



# Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 07:16 pm BST

PDB ID : 3B1Q  
Title : Structure of Burkholderia thailandensis nucleoside kinase (BthNK) in complex with inosine  
Authors : Yasutake, Y.; Ota, H.; Hino, E.; Sakasegawa, S.; Tamura, T.  
Deposited on : 2011-07-05  
Resolution : 1.70 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at [validation@mail.wwpdb.org](mailto: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.

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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

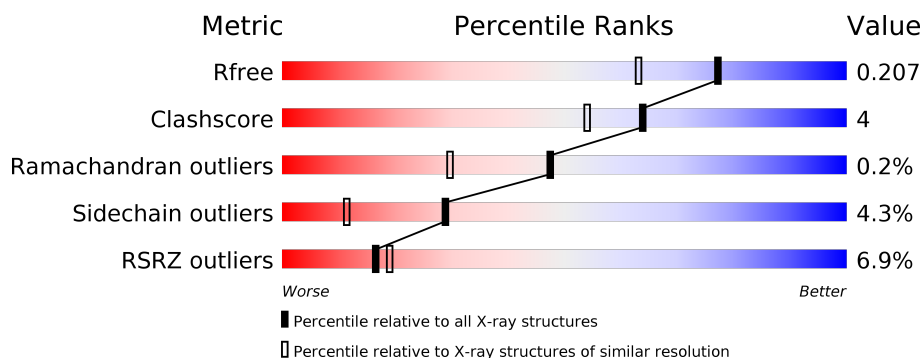
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.70 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	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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  $\geq 3$ , 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	326	<div> <div>8%</div> <div>83% 9% • 7%</div> </div>
1	B	326	<div> <div>8%</div> <div>85% 9% • 6%</div> </div>
1	C	326	<div> <div>6%</div> <div>84% 8% • 6%</div> </div>
1	D	326	<div> <div>5%</div> <div>82% 11% 7%</div> </div>
1	E	326	<div> <div>5%</div> <div>81% 11% • 6%</div> </div>
1	F	326	<div> <div>6%</div> <div>83% 6% • 9%</div> </div>

## 2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 15318 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 Ribokinase, putative.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	2	0
			2325	1460	414	436	15			
1	B	306	Total	C	N	O	S	0	2	0
			2346	1474	417	440	15			
1	C	305	Total	C	N	O	S	0	1	0
			2333	1466	414	438	15			
1	D	303	Total	C	N	O	S	0	2	0
			2315	1456	408	435	16			
1	E	306	Total	C	N	O	S	0	4	0
			2354	1480	417	442	15			
1	F	298	Total	C	N	O	S	0	2	0
			2277	1429	404	430	14			

There are 84 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	313	GLY	-	EXPRESSION TAG	UNP Q2SZE4
A	314	SER	-	EXPRESSION TAG	UNP Q2SZE4
A	315	LYS	-	EXPRESSION TAG	UNP Q2SZE4
A	316	LEU	-	EXPRESSION TAG	UNP Q2SZE4
A	317	ARG	-	EXPRESSION TAG	UNP Q2SZE4
A	318	SER	-	EXPRESSION TAG	UNP Q2SZE4
A	319	LEU	-	EXPRESSION TAG	UNP Q2SZE4
A	320	GLU	-	EXPRESSION TAG	UNP Q2SZE4
A	321	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	322	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	323	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	324	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	325	HIS	-	EXPRESSION TAG	UNP Q2SZE4
A	326	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	313	GLY	-	EXPRESSION TAG	UNP Q2SZE4
B	314	SER	-	EXPRESSION TAG	UNP Q2SZE4
B	315	LYS	-	EXPRESSION TAG	UNP Q2SZE4

