



wwPDB X-ray Structure Validation Summary Report ⓘ

May 14, 2020 – 12:59 pm BST

PDB ID : 5THI
Title : Comprehensive Analysis of a Novel Ketoreductase for Pentangular Polyphenol Biosynthesis
Authors : Valentic, T.R.; Tsai, S.C.; Brady, S.F.
Deposited on : 2016-10-03
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 : 2.11
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) : 2.11

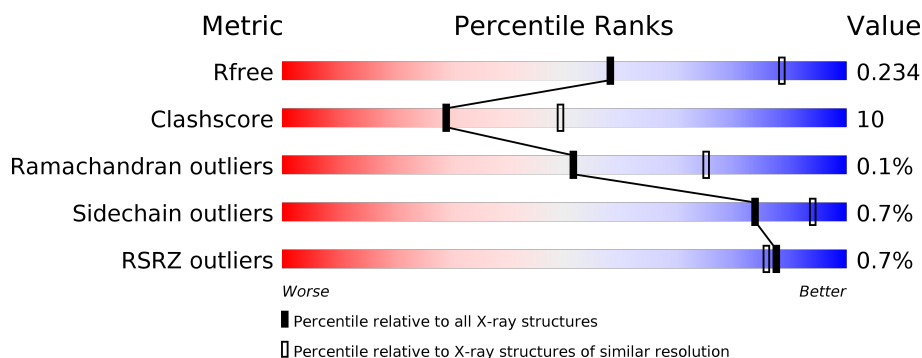
1 Overall quality at a glance

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 on 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	272	
1	B	272	
1	C	272	
1	D	272	
1	E	272	
1	F	272	

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Mol	Chain	Length	Quality of chain
1	G	272	<div><div></div><div>73%</div><div>12%</div><div>•</div><div>15%</div></div>
1	H	272	<div>%<div><div></div><div>71%</div><div>15%</div><div>14%</div></div></div>

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 14887 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 3-oxoacyl-ACP reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	241	Total	C	N	O	S	0	0	0
			1801	1132	329	338	2			
1	D	244	Total	C	N	O	S	0	0	0
			1828	1149	334	343	2			
1	E	238	Total	C	N	O	S	0	0	0
			1776	1118	326	330	2			
1	G	232	Total	C	N	O	S	0	0	0
			1729	1090	319	319	1			
1	H	233	Total	C	N	O	S	0	0	0
			1734	1093	320	320	1			
1	B	241	Total	C	N	O	S	0	0	0
			1800	1134	331	334	1			
1	C	236	Total	C	N	O	S	0	0	0
			1759	1107	324	326	2			
1	F	250	Total	C	N	O	S	0	0	0
			1875	1177	343	353	2			

There are 160 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	initiating methionine	UNP A0A023PKG5
A	-18	GLY	-	expression tag	UNP A0A023PKG5
A	-17	SER	-	expression tag	UNP A0A023PKG5
A	-16	SER	-	expression tag	UNP A0A023PKG5
A	-15	HIS	-	expression tag	UNP A0A023PKG5
A	-14	HIS	-	expression tag	UNP A0A023PKG5
A	-13	HIS	-	expression tag	UNP A0A023PKG5
A	-12	HIS	-	expression tag	UNP A0A023PKG5
A	-11	HIS	-	expression tag	UNP A0A023PKG5
A	-10	HIS	-	expression tag	UNP A0A023PKG5
A	-9	SER	-	expression tag	UNP A0A023PKG5
A	-8	SER	-	expression tag	UNP A0A023PKG5
A	-7	GLY	-	expression tag	UNP A0A023PKG5

