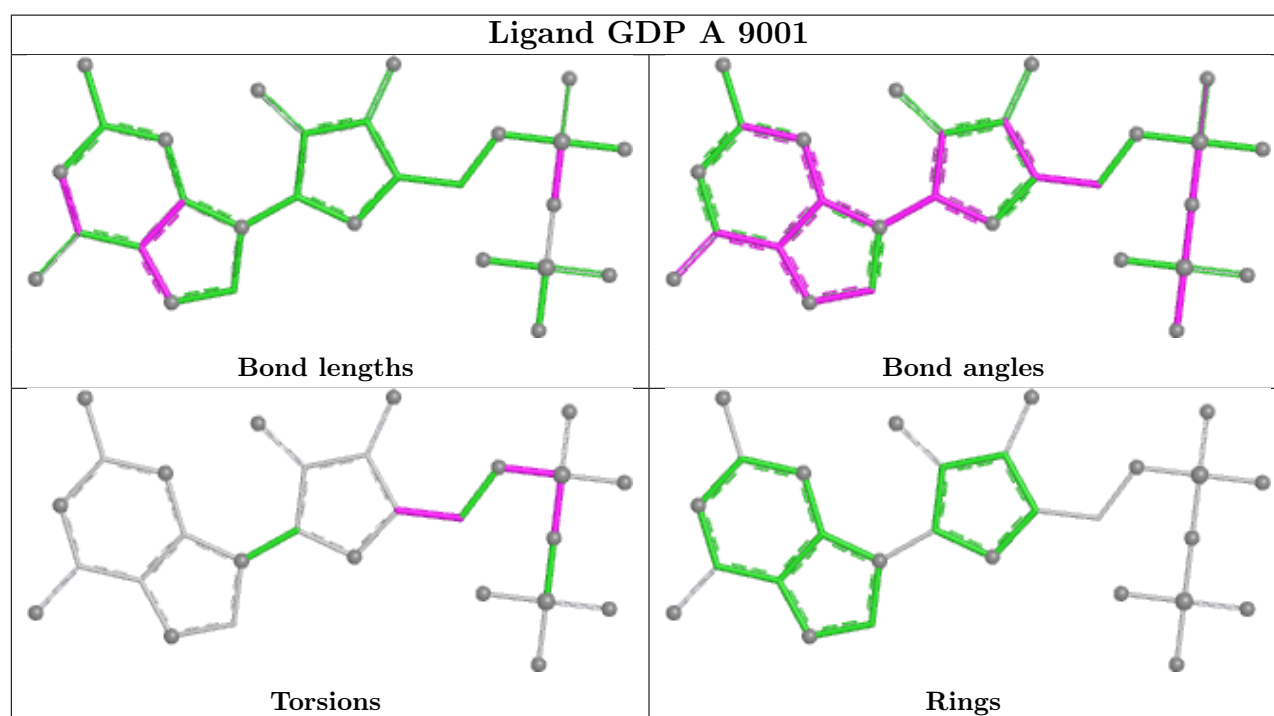
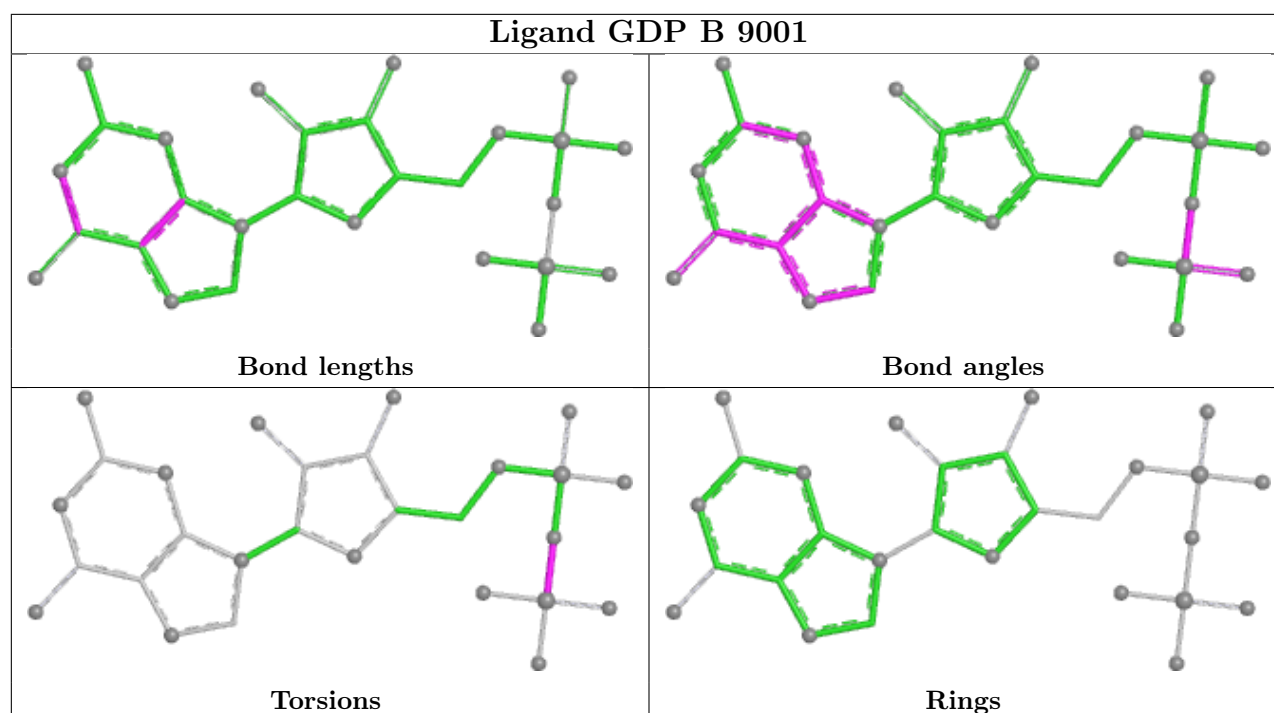
Mol	Chain	Res	Type	Atoms
2	A	9001	GDP	C5'-O5'-PA-O3A
2	A	9001	GDP	O4'-C4'-C5'-O5'
2	D	9001	GDP	C5'-O5'-PA-O3A
2	D	9001	GDP	C5'-O5'-PA-O2A
2	A	9001	GDP	C3'-C4'-C5'-O5'