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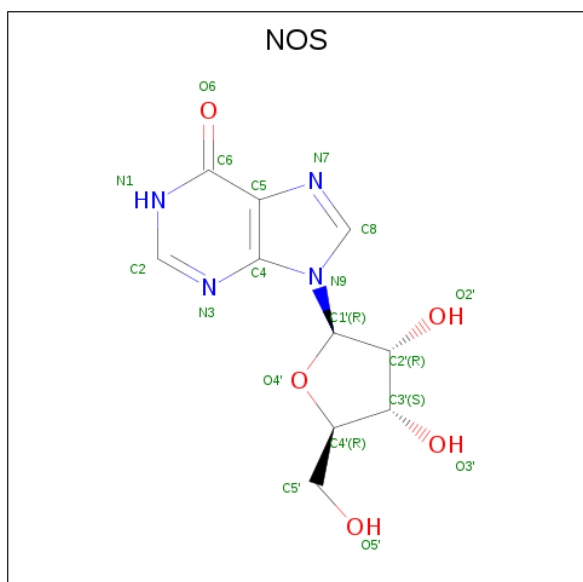
Chain	Residue	Modelled	Actual	Comment	Reference
B	316	LEU	-	EXPRESSION TAG	UNP Q2SZE4
B	317	ARG	-	EXPRESSION TAG	UNP Q2SZE4
B	318	SER	-	EXPRESSION TAG	UNP Q2SZE4
B	319	LEU	-	EXPRESSION TAG	UNP Q2SZE4
B	320	GLU	-	EXPRESSION TAG	UNP Q2SZE4
B	321	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	322	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	323	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	324	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	325	HIS	-	EXPRESSION TAG	UNP Q2SZE4
B	326	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	313	GLY	-	EXPRESSION TAG	UNP Q2SZE4
C	314	SER	-	EXPRESSION TAG	UNP Q2SZE4
C	315	LYS	-	EXPRESSION TAG	UNP Q2SZE4
C	316	LEU	-	EXPRESSION TAG	UNP Q2SZE4
C	317	ARG	-	EXPRESSION TAG	UNP Q2SZE4
C	318	SER	-	EXPRESSION TAG	UNP Q2SZE4
C	319	LEU	-	EXPRESSION TAG	UNP Q2SZE4
C	320	GLU	-	EXPRESSION TAG	UNP Q2SZE4
C	321	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	322	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	323	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	324	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	325	HIS	-	EXPRESSION TAG	UNP Q2SZE4
C	326	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	313	GLY	-	EXPRESSION TAG	UNP Q2SZE4
D	314	SER	-	EXPRESSION TAG	UNP Q2SZE4
D	315	LYS	-	EXPRESSION TAG	UNP Q2SZE4
D	316	LEU	-	EXPRESSION TAG	UNP Q2SZE4
D	317	ARG	-	EXPRESSION TAG	UNP Q2SZE4
D	318	SER	-	EXPRESSION TAG	UNP Q2SZE4
D	319	LEU	-	EXPRESSION TAG	UNP Q2SZE4
D	320	GLU	-	EXPRESSION TAG	UNP Q2SZE4
D	321	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	322	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	323	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	324	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	325	HIS	-	EXPRESSION TAG	UNP Q2SZE4
D	326	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	313	GLY	-	EXPRESSION TAG	UNP Q2SZE4
E	314	SER	-	EXPRESSION TAG	UNP Q2SZE4
E	315	LYS	-	EXPRESSION TAG	UNP Q2SZE4

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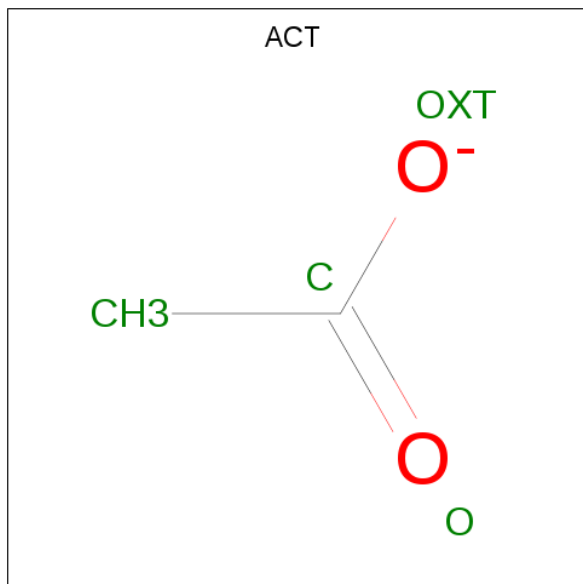
Chain	Residue	Modelled	Actual	Comment	Reference
E	316	LEU	-	EXPRESSION TAG	UNP Q2SZE4
E	317	ARG	-	EXPRESSION TAG	UNP Q2SZE4
E	318	SER	-	EXPRESSION TAG	UNP Q2SZE4
E	319	LEU	-	EXPRESSION TAG	UNP Q2SZE4
E	320	GLU	-	EXPRESSION TAG	UNP Q2SZE4
E	321	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	322	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	323	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	324	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	325	HIS	-	EXPRESSION TAG	UNP Q2SZE4
E	326	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	313	GLY	-	EXPRESSION TAG	UNP Q2SZE4
F	314	SER	-	EXPRESSION TAG	UNP Q2SZE4
F	315	LYS	-	EXPRESSION TAG	UNP Q2SZE4
F	316	LEU	-	EXPRESSION TAG	UNP Q2SZE4
F	317	ARG	-	EXPRESSION TAG	UNP Q2SZE4
F	318	SER	-	EXPRESSION TAG	UNP Q2SZE4
F	319	LEU	-	EXPRESSION TAG	UNP Q2SZE4
F	320	GLU	-	EXPRESSION TAG	UNP Q2SZE4
F	321	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	322	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	323	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	324	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	325	HIS	-	EXPRESSION TAG	UNP Q2SZE4
F	326	HIS	-	EXPRESSION TAG	UNP Q2SZE4