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-6	LEU	-	expression tag	UNP A0A023PKG5
A	-5	VAL	-	expression tag	UNP A0A023PKG5
A	-4	PRO	-	expression tag	UNP A0A023PKG5
A	-3	ARG	-	expression tag	UNP A0A023PKG5
A	-2	GLY	-	expression tag	UNP A0A023PKG5
A	-1	SER	-	expression tag	UNP A0A023PKG5
A	0	HIS	-	expression tag	UNP A0A023PKG5
D	-19	MET	-	initiating methionine	UNP A0A023PKG5
D	-18	GLY	-	expression tag	UNP A0A023PKG5
D	-17	SER	-	expression tag	UNP A0A023PKG5
D	-16	SER	-	expression tag	UNP A0A023PKG5
D	-15	HIS	-	expression tag	UNP A0A023PKG5
D	-14	HIS	-	expression tag	UNP A0A023PKG5
D	-13	HIS	-	expression tag	UNP A0A023PKG5
D	-12	HIS	-	expression tag	UNP A0A023PKG5
D	-11	HIS	-	expression tag	UNP A0A023PKG5
D	-10	HIS	-	expression tag	UNP A0A023PKG5
D	-9	SER	-	expression tag	UNP A0A023PKG5
D	-8	SER	-	expression tag	UNP A0A023PKG5
D	-7	GLY	-	expression tag	UNP A0A023PKG5
D	-6	LEU	-	expression tag	UNP A0A023PKG5
D	-5	VAL	-	expression tag	UNP A0A023PKG5
D	-4	PRO	-	expression tag	UNP A0A023PKG5
D	-3	ARG	-	expression tag	UNP A0A023PKG5
D	-2	GLY	-	expression tag	UNP A0A023PKG5
D	-1	SER	-	expression tag	UNP A0A023PKG5
D	0	HIS	-	expression tag	UNP A0A023PKG5
E	-19	MET	-	initiating methionine	UNP A0A023PKG5
E	-18	GLY	-	expression tag	UNP A0A023PKG5
E	-17	SER	-	expression tag	UNP A0A023PKG5
E	-16	SER	-	expression tag	UNP A0A023PKG5
E	-15	HIS	-	expression tag	UNP A0A023PKG5
E	-14	HIS	-	expression tag	UNP A0A023PKG5
E	-13	HIS	-	expression tag	UNP A0A023PKG5
E	-12	HIS	-	expression tag	UNP A0A023PKG5
E	-11	HIS	-	expression tag	UNP A0A023PKG5
E	-10	HIS	-	expression tag	UNP A0A023PKG5
E	-9	SER	-	expression tag	UNP A0A023PKG5
E	-8	SER	-	expression tag	UNP A0A023PKG5
E	-7	GLY	-	expression tag	UNP A0A023PKG5
E	-6	LEU	-	expression tag	UNP A0A023PKG5
E	-5	VAL	-	expression tag	UNP A0A023PKG5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	-4	PRO	-	expression tag	UNP A0A023PKG5
E	-3	ARG	-	expression tag	UNP A0A023PKG5
E	-2	GLY	-	expression tag	UNP A0A023PKG5
E	-1	SER	-	expression tag	UNP A0A023PKG5
E	0	HIS	-	expression tag	UNP A0A023PKG5
G	-19	MET	-	initiating methionine	UNP A0A023PKG5
G	-18	GLY	-	expression tag	UNP A0A023PKG5
G	-17	SER	-	expression tag	UNP A0A023PKG5
G	-16	SER	-	expression tag	UNP A0A023PKG5
G	-15	HIS	-	expression tag	UNP A0A023PKG5
G	-14	HIS	-	expression tag	UNP A0A023PKG5
G	-13	HIS	-	expression tag	UNP A0A023PKG5
G	-12	HIS	-	expression tag	UNP A0A023PKG5
G	-11	HIS	-	expression tag	UNP A0A023PKG5
G	-10	HIS	-	expression tag	UNP A0A023PKG5
G	-9	SER	-	expression tag	UNP A0A023PKG5
G	-8	SER	-	expression tag	UNP A0A023PKG5
G	-7	GLY	-	expression tag	UNP A0A023PKG5
G	-6	LEU	-	expression tag	UNP A0A023PKG5
G	-5	VAL	-	expression tag	UNP A0A023PKG5
G	-4	PRO	-	expression tag	UNP A0A023PKG5
G	-3	ARG	-	expression tag	UNP A0A023PKG5
G	-2	GLY	-	expression tag	UNP A0A023PKG5
G	-1	SER	-	expression tag	UNP A0A023PKG5
G	0	HIS	-	expression tag	UNP A0A023PKG5
H	-19	MET	-	initiating methionine	UNP A0A023PKG5
H	-18	GLY	-	expression tag	UNP A0A023PKG5
H	-17	SER	-	expression tag	UNP A0A023PKG5
H	-16	SER	-	expression tag	UNP A0A023PKG5
H	-15	HIS	-	expression tag	UNP A0A023PKG5
H	-14	HIS	-	expression tag	UNP A0A023PKG5
H	-13	HIS	-	expression tag	UNP A0A023PKG5
H	-12	HIS	-	expression tag	UNP A0A023PKG5
H	-11	HIS	-	expression tag	UNP A0A023PKG5
H	-10	HIS	-	expression tag	UNP A0A023PKG5
H	-9	SER	-	expression tag	UNP A0A023PKG5
H	-8	SER	-	expression tag	UNP A0A023PKG5
H	-7	GLY	-	expression tag	UNP A0A023PKG5
H	-6	LEU	-	expression tag	UNP A0A023PKG5
H	-5	VAL	-	expression tag	UNP A0A023PKG5
H	-4	PRO	-	expression tag	UNP A0A023PKG5
H	-3	ARG	-	expression tag	UNP A0A023PKG5

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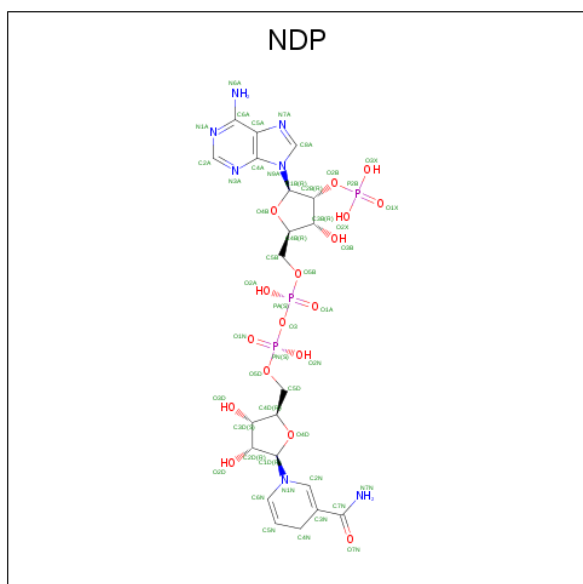
Chain	Residue	Modelled	Actual	Comment	Reference
H	-2	GLY	-	expression tag	UNP A0A023PKG5
H	-1	SER	-	expression tag	UNP A0A023PKG5
H	0	HIS	-	expression tag	UNP A0A023PKG5
B	-19	MET	-	initiating methionine	UNP A0A023PKG5
B	-18	GLY	-	expression tag	UNP A0A023PKG5
B	-17	SER	-	expression tag	UNP A0A023PKG5
B	-16	SER	-	expression tag	UNP A0A023PKG5
B	-15	HIS	-	expression tag	UNP A0A023PKG5
B	-14	HIS	-	expression tag	UNP A0A023PKG5
B	-13	HIS	-	expression tag	UNP A0A023PKG5
B	-12	HIS	-	expression tag	UNP A0A023PKG5
B	-11	HIS	-	expression tag	UNP A0A023PKG5
B	-10	HIS	-	expression tag	UNP A0A023PKG5
B	-9	SER	-	expression tag	UNP A0A023PKG5
B	-8	SER	-	expression tag	UNP A0A023PKG5
B	-7	GLY	-	expression tag	UNP A0A023PKG5
B	-6	LEU	-	expression tag	UNP A0A023PKG5
B	-5	VAL	-	expression tag	UNP A0A023PKG5
B	-4	PRO	-	expression tag	UNP A0A023PKG5
B	-3	ARG	-	expression tag	UNP A0A023PKG5
B	-2	GLY	-	expression tag	UNP A0A023PKG5
B	-1	SER	-	expression tag	UNP A0A023PKG5
B	0	HIS	-	expression tag	UNP A0A023PKG5
C	-19	MET	-	initiating methionine	UNP A0A023PKG5
C	-18	GLY	-	expression tag	UNP A0A023PKG5
C	-17	SER	-	expression tag	UNP A0A023PKG5
C	-16	SER	-	expression tag	UNP A0A023PKG5
C	-15	HIS	-	expression tag	UNP A0A023PKG5
C	-14	HIS	-	expression tag	UNP A0A023PKG5
C	-13	HIS	-	expression tag	UNP A0A023PKG5
C	-12	HIS	-	expression tag	UNP A0A023PKG5
C	-11	HIS	-	expression tag	UNP A0A023PKG5
C	-10	HIS	-	expression tag	UNP A0A023PKG5
C	-9	SER	-	expression tag	UNP A0A023PKG5
C	-8	SER	-	expression tag	UNP A0A023PKG5
C	-7	GLY	-	expression tag	UNP A0A023PKG5
C	-6	LEU	-	expression tag	UNP A0A023PKG5
C	-5	VAL	-	expression tag	UNP A0A023PKG5
C	-4	PRO	-	expression tag	UNP A0A023PKG5
C	-3	ARG	-	expression tag	UNP A0A023PKG5
C	-2	GLY	-	expression tag	UNP A0A023PKG5
C	-1	SER	-	expression tag	UNP A0A023PKG5