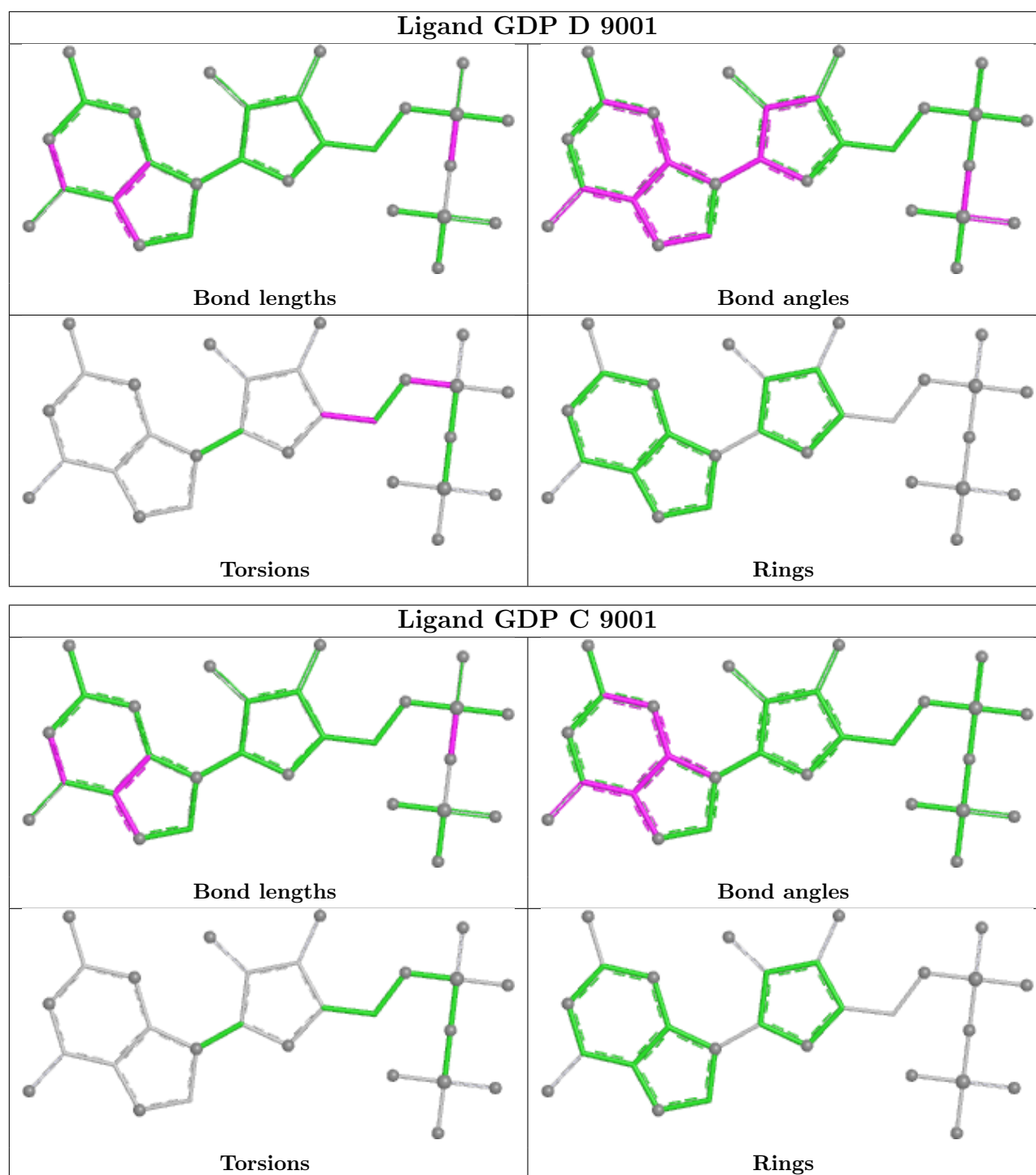
There are no ring outliers.