- Molecule 2 is INOSINE (three-letter code: NOS) (formula: C<sub>10</sub>H<sub>12</sub>N<sub>4</sub>O<sub>5</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			19	10	4	5		
2	B	1	Total	C	N	O	0	0
			19	10	4	5		
2	C	1	Total	C	N	O	0	0
			19	10	4	5		
2	D	1	Total	C	N	O	0	0
			19	10	4	5		
2	E	1	Total	C	N	O	0	0
			19	10	4	5		
2	F	1	Total	C	N	O	0	0
			19	10	4	5		

- Molecule 3 is ACETATE ION (three-letter code: ACT) (formula:  $C_2H_3O_2$ ).



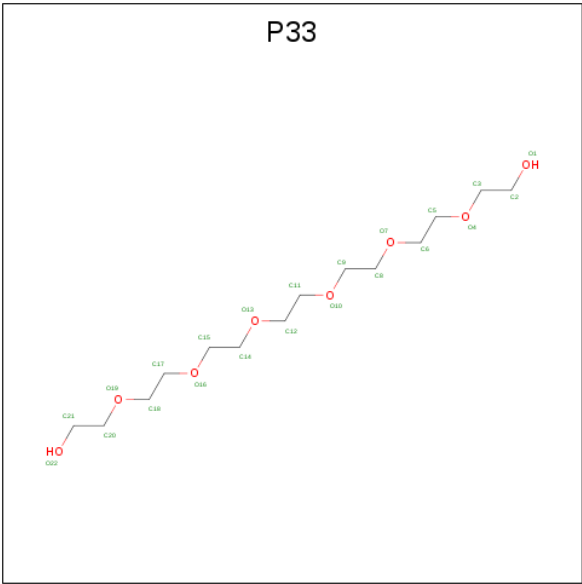
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	C	1	Total	C	O	0	0
			4	2	2		
3	C	1	Total	C	O	0	0
			4	2	2		
3	D	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is 3,6,9,12,15,18-HEXAOXAICOSANE-1,20-DIOL (three-letter code: P33) (formula: C<sub>14</sub>H<sub>30</sub>O<sub>8</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			22	14	8		

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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			22	14	8		
4	B	1	Total	C	O	0	0
			14	9	5		
4	C	1	Total	C	O	0	0
			19	12	7		
4	C	1	Total	C	O	0	0
			22	14	8		
4	E	1	Total	C	O	0	0
			22	14	8		

- Molecule 5 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	D	1	Total	Na	0	0
			1	1		
5	E	4	Total	Na	0	0
			4	4		
5	B	3	Total	Na	0	0
			3	3		
5	C	2	Total	Na	0	0
			2	2		
5	A	3	Total	Na	0	0
			3	3		
5	F	2	Total	Na	0	0
			2	2		