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Chain	Residue	Modelled	Actual	Comment	Reference
C	0	HIS	-	expression tag	UNP A0A023PKG5
F	-19	MET	-	initiating methionine	UNP A0A023PKG5
F	-18	GLY	-	expression tag	UNP A0A023PKG5
F	-17	SER	-	expression tag	UNP A0A023PKG5
F	-16	SER	-	expression tag	UNP A0A023PKG5
F	-15	HIS	-	expression tag	UNP A0A023PKG5
F	-14	HIS	-	expression tag	UNP A0A023PKG5
F	-13	HIS	-	expression tag	UNP A0A023PKG5
F	-12	HIS	-	expression tag	UNP A0A023PKG5
F	-11	HIS	-	expression tag	UNP A0A023PKG5
F	-10	HIS	-	expression tag	UNP A0A023PKG5
F	-9	SER	-	expression tag	UNP A0A023PKG5
F	-8	SER	-	expression tag	UNP A0A023PKG5
F	-7	GLY	-	expression tag	UNP A0A023PKG5
F	-6	LEU	-	expression tag	UNP A0A023PKG5
F	-5	VAL	-	expression tag	UNP A0A023PKG5
F	-4	PRO	-	expression tag	UNP A0A023PKG5
F	-3	ARG	-	expression tag	UNP A0A023PKG5
F	-2	GLY	-	expression tag	UNP A0A023PKG5
F	-1	SER	-	expression tag	UNP A0A023PKG5
F	0	HIS	-	expression tag	UNP A0A023PKG5

- Molecule 2 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: $C_{21}H_{30}N_7O_{17}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	E	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
2	F	1	Total	C	N	O	P	0	0
			48	21	7	17	3		


- Molecule 3 is water.

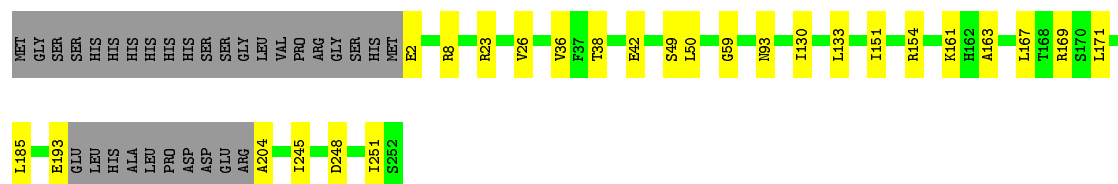
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	75	Total	O	0	0
			75	75		
3	D	53	Total	O	0	0
			53	53		
3	E	45	Total	O	0	0
			45	45		
3	G	52	Total	O	0	0
			52	52		
3	H	37	Total	O	0	0
			37	37		
3	B	62	Total	O	0	0
			62	62		
3	C	62	Total	O	0	0
			62	62		
3	F	55	Total	O	0	0
			55	55		

3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

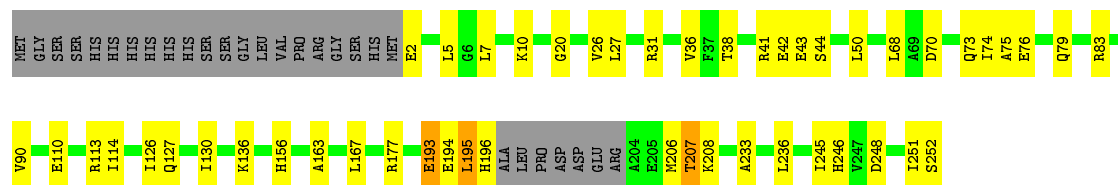
- Molecule 1: 3-oxoacyl-ACP reductase

Chain A: 



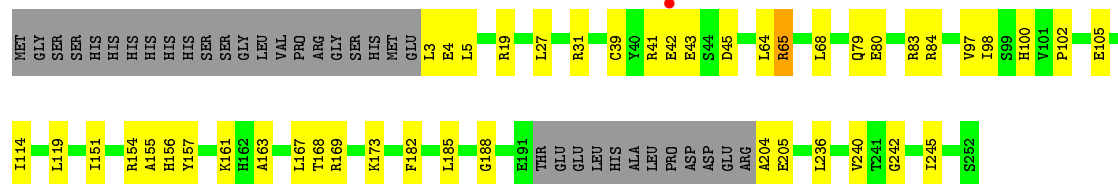
- Molecule 1: 3-oxoacyl-ACP reductase

Chain D: 