4 monomers are involved in 28 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	9001	GDP	7	0
2	A	9001	GDP	7	0
2	D	9001	GDP	8	0
2	C	9001	GDP	6	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.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

In the following table, the column labelled ‘#RSRZ> 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q< 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	339/360 (94%)	0.35	14 (4%) 41 23	20, 44, 118, 146	0
1	B	339/360 (94%)	0.17	15 (4%) 39 22	18, 38, 104, 162	0
1	C	339/360 (94%)	0.35	13 (3%) 44 25	22, 51, 130, 174	0
1	D	339/360 (94%)	0.52	13 (3%) 44 25	31, 62, 118, 173	0
All	All	1356/1440 (94%)	0.35	55 (4%) 41 23	18, 48, 118, 174	0

The worst 5 of 55 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	65	GLY	3.9
1	C	21	HIS	3.7
1	C	584	GLU	3.7
1	B	20	ASP	3.5
1	D	584	GLU	3.4

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](#)

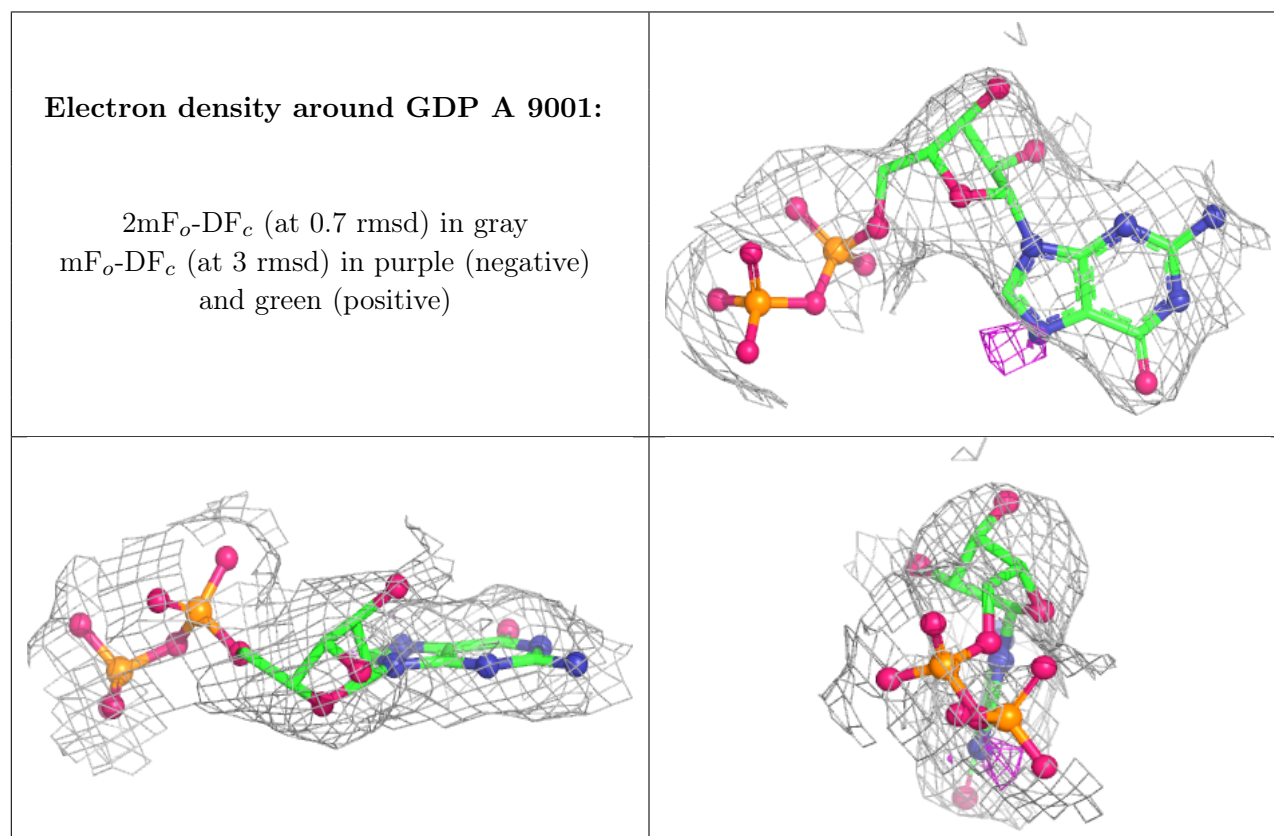
There are no oligosaccharides in this entry.

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.

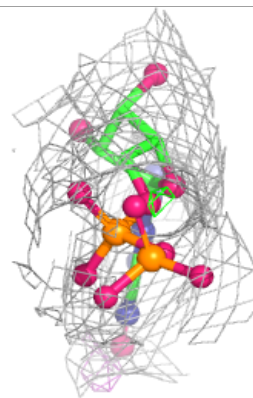
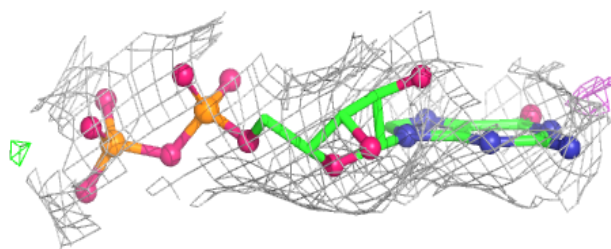
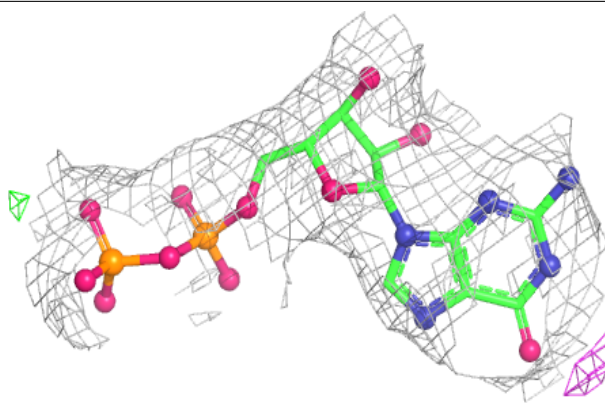
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GDP	A	9001	28/28	0.93	0.11	24,41,56,61	0
2	GDP	D	9001	28/28	0.93	0.09	34,42,47,48	0
2	GDP	C	9001	28/28	0.94	0.10	33,47,52,54	0
2	GDP	B	9001	28/28	0.97	0.07	22,27,33,37	0

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.