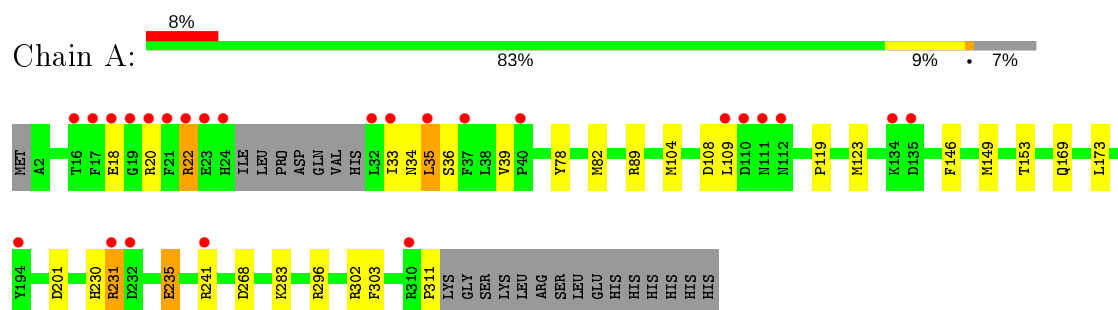
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	190	Total	O	0	0
			190	190		
6	B	160	Total	O	0	3
			163	163		
6	C	207	Total	O	0	0
			207	207		
6	D	141	Total	O	0	1
			142	142		
6	E	204	Total	O	0	1
			205	205		
6	F	147	Total	O	0	0
			147	147		

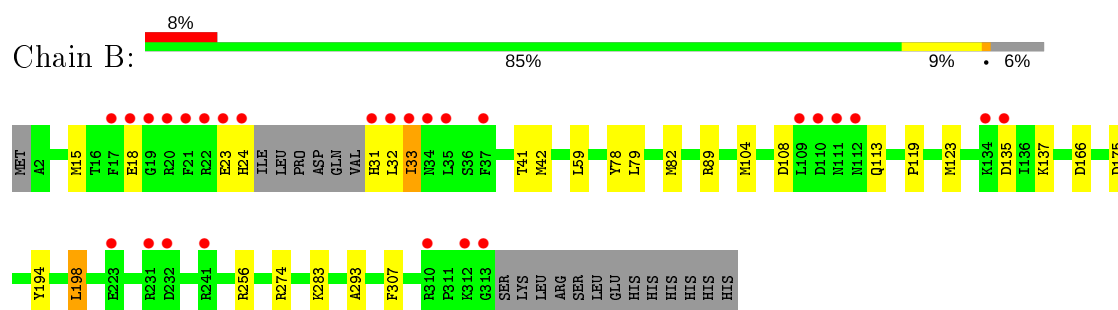
### 3 Residue-property plots [i](#)

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.

