



wwPDB X-ray Structure Validation Summary Report ⓘ

Nov 1, 2021 – 05:13 PM EDT

PDB ID : 3A58
Title : Crystal structure of Sec3p - Rho1p complex from *Saccharomyces cerevisiae*
Authors : Yamashita, M.; Sato, Y.; Yamagata, A.; Mimura, H.; Yoshikawa, A.; Fukai, S.
Deposited on : 2009-08-03
Resolution : 2.60 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.23.2

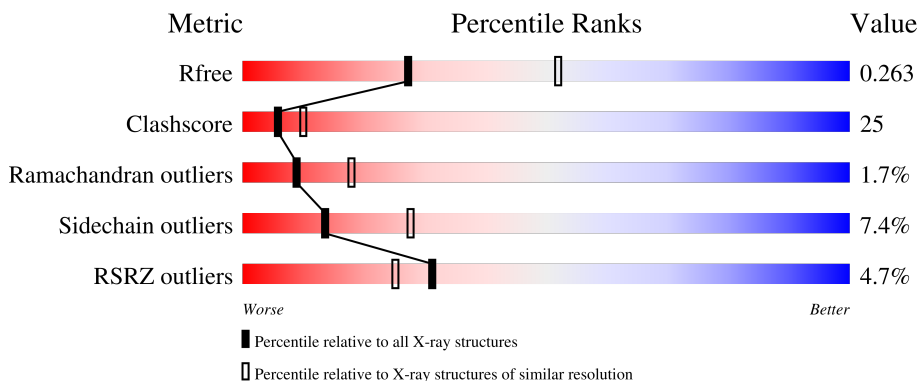
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



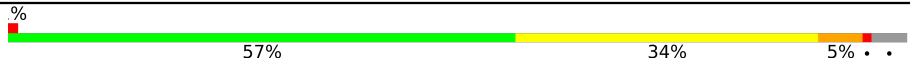
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	320	
1	C	320	
1	E	320	
2	B	188	
2	D	188	

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Mol	Chain	Length	Quality of chain
2	F	188	 <p>A horizontal bar chart representing the quality of chain. The bar is divided into three segments: a green segment on the left labeled '57%', a yellow segment in the middle labeled '34%', and a red segment on the right labeled '5%'. There are two small black dots at the far right end of the bar. A '%' symbol is located at the top left of the bar.</p>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8792 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 Exocyst complex component SEC3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	C	N	O	S				Se
1	A	185	1522	969	268	282	2	1	0	0	0
1	C	180	1485	944	262	276	2	1	0	0	0
1	E	166	1377	882	238	254	2	1	0	0	0

- Molecule 2 is a protein called GTP-binding protein RHO1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	178	1385	871	235	272	7	0	0	0
2	D	178	1385	871	235	272	7	0	0	0
2	F	181	1406	883	240	276	7	0	0	0

There are 3 discrepancies between the modelled and reference sequences:

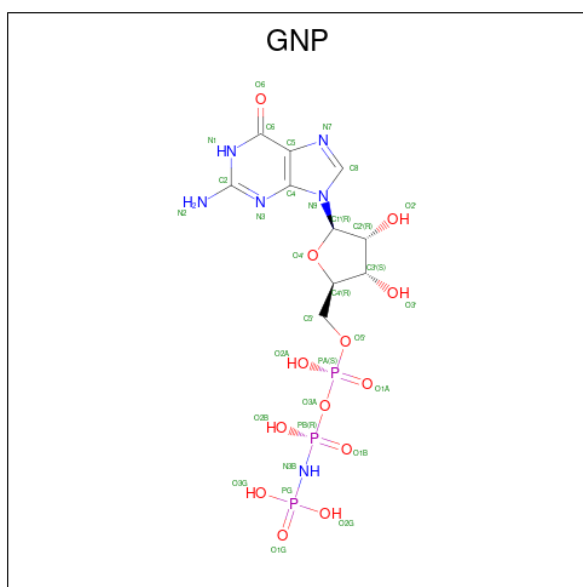
Chain	Residue	Modelled	Actual	Comment	Reference
B	30	ASN	PHE	engineered mutation	UNP P06780
D	30	ASN	PHE	engineered mutation	UNP P06780
F	30	ASN	PHE	engineered mutation	UNP P06780