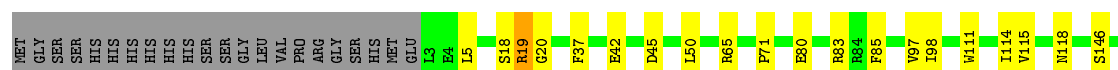
- Molecule 1: 3-oxoacyl-ACP reductase

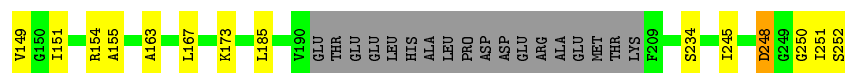
Chain E: 



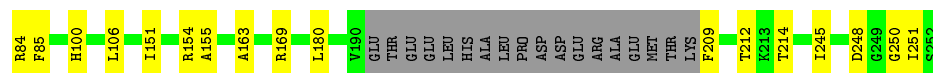
- Molecule 1: 3-oxoacyl-ACP reductase

Chain G: 

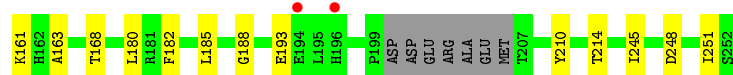
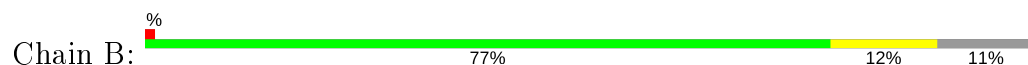




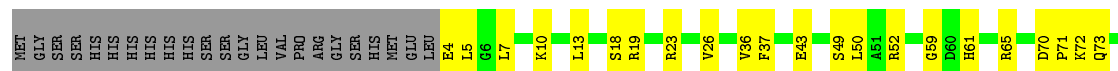
• Molecule 1: 3-oxoacyl-ACP reductase



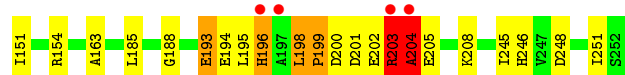
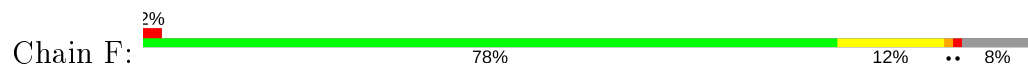
• Molecule 1: 3-oxoacyl-ACP reductase



• Molecule 1: 3-oxoacyl-ACP reductase



• Molecule 1: 3-oxoacyl-ACP reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.38Å 86.65Å 107.32Å 90.00° 108.97° 90.00°	Depositor
Resolution (Å)	52.67 – 2.60 99.66 – 2.60	Depositor EDS
% Data completeness (in resolution range)	93.3 (52.67-2.60) 93.1 (99.66-2.60)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.98 (at 2.62Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.177 , 0.234 0.177 , 0.234	Depositor DCC
R_{free} test set	2011 reflections (3.72%)	wwPDB-VP
Wilson B-factor (Å ²)	26.5	Xtriage
Anisotropy	0.394	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.022 for l,-k,h	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14887	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 23.41 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.6838e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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: NDP

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	0.25	0/1828	0.44	0/2474
1	B	0.28	0/1829	0.45	0/2478
1	C	0.26	0/1786	0.46	0/2417
1	D	0.34	1/1856 (0.1%)	0.55	4/2512 (0.2%)
1	E	0.26	0/1803	0.46	1/2440 (0.0%)
1	F	0.34	0/1905	0.83	8/2581 (0.3%)
1	G	0.25	0/1756	0.43	0/2378
1	H	0.27	0/1761	0.45	0/2385
All	All	0.28	1/14524 (0.0%)	0.53	13/19665 (0.1%)

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	D	0	1
1	F	0	3
All	All	0	4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	195	LEU	CG-CD2	-6.74	1.26	1.51

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	203	ARG	CB-CA-C	-19.15	72.09	110.40
1	F	204	ALA	CB-CA-C	-15.45	86.92	110.10

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	205	GLU	N-CA-CB	13.09	134.16	110.60
1	F	205	GLU	N-CA-C	-12.22	78.00	111.00
1	D	195	LEU	CB-CG-CD2	-7.33	98.53	111.00

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	193	GLU	Peptide
1	F	193	GLU	Peptide
1	F	203	ARG	Peptide
1	F	204	ALA	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	1801	0	1834	23	0
1	B	1800	0	1838	26	0
1	C	1759	0	1798	29	0
1	D	1828	0	1858	44	1
1	E	1776	0	1815	56	1
1	F	1875	0	1903	52	0
1	G	1729	0	1769	25	0
1	H	1734	0	1771	37	0
2	B	48	0	24	3	0
2	E	48	0	24	8	0
2	F	48	0	24	3	0
3	A	75	0	0	9	0
3	B	62	0	0	8	0
3	C	62	0	0	10	0
3	D	53	0	0	20	0
3	E	45	0	0	12	0
3	F	55	0	0	7	0
3	G	52	0	0	3	0
3	H	37	0	0	4	0
All	All	14887	0	14658	278	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 10.