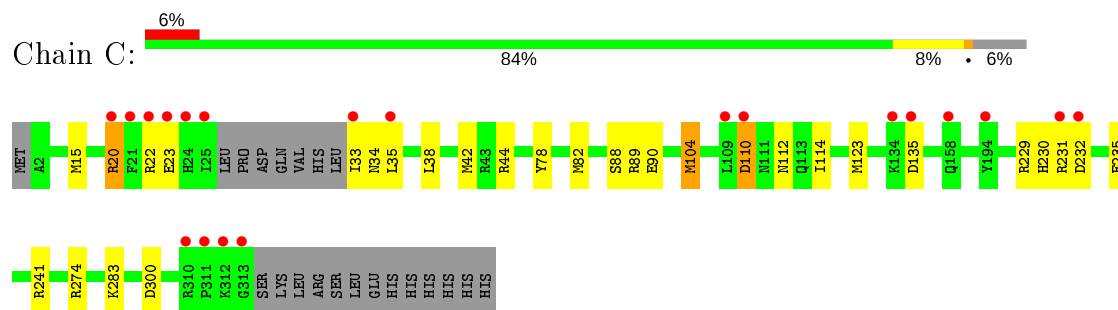
- Molecule 1: Ribokinase, putative



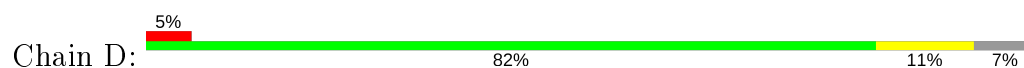
- Molecule 1: Ribokinase, putative

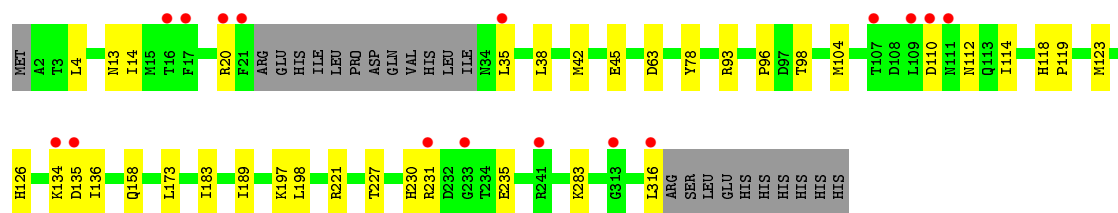


- Molecule 1: Ribokinase, putative

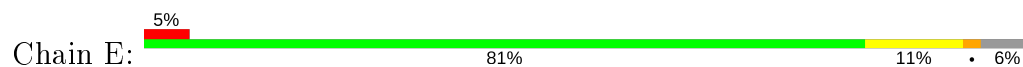


- Molecule 1: Ribokinase, putative

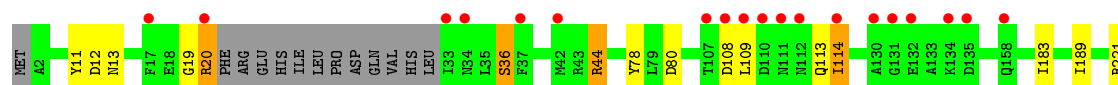
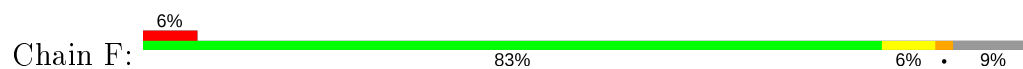




- Molecule 1: Ribokinase, putative



- Molecule 1: Ribokinase, putative



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	83.11Å 85.90Å 86.87Å 66.33° 68.47° 67.81°	Depositor
Resolution (Å)	47.78 – 1.70 38.48 – 1.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (47.78-1.70) 96.9 (38.48-1.70)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.92 (at 1.71Å)	Xtriage
Refinement program	REFMAC 5.5.0109	Depositor
R, $R_{free}$	0.176 , 0.207 0.176 , 0.207	Depositor DCC
$R_{free}$ test set	10501 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	20.3	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.40 , 53.1	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.007 for k,l,h 0.007 for l,h,k 0.008 for -k,-h,-l 0.008 for -l,-k,-h 0.009 for -h,-l,-k	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	15318	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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: NA, ACT, P33, NOS

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	0.90	0/2378	0.94	4/3219 (0.1%)
1	B	0.85	0/2400	0.89	3/3248 (0.1%)
1	C	0.93	1/2383 (0.0%)	0.93	3/3225 (0.1%)
1	D	0.88	0/2367	0.87	2/3202 (0.1%)
1	E	0.95	0/2414	0.95	5/3268 (0.2%)
1	F	0.84	0/2328	0.93	6/3154 (0.2%)
All	All	0.89	1/14270 (0.0%)	0.92	23/19316 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	104	MET	CG-SD	-5.61	1.66	1.81

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	221	ARG	NE-CZ-NH1	-10.56	115.02	120.30
1	C	104	MET	CG-SD-CE	-9.94	84.29	100.20
1	F	221	ARG	NE-CZ-NH2	8.73	124.67	120.30
1	A	268	ASP	CB-CG-OD1	6.99	124.59	118.30
1	E	229	ARG	NE-CZ-NH2	6.45	123.52	120.30
1	E	268	ASP	CB-CG-OD1	6.08	123.78	118.30
1	B	108	ASP	CB-CG-OD1	6.02	123.72	118.30
1	E	244	ARG	NE-CZ-NH1	-5.88	117.36	120.30
1	A	35	LEU	CA-CB-CG	5.78	128.59	115.30
1	D	63	ASP	CB-CG-OD1	5.59	123.33	118.30
1	E	274	ARG	NE-CZ-NH1	5.44	123.02	120.30
1	F	302	ARG	NE-CZ-NH2	5.34	122.97	120.30
1	E	274	ARG	NE-CZ-NH2	-5.33	117.63	120.30
1	F	80	ASP	CB-CG-OD1	5.32	123.09	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	201	ASP	CB-CG-OD1	5.32	123.09	118.30
1	C	104	MET	CA-CB-CG	-5.28	104.32	113.30
1	A	108	ASP	CB-CG-OD1	5.28	123.05	118.30
1	F	12	ASP	CB-CG-OD1	5.25	123.02	118.30
1	C	274	ARG	NE-CZ-NH2	-5.25	117.68	120.30
1	B	175	ASP	CB-CG-OD2	5.12	122.91	118.30
1	D	316	LEU	CA-CB-CG	5.11	127.05	115.30
1	B	59	LEU	CB-CG-CD2	5.07	119.62	111.00
1	F	302	ARG	NE-CZ-NH1	-5.06	117.77	120.30

There are no chirality outliers.