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O₄P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	C	1	Total O P 5 4 1	0	0
3	E	1	Total O P 5 4 1	0	0

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-GUANYLATE ESTER (three-letter code: GNP) (formula: C₁₀H₁₇N₆O₁₃P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
4	B	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	D	1	Total	C	N	O	P	0	0
			32	10	6	13	3		
4	F	1	Total	C	N	O	P	0	0
			32	10	6	13	3		

- Molecule 5 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Mg		
5	B	1	Total	Mg	0	0
			1	1		
5	D	1	Total	Mg	0	0
			1	1		
5	F	1	Total	Mg	0	0
			1	1		

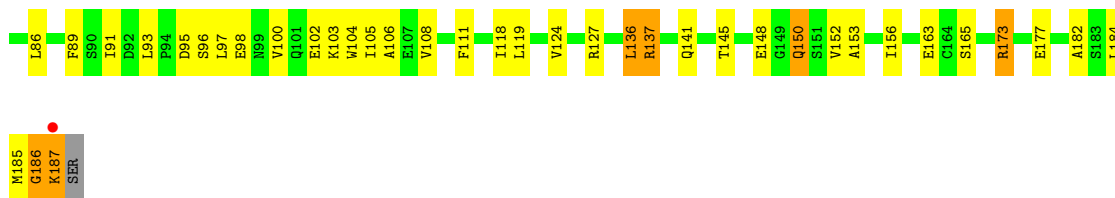
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	29	Total	O	0	0
			29	29		
6	B	7	Total	O	0	0
			7	7		
6	C	24	Total	O	0	0
			24	24		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	D	25	Total 25	O 25	0	0
6	E	6	Total 6	O 6	0	0
6	F	7	Total 7	O 7	0	0



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	116.00Å 116.05Å 247.68Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.85 – 2.60 47.85 – 2.60	Depositor EDS
% Data completeness (in resolution range)	99.8 (47.85-2.60) 99.6 (47.85-2.60)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.02 (at 2.61Å)	Xtrriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.234 , 0.265 0.231 , 0.263	Depositor DCC
R_{free} test set	2663 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	54.4	Xtrriage
Anisotropy	0.159	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 53.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8792	wwPDB-VP
Average B, all atoms (Å ²)	70.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.28% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: PO4, MG, GNP

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	0.45	0/1556	0.67	0/2101
1	C	0.41	0/1518	0.65	0/2049
1	E	0.33	0/1406	0.59	0/1895
2	B	0.38	0/1409	0.64	0/1915
2	D	0.47	0/1409	0.69	0/1915
2	F	0.36	0/1430	0.61	0/1942
All	All	0.40	0/8728	0.64	0/11817

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

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	1522	0	1533	55	0
1	C	1485	0	1488	67	0
1	E	1377	0	1387	113	0
2	B	1385	0	1361	79	0
2	D	1385	0	1360	52	0
2	F	1406	0	1383	87	0
3	A	15	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	C	15	0	0	1	0
3	E	5	0	0	0	0
4	B	32	0	13	2	0
4	D	32	0	13	1	0
4	F	32	0	13	0	0
5	B	1	0	0	0	0
5	D	1	0	0	0	0
5	F	1	0	0	0	0
6	A	29	0	0	0	0
6	B	7	0	0	0	0
6	C	24	0	0	0	0
6	D	25	0	0	4	0
6	E	6	0	0	0	0
6	F	7	0	0	0	0
All	All	8792	0	8551	434	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 25.