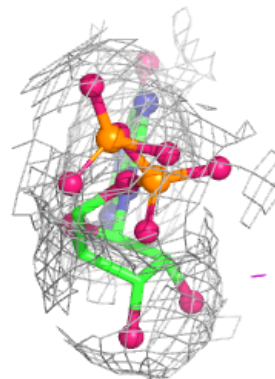
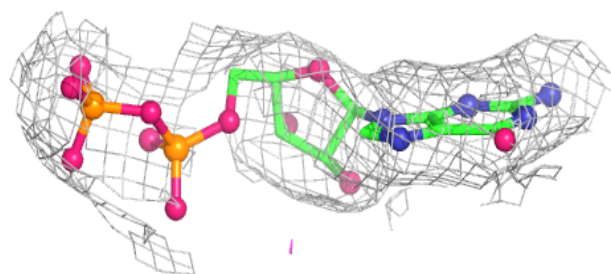


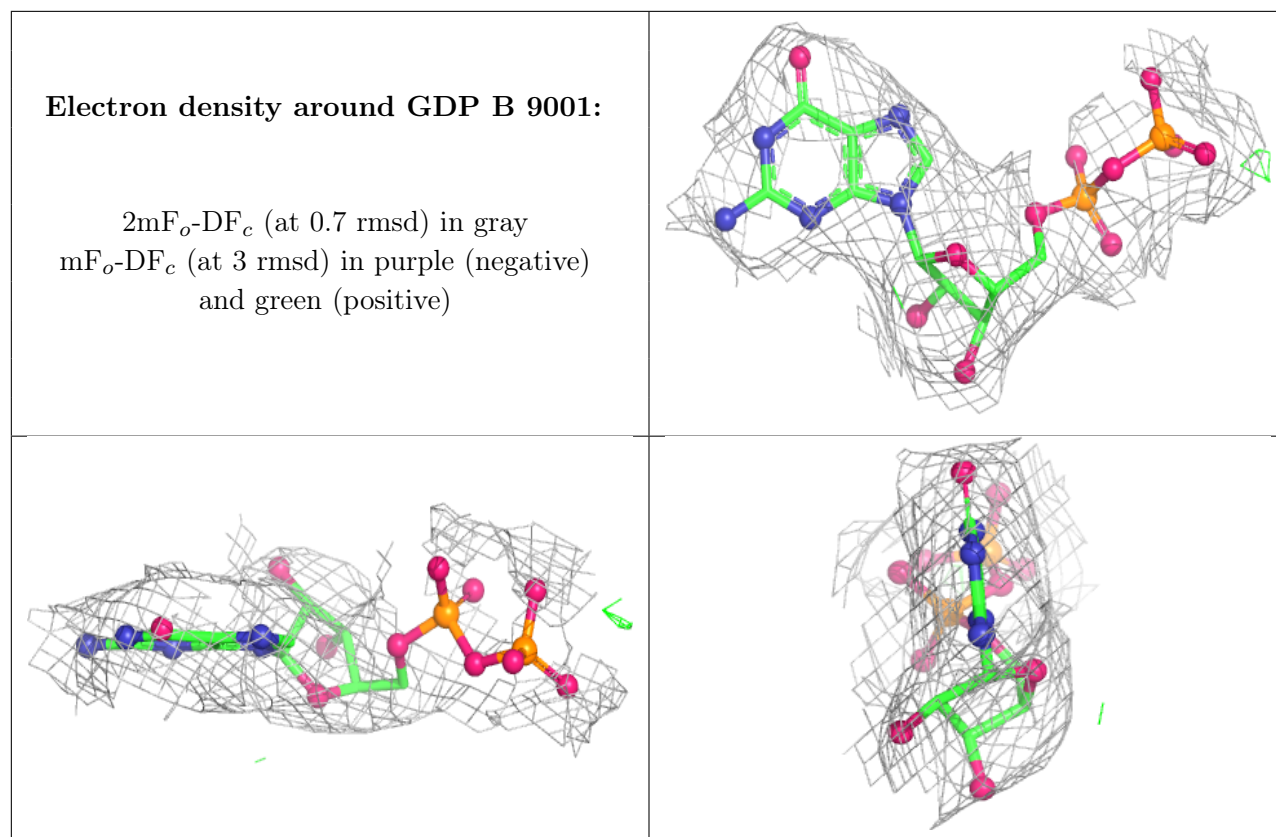
Electron density around GDP D 9001:

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

**Electron density around GDP C 9001:**

$2mF_o-DF_c$ (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.