The worst 5 of 278 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:D:113:ARG:HB3	3:D:303:HOH:O	1.40	1.17
1:F:199:PRO:O	1:F:203:ARG:N	1.83	1.11
1:F:200:ASP:HA	1:F:203:ARG:CG	1.82	1.10
1:E:42:GLU:HA	3:E:403:HOH:O	1.53	1.06
1:C:52:ARG:NE	3:C:301:HOH:O	1.80	1.03

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:D:83:ARG:NH1	1:E:45:ASP:OD2[2_756]	2.11	0.09

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	237/272 (87%)	230 (97%)	7 (3%)	0	100	100
1	B	237/272 (87%)	231 (98%)	6 (2%)	0	100	100
1	C	232/272 (85%)	226 (97%)	6 (3%)	0	100	100
1	D	240/272 (88%)	232 (97%)	8 (3%)	0	100	100
1	E	234/272 (86%)	229 (98%)	5 (2%)	0	100	100
1	F	248/272 (91%)	237 (96%)	10 (4%)	1 (0%)	34	57
1	G	228/272 (84%)	222 (97%)	6 (3%)	0	100	100
1	H	229/272 (84%)	224 (98%)	5 (2%)	0	100	100
All	All	1885/2176 (87%)	1831 (97%)	53 (3%)	1 (0%)	51	75

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	F	199	PRO

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	185/212 (87%)	183 (99%)	2 (1%)	73	88
1	B	185/212 (87%)	184 (100%)	1 (0%)	88	96
1	C	180/212 (85%)	179 (99%)	1 (1%)	86	95
1	D	188/212 (89%)	188 (100%)	0	100	100
1	E	182/212 (86%)	182 (100%)	0	100	100
1	F	193/212 (91%)	191 (99%)	2 (1%)	76	90
1	G	177/212 (84%)	175 (99%)	2 (1%)	73	88
1	H	177/212 (84%)	175 (99%)	2 (1%)	73	88
All	All	1467/1696 (86%)	1457 (99%)	10 (1%)	84	94

5 of 10 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	H	60	ASP
1	H	77	LEU
1	C	19	ARG
1	G	248	ASP
1	B	193	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	56	GLN
1	H	61	HIS
1	H	62	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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

3 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	NDP	B	301	-	45,52,52	4.08	20 (44%)	53,80,80	2.24	6 (11%)
2	NDP	F	301	-	45,52,52	4.05	20 (44%)	53,80,80	2.17	7 (13%)
2	NDP	E	301	-	45,52,52	4.07	20 (44%)	53,80,80	2.40	8 (15%)

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	NDP	B	301	-	-	12/30/77/77	0/5/5/5
2	NDP	F	301	-	-	8/30/77/77	0/5/5/5
2	NDP	E	301	-	-	8/30/77/77	0/5/5/5

The worst 5 of 60 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301	NDP	O4B-C1B	15.46	1.62	1.41
2	E	301	NDP	O4B-C1B	15.34	1.62	1.41
2	F	301	NDP	O4B-C1B	15.06	1.62	1.41
2	F	301	NDP	C6N-C5N	12.34	1.55	1.33
2	E	301	NDP	C6N-C5N	12.34	1.55	1.33

The worst 5 of 21 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	301	NDP	C5A-C6A-N6A	10.15	135.78	120.35
2	F	301	NDP	C5A-C6A-N6A	10.02	135.57	120.35
2	B	301	NDP	C5A-C6A-N6A	9.92	135.43	120.35
2	E	301	NDP	C1B-N9A-C4A	-7.89	112.78	126.64
2	B	301	NDP	C1B-N9A-C4A	-7.47	113.52	126.64

There are no chirality outliers.

5 of 28 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301	NDP	C4B-C5B-O5B-PA
2	B	301	NDP	C5D-O5D-PN-O1N
2	B	301	NDP	C5D-O5D-PN-O2N
2	F	301	NDP	C2B-O2B-P2B-O1X
2	F	301	NDP	C5D-O5D-PN-O1N

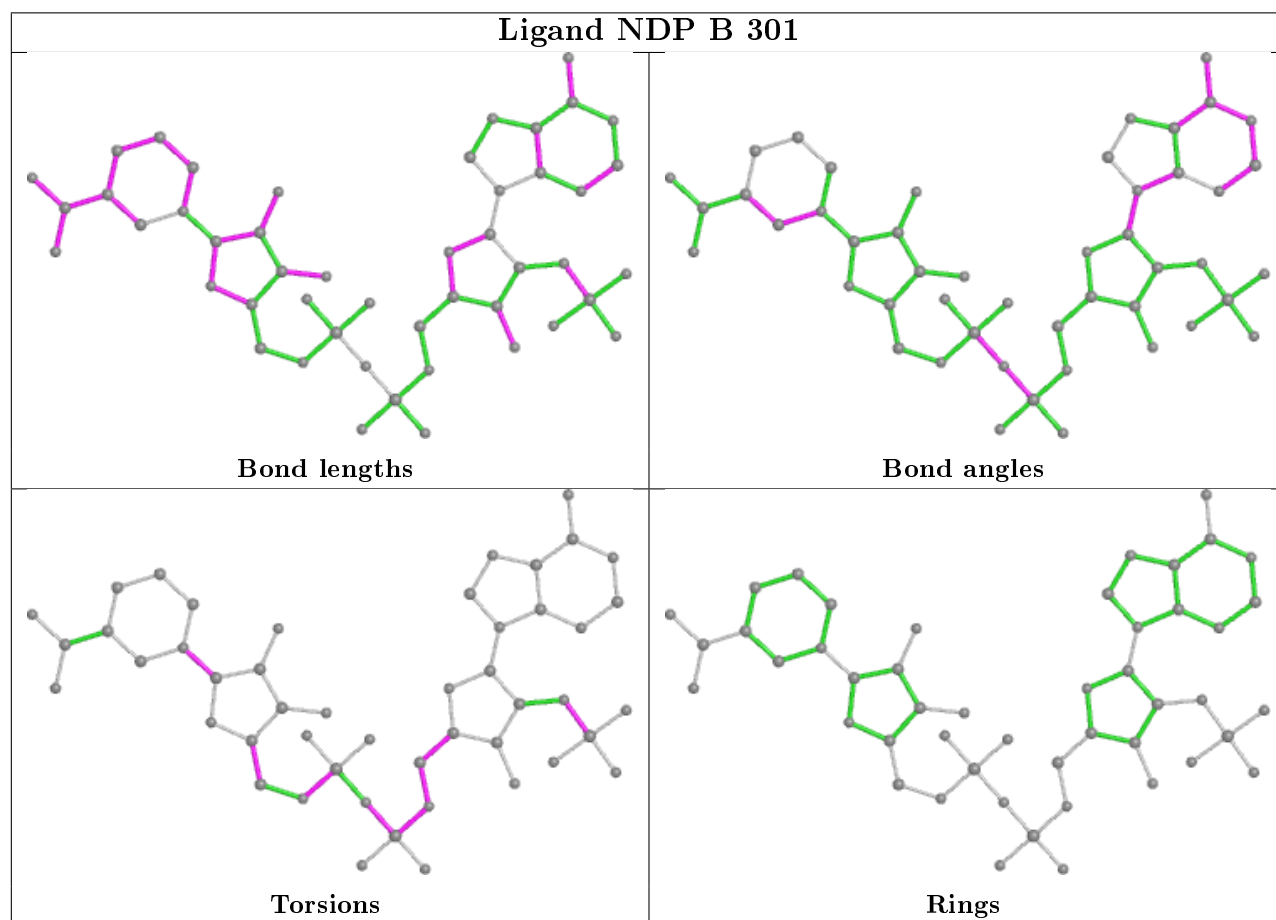
There are no ring outliers.