The worst 5 of 434 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:34:GLN:HE21	2:D:34:GLN:HA	1.16	1.10
1:C:102:GLY:HA3	2:F:11:ARG:HH22	1.15	1.06
1:E:147:ASN:HD22	1:E:150:LEU:HG	1.16	1.03
1:E:112:VAL:HG11	1:E:209:PHE:HB2	1.41	1.02
2:B:97:LEU:HD11	2:B:152:VAL:HG21	1.40	1.00

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	183/320 (57%)	172 (94%)	9 (5%)	2 (1%)	14	30
1	C	178/320 (56%)	161 (90%)	12 (7%)	5 (3%)	5	7
1	E	162/320 (51%)	144 (89%)	17 (10%)	1 (1%)	25	47
2	B	176/188 (94%)	166 (94%)	7 (4%)	3 (2%)	9	18
2	D	176/188 (94%)	167 (95%)	6 (3%)	3 (2%)	9	18
2	F	179/188 (95%)	166 (93%)	9 (5%)	4 (2%)	6	12
All	All	1054/1524 (69%)	976 (93%)	60 (6%)	18 (2%)	9	18

5 of 18 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	80	PRO
1	C	97	PRO
2	D	80	PRO
2	F	80	PRO
1	C	160	SER

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	172/290 (59%)	159 (92%)	13 (8%)	13	26
1	C	167/290 (58%)	151 (90%)	16 (10%)	8	16
1	E	155/290 (53%)	148 (96%)	7 (4%)	27	52
2	B	153/161 (95%)	145 (95%)	8 (5%)	23	46
2	D	153/161 (95%)	137 (90%)	16 (10%)	7	13
2	F	155/161 (96%)	144 (93%)	11 (7%)	14	29
All	All	955/1353 (71%)	884 (93%)	71 (7%)	13	28

5 of 71 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	192	MSE

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Mol	Chain	Res	Type
1	E	241	ARG
2	F	93	LEU
1	C	172	LEU
1	C	171	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 39 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	147	ASN
2	F	141	GLN
1	E	152	GLN
2	F	68	GLN
2	F	150	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 13 ligands modelled in this entry, 3 are monoatomic - leaving 10 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
3	PO4	C	322	-	4,4,4	1.67	0	6,6,6	0.46	0
4	GNP	B	301	5	28,34,34	2.36	8 (28%)	30,54,54	2.14	8 (26%)
3	PO4	A	322	-	4,4,4	1.64	0	6,6,6	0.42	0
4	GNP	D	301	5	28,34,34	2.25	9 (32%)	30,54,54	2.09	8 (26%)
3	PO4	C	321	-	4,4,4	1.61	0	6,6,6	0.46	0
3	PO4	E	321	-	4,4,4	1.60	0	6,6,6	0.43	0
3	PO4	A	321	-	4,4,4	1.63	0	6,6,6	0.43	0
3	PO4	A	323	-	4,4,4	1.62	0	6,6,6	0.42	0
4	GNP	F	301	5	28,34,34	2.57	9 (32%)	30,54,54	2.17	9 (30%)
3	PO4	C	323	-	4,4,4	1.67	0	6,6,6	0.44	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	GNP	F	301	5	-	5/17/38/38	0/3/3/3
4	GNP	D	301	5	-	5/17/38/38	0/3/3/3
4	GNP	B	301	5	-	4/17/38/38	0/3/3/3

The worst 5 of 26 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	F	301	GNP	C4-N9	-7.11	1.38	1.47
4	B	301	GNP	C4-N9	-6.89	1.38	1.47
4	D	301	GNP	C4-N9	-6.15	1.39	1.47
4	B	301	GNP	C6-N1	5.65	1.42	1.33
4	F	301	GNP	PB-O3A	-5.50	1.52	1.59

The worst 5 of 25 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	F	301	GNP	C4-C5-N7	6.26	110.76	102.46
4	B	301	GNP	C4-C5-N7	6.24	110.73	102.46
4	D	301	GNP	C4-C5-N7	5.97	110.37	102.46
4	B	301	GNP	C5-C6-N1	-4.48	112.67	118.19
4	D	301	GNP	C5-C6-N1	-4.40	112.76	118.19

There are no chirality outliers.