There are no planarity outliers.

## 5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	2325	0	2269	22	0
1	B	2346	0	2293	14	0
1	C	2333	0	2281	31	0
1	D	2315	0	2271	19	0
1	E	2354	0	2307	34	0
1	F	2277	0	2225	21	0
2	A	19	0	11	0	0
2	B	19	0	11	0	0
2	C	19	0	11	0	0
2	D	19	0	11	0	0
2	E	19	0	11	0	0
2	F	19	0	11	0	0
3	A	16	0	12	1	0
3	B	4	0	3	0	0
3	C	12	0	9	0	0
3	D	4	0	3	0	0
3	E	20	0	15	0	0
3	F	8	0	6	2	0
4	A	22	0	30	4	0
4	B	36	0	47	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	C	41	0	55	1	0
4	E	22	0	30	2	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
5	C	2	0	0	0	0
5	D	1	0	0	0	0
5	E	4	0	0	0	0
5	F	2	0	0	0	0
6	A	190	0	0	3	0
6	B	163	0	0	2	0
6	C	207	0	0	1	0
6	D	142	0	0	3	0
6	E	205	0	0	3	0
6	F	147	0	0	1	0
All	All	15318	0	13922	119	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 4.

All (119) 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:F:44[A]:ARG:HB2	1:F:44[A]:ARG:HH11	1.28	0.99
1:F:13:ASN:OD1	1:F:44[B]:ARG:HD3	1.70	0.90
1:A:230:HIS:HE1	1:A:235:GLU:OE2	1.55	0.90
1:B:33:ILE:HD13	1:D:112:ASN:HB3	1.57	0.86
1:C:33:ILE:HA	1:E:112:ASN:HD22	1.45	0.80
1:D:93:ARG:HD2	6:D:1028:HOH:O	1.82	0.79
1:D:183:ILE:HG23	1:D:189:ILE:HD11	1.66	0.76
1:C:33:ILE:HA	1:E:112:ASN:ND2	2.01	0.76
1:D:104[B]:MET:HA	1:D:104[B]:MET:HE3	1.68	0.74
1:F:13:ASN:OD1	1:F:44[A]:ARG:HD3	1.88	0.74
1:E:82:MET:HE1	1:E:89:ARG:HG2	1.70	0.74
1:A:230:HIS:CE1	1:A:235:GLU:OE2	2.39	0.73
1:F:44[A]:ARG:HB2	1:F:44[A]:ARG:NH1	2.03	0.73
4:E:332:P33:H201	6:E:616:HOH:O	1.89	0.71
1:E:20:ARG:HD3	1:E:110:ASP:OD2	1.91	0.71
1:B:82:MET:HE1	1:B:89:ARG:HG2	1.74	0.69
1:C:112:ASN:HD22	1:E:33:ILE:H	1.43	0.67
1:E:230:HIS:O	1:E:232:ASP:N	2.29	0.65
1:C:20:ARG:NE	1:C:110:ASP:OD1	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:123[B]:MET:CE	1:E:40:PRO:HB3	2.26	0.65
1:C:42:MET:CE	1:E:118:HIS:HB2	2.27	0.65
1:A:82:MET:HE1	1:A:89:ARG:HG2	1.80	0.64
1:C:112:ASN:ND2	1:E:33:ILE:H	1.95	0.63
1:A:302:ARG:HG2	4:A:331:P33:H141	1.79	0.63
1:A:18:GLU:HA	1:A:109:LEU:HD13	1.81	0.61
1:A:35:LEU:HD22	1:F:114:ILE:HG13	1.82	0.61
1:C:38:LEU:HD22	1:E:173:LEU:HD11	1.83	0.60
1:F:13:ASN:OD1	1:F:44[B]:ARG:CD	2.45	0.60
1:A:302:ARG:HH21	4:A:331:P33:H171	1.67	0.59
1:A:169:GLN:HG2	1:F:36:SER:OG	2.03	0.58
1:F:230:HIS:NE2	1:F:235:GLU:OE2	2.24	0.58