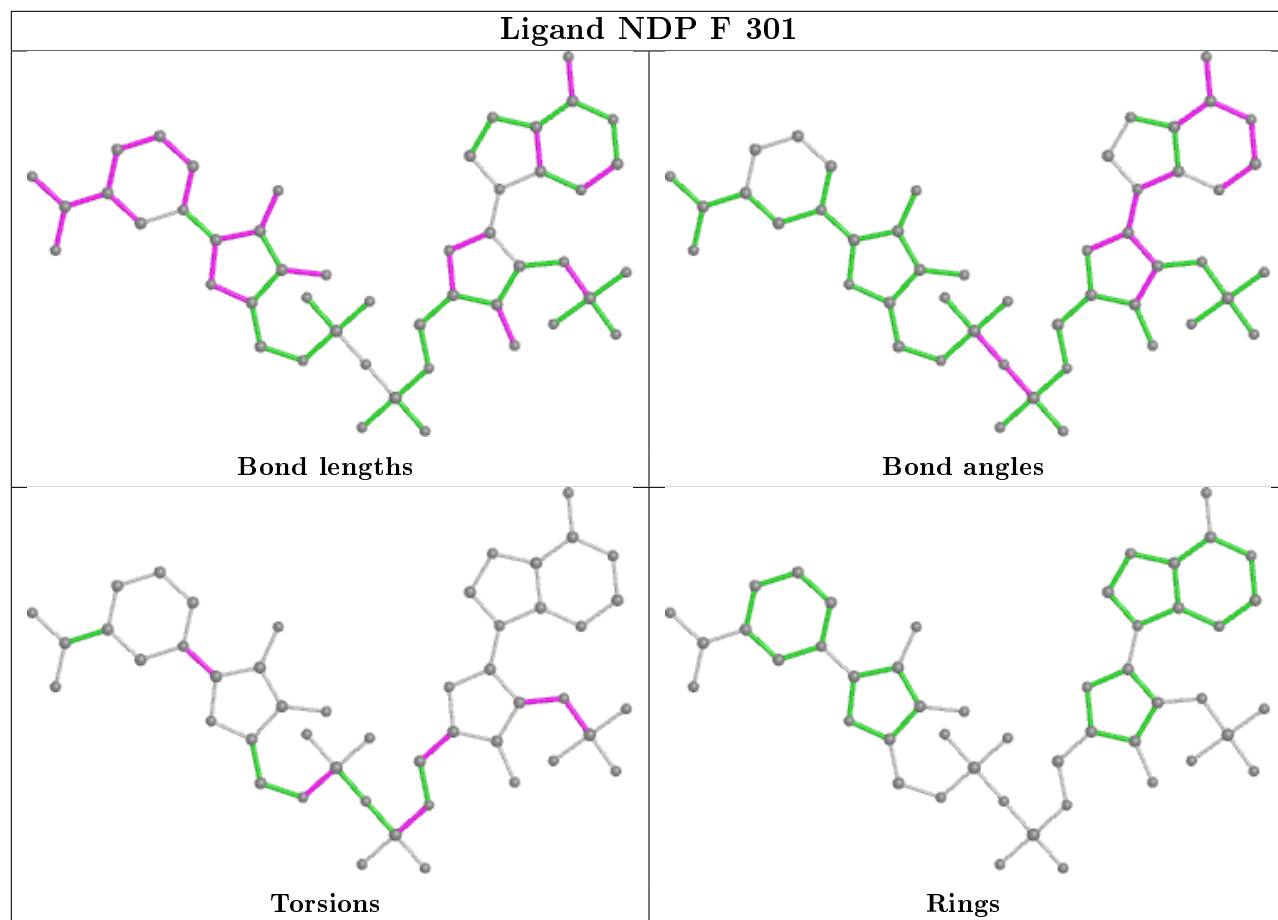
3 monomers are involved in 14 short contacts:

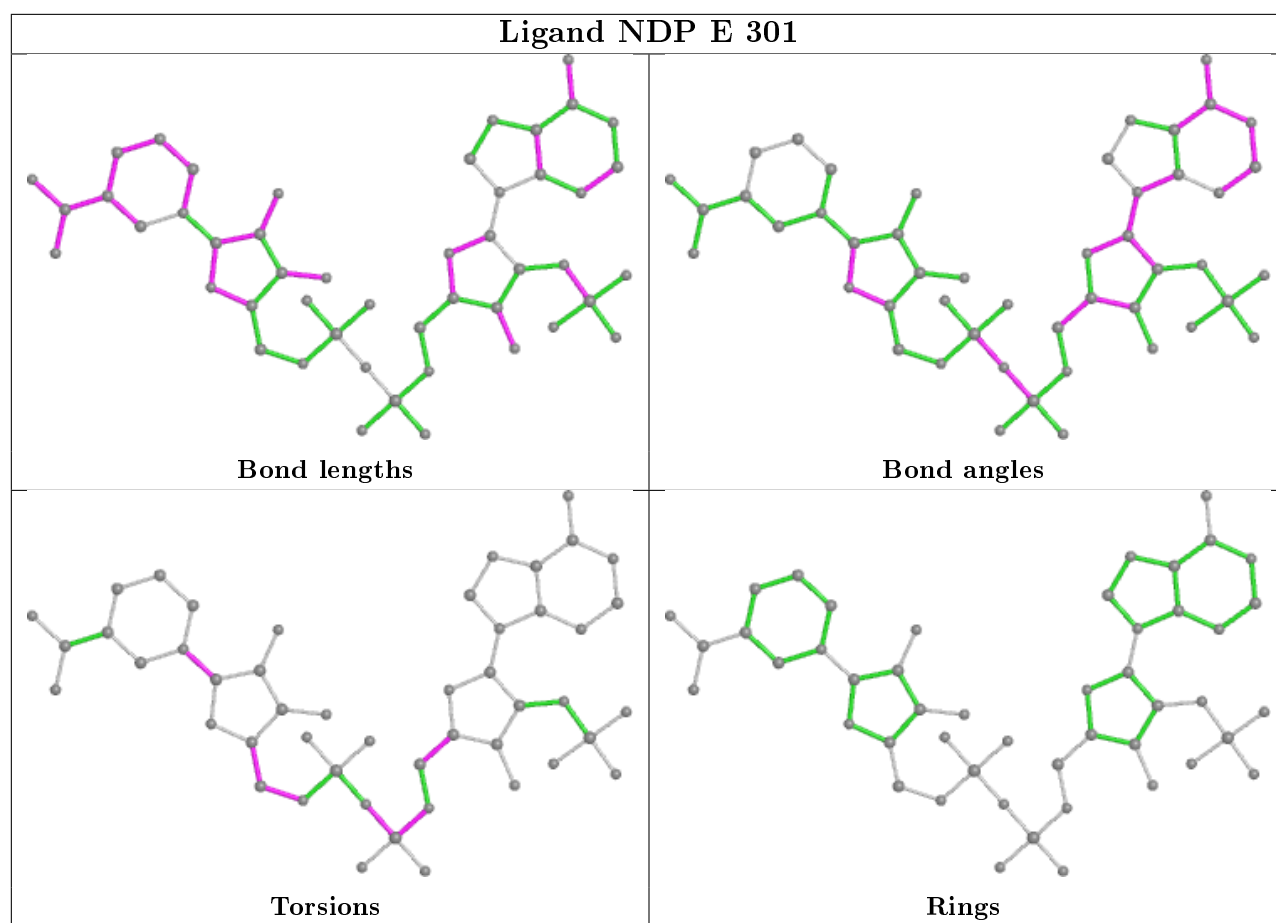
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	301	NDP	3	0
2	F	301	NDP	3	0
2	E	301	NDP	8	0

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.







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	241/272 (88%)	-0.38	0 100 100	14, 23, 42, 69	0
1	B	241/272 (88%)	-0.34	2 (0%) 86 84	12, 24, 44, 86	0
1	C	236/272 (86%)	-0.35	1 (0%) 92 91	14, 23, 45, 68	0
1	D	244/272 (89%)	-0.31	0 100 100	18, 27, 48, 76	0
1	E	238/272 (87%)	-0.30	1 (0%) 92 91	18, 29, 51, 67	0
1	F	250/272 (91%)	-0.24	6 (2%) 59 53	15, 24, 58, 98	0
1	G	232/272 (85%)	-0.24	0 100 100	18, 30, 49, 60	0
1	H	233/272 (85%)	-0.16	3 (1%) 77 73	18, 32, 61, 84	0
All	All	1915/2176 (88%)	-0.29	13 (0%) 87 86	12, 26, 52, 98	0

The worst 5 of 13 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	203	ARG	5.4
1	F	204	ALA	4.6
1	F	196	HIS	3.5
1	B	196	HIS	3.4
1	F	135	ASP	3.3