5 of 14 torsion outliers are listed below:

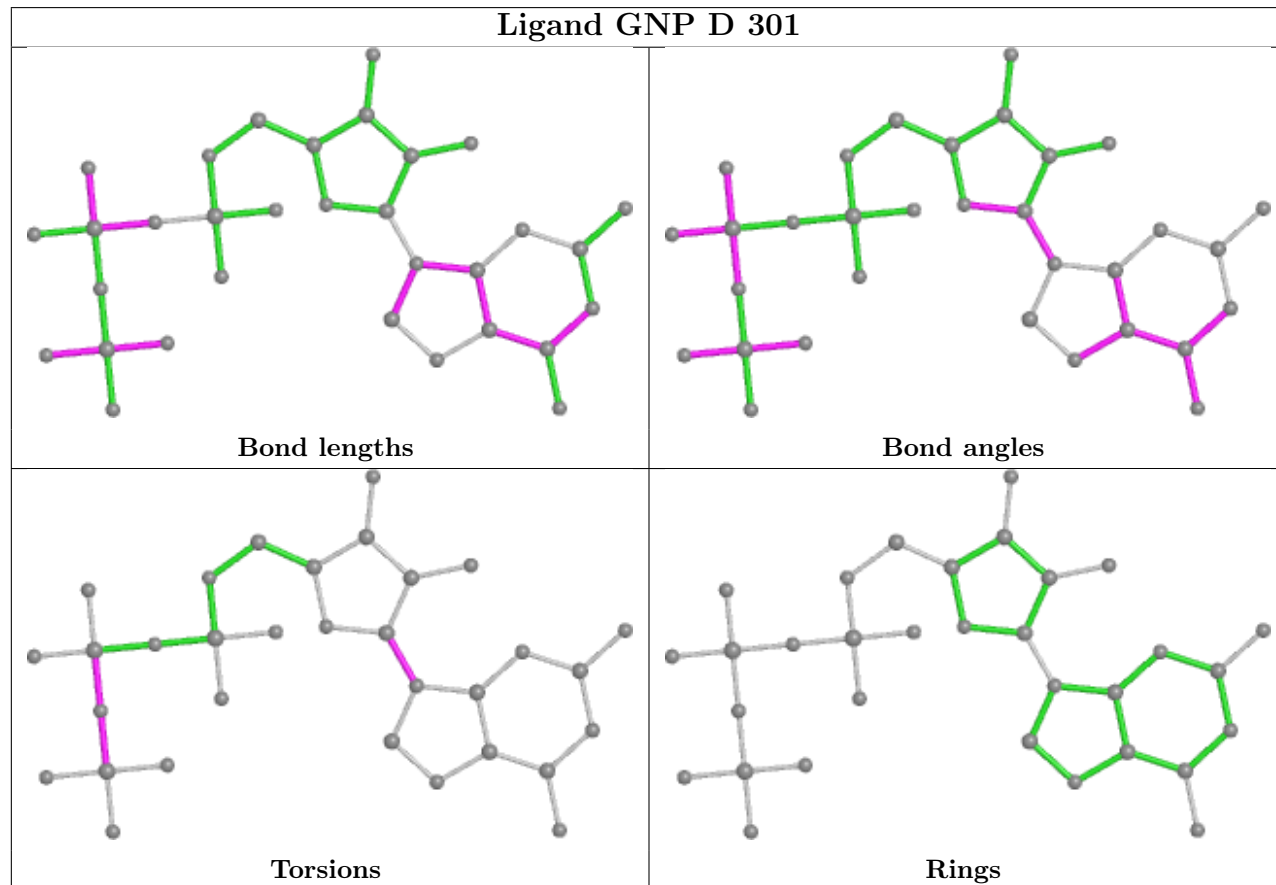
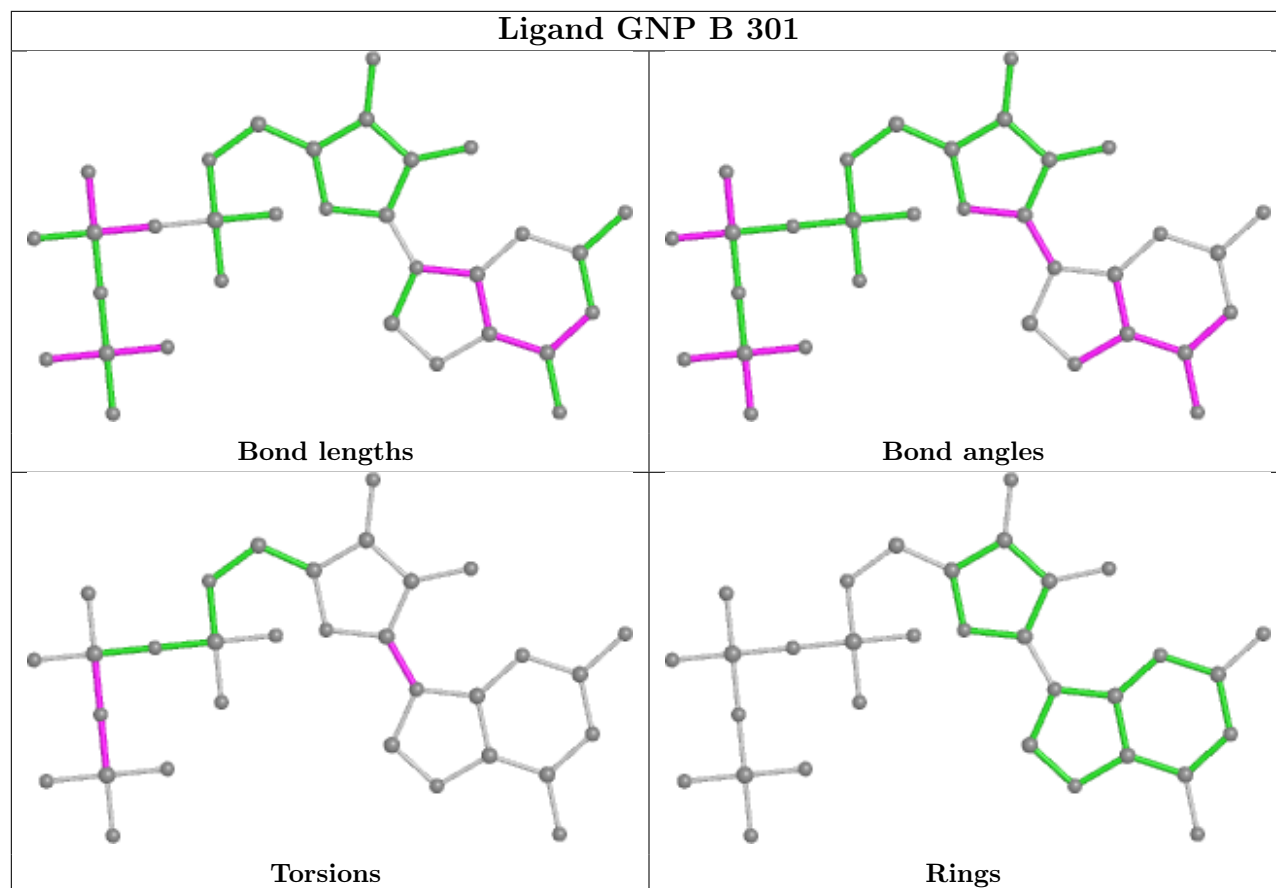
Mol	Chain	Res	Type	Atoms
4	B	301	GNP	PB-N3B-PG-O1G
4	B	301	GNP	PG-N3B-PB-O1B
4	B	301	GNP	PG-N3B-PB-O3A
4	B	301	GNP	C2'-C1'-N9-C4
4	D	301	GNP	PB-N3B-PG-O1G

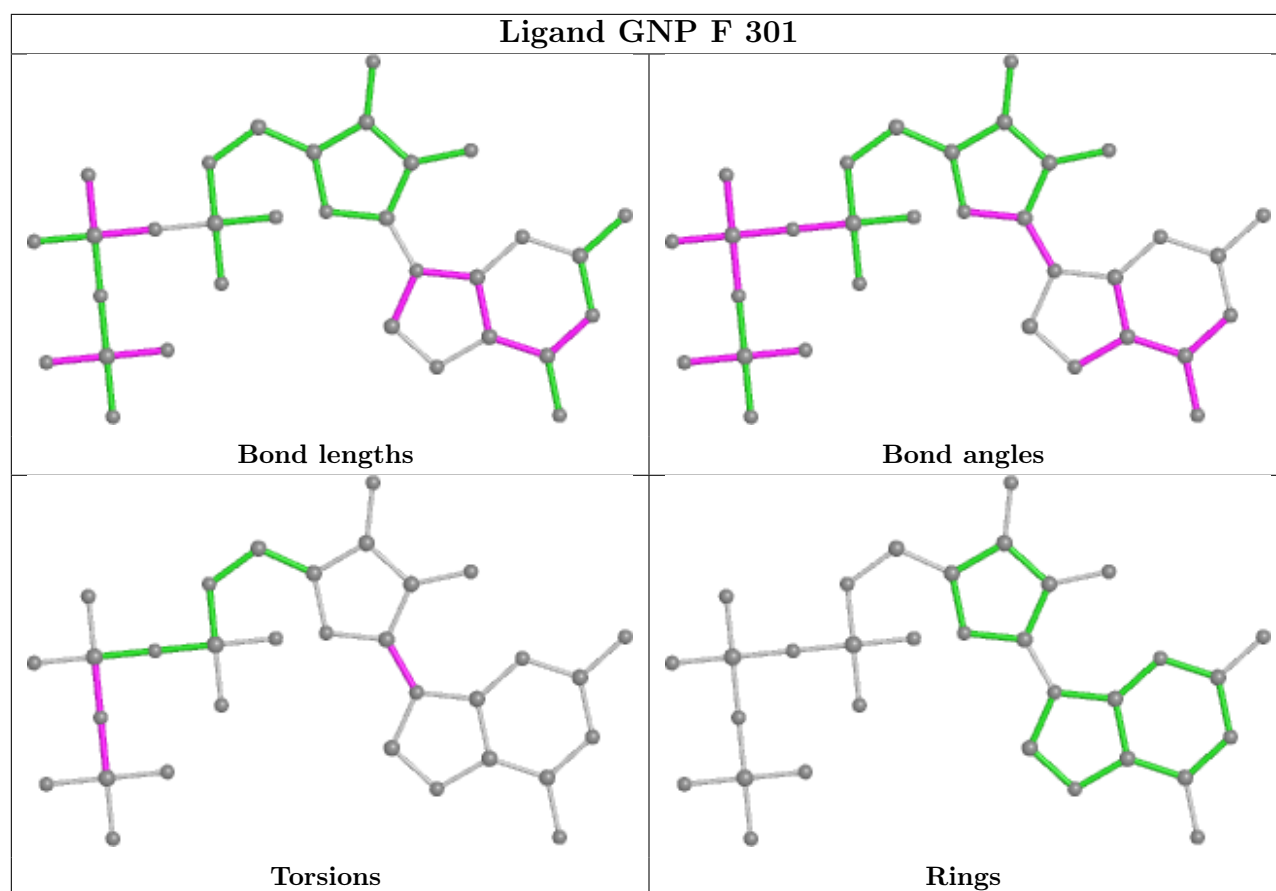
There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	301	GNP	2	0
4	D	301	GNP	1	0
3	C	321	PO4	1	0
3	A	323	PO4	1	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	184/320 (57%)	0.08	5 (2%) 54 48	31, 53, 84, 119	0
1	C	179/320 (55%)	-0.10	0 100 100	36, 57, 97, 123	0
1	E	165/320 (51%)	1.17	29 (17%) 1 0	72, 108, 129, 133	0
2	B	178/188 (94%)	0.64	13 (7%) 15 11	52, 74, 97, 108	0
2	D	178/188 (94%)	0.28	1 (0%) 89 88	34, 47, 78, 99	0
2	F	181/188 (96%)	0.31	2 (1%) 80 78	51, 76, 95, 108	0
All	All	1065/1524 (69%)	0.38	50 (4%) 31 25	31, 67, 116, 133	0