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

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

6.3 Carbohydrates ⓘ

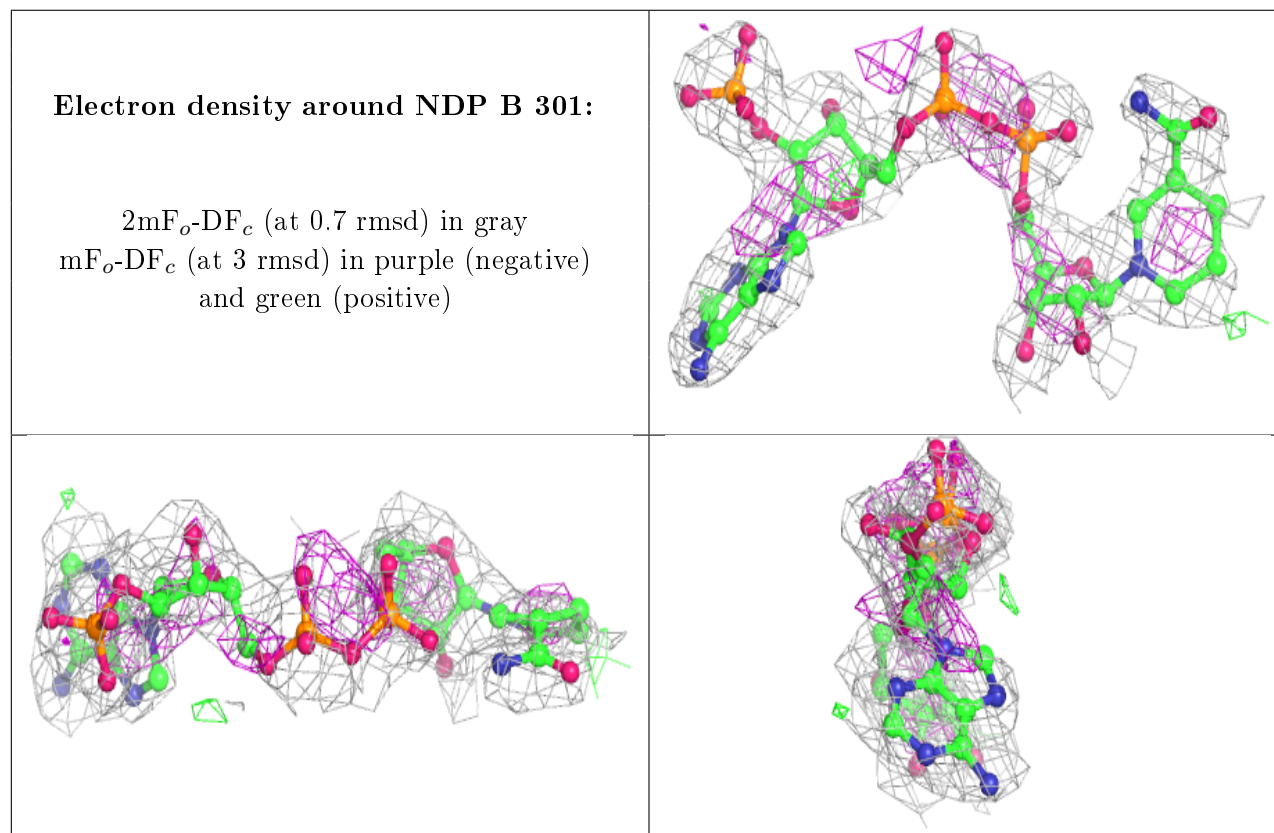
There are no carbohydrates in this entry.

6.4 Ligands ⓘ

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. 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.

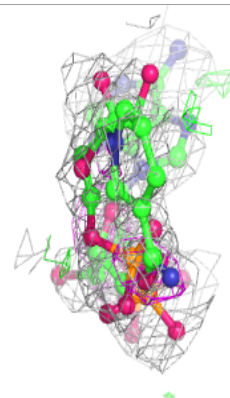
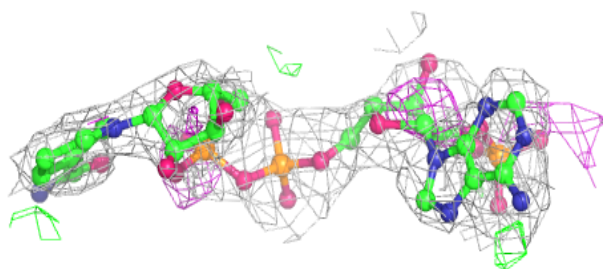
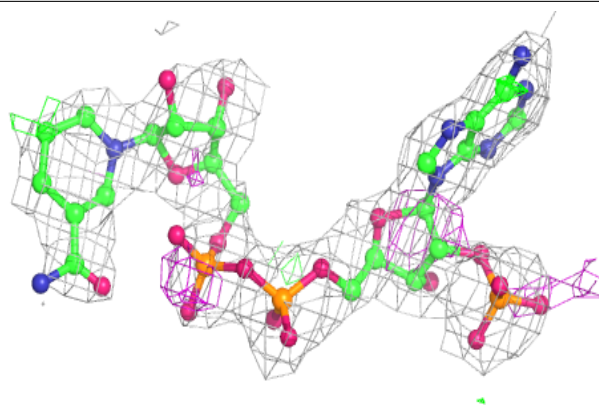
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NDP	B	301	48/48	0.86	0.29	27,46,58,74	0
2	NDP	E	301	48/48	0.86	0.30	32,51,68,72	0
2	NDP	F	301	48/48	0.92	0.26	26,37,46,57	0

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.

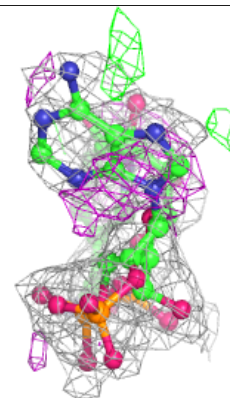
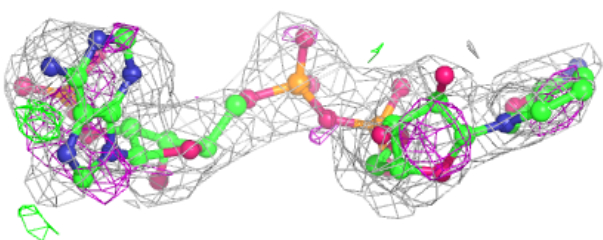
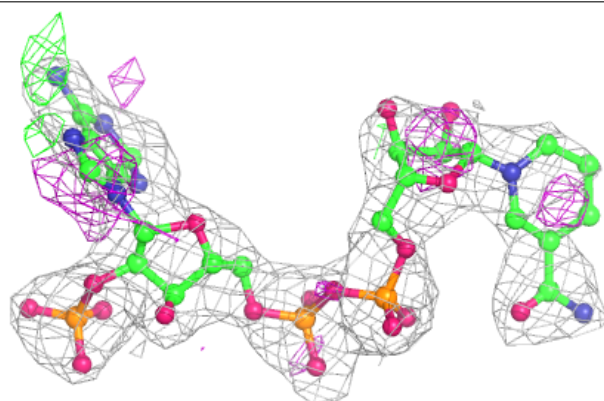


Electron density around NDP E 301:

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

**Electron density around NDP F 301:**

$2mF_o-DF_c$ (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.