The worst 5 of 50 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	150	LEU	6.1
1	E	164	PHE	4.8
2	B	31	SER	4.8
1	E	170	TRP	4.7
1	E	162	GLY	4.6

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

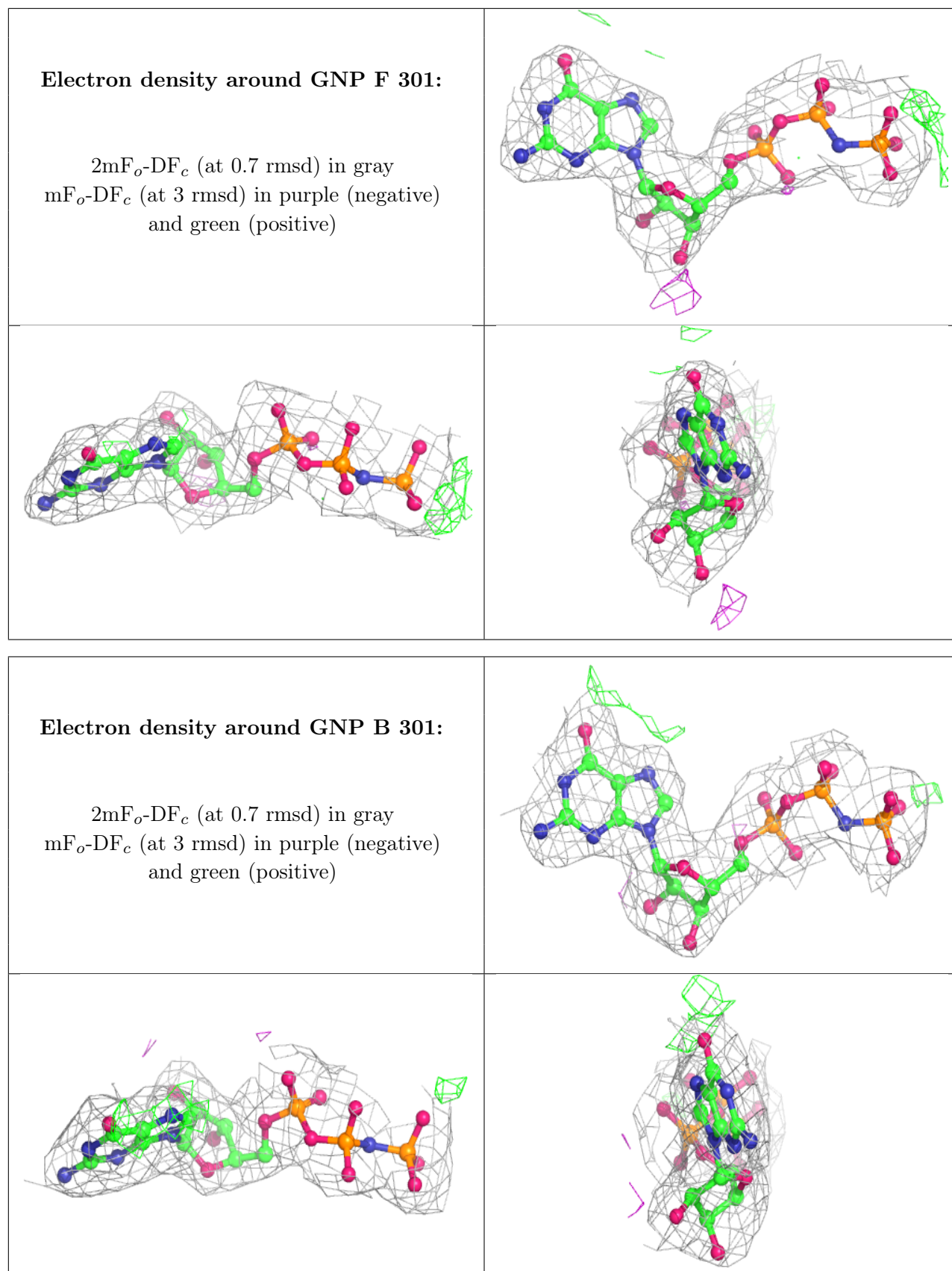
There are no monosaccharides in this entry.

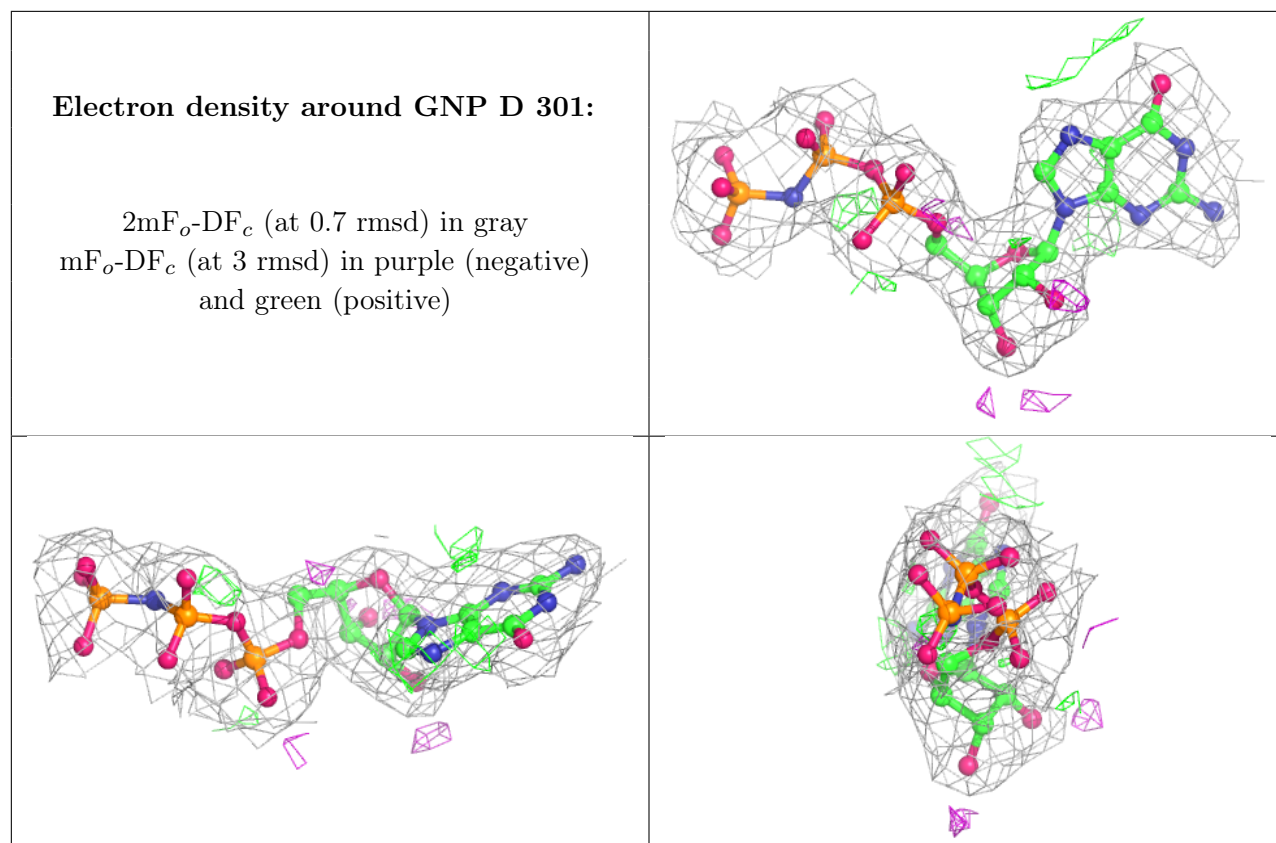
6.4 Ligands

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 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
3	PO4	E	321	5/5	0.53	0.26	146,147,147,147	0
3	PO4	A	323	5/5	0.82	0.24	110,110,111,111	0
3	PO4	A	321	5/5	0.87	0.17	109,110,110,110	0
5	MG	F	401	1/1	0.88	0.11	57,57,57,57	0
3	PO4	C	322	5/5	0.94	0.14	67,67,68,70	0
3	PO4	A	322	5/5	0.96	0.18	82,83,83,84	0
5	MG	D	401	1/1	0.96	0.16	38,38,38,38	0
3	PO4	C	323	5/5	0.96	0.18	93,94,95,95	0
5	MG	B	401	1/1	0.97	0.12	46,46,46,46	0
3	PO4	C	321	5/5	0.97	0.10	71,72,72,73	0
4	GNP	F	301	32/32	0.97	0.18	58,62,65,68	0
4	GNP	B	301	32/32	0.98	0.15	49,57,60,61	0
4	GNP	D	301	32/32	0.99	0.20	27,34,39,42	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.