1:E:134:LYS:O	1:E:135:ASP:HB2	2.03	0.58
6:C:404:HOH:O	4:E:332:P33:H172	2.03	0.57
1:F:20:ARG:HD2	1:F:108:ASP:OD1	2.04	0.57
1:F:229:ARG:HD2	6:F:1049:HOH:O	2.05	0.57
1:A:231:ARG:HG2	6:A:789:HOH:O	2.05	0.57
1:D:20:ARG:HD2	1:D:110:ASP:OD2	2.05	0.56
1:D:14:ILE:HD12	1:D:45:GLU:HG3	1.88	0.56
1:A:146:PHE:HB2	1:A:173:LEU:HD13	1.89	0.55
1:B:82:MET:CE	1:B:89:ARG:HG2	2.35	0.55
1:C:82:MET:HE1	1:C:89:ARG:HG2	1.86	0.55
1:C:15:MET:SD	1:C:42:MET:HE2	2.46	0.55
1:F:19:GLY:O	1:F:109:LEU:HB2	2.07	0.54
1:A:20:ARG:NH1	1:A:109:LEU:HD23	2.22	0.54
1:A:296[B]:ARG:HB2	3:A:330:ACT:C	2.37	0.54
4:A:331:P33:H142	6:A:500:HOH:O	2.07	0.54
1:A:34:ASN:HD21	3:F:328:ACT:H3	1.73	0.54
1:C:42:MET:HE3	1:E:118:HIS:CG	2.43	0.53
1:C:112:ASN:HD22	1:E:33:ILE:N	2.05	0.53
1:D:126:HIS:CD2	1:D:126:HIS:H	2.26	0.53
1:D:96:PRO:O	1:D:98:THR:HG23	2.09	0.53
1:D:13:ASN:HB2	1:D:104[B]:MET:HE3	1.91	0.53
1:B:119:PRO:HG3	1:D:38:LEU:HD22	1.91	0.52
1:D:119:PRO:HB2	1:D:123:MET:HG3	1.92	0.52
1:F:11:TYR:HB3	1:F:44[A]:ARG:HD2	1.92	0.51
1:A:22:ARG:HD2	1:A:22:ARG:O	2.10	0.51
1:C:123[B]:MET:HE2	1:E:40:PRO:HB3	1.91	0.51
1:F:302:ARG:HG2	3:F:327:ACT:H3	1.93	0.51
1:A:302:ARG:NH2	4:A:331:P33:H171	2.26	0.50
1:C:104:MET:HG2	1:E:104:MET:SD	2.51	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:183:ILE:HG23	1:F:189:ILE:HD11	1.93	0.50
1:A:36:SER:HB2	6:A:744:HOH:O	2.10	0.50
1:B:15:MET:HG3	1:B:42:MET:HG3	1.93	0.50
1:B:194:TYR:CE1	1:B:198:LEU:HD21	2.47	0.49
1:C:232:ASP:N	1:C:232:ASP:OD1	2.36	0.48
1:D:230:HIS:HE1	1:D:235:GLU:OE2	1.96	0.48
1:F:20:ARG:CD	1:F:108:ASP:OD1	2.60	0.48
1:C:123[B]:MET:HE1	1:E:40:PRO:HB3	1.95	0.48
1:B:274:ARG:HB3	1:B:307:PHE:CE2	2.49	0.48
1:E:274:ARG:HB3	1:E:307:PHE:CE2	2.49	0.48
1:E:179:LEU:HD22	1:E:202:LYS:HD2	1.96	0.47
1:E:20:ARG:HB2	1:E:23:GLU:HG3	1.97	0.47
1:C:229:ARG:HB3	1:C:229:ARG:HH11	1.80	0.47
1:E:35:LEU:HD23	1:E:35:LEU:O	2.15	0.47
1:B:79:LEU:HD22	1:B:89:ARG:HD2	1.98	0.46
1:A:303:PHE:CD2	1:A:311:PRO:HD3	2.51	0.46
1:E:19:GLY:O	1:E:108:ASP:HB2	2.16	0.45
1:E:195:GLU:O	1:E:199:VAL:HG23	2.16	0.45
1:A:82:MET:CE	1:A:89:ARG:HG2	2.46	0.45
1:B:113:GLN:NE2	6:B:1031:HOH:O	2.50	0.45
1:E:18:GLU:HG2	6:E:945:HOH:O	2.17	0.45
1:C:230:HIS:HE1	1:C:235:GLU:OE1	2.00	0.45
1:C:88:SER:OG	1:C:90:GLU:HG3	2.17	0.45
1:C:42:MET:CE	1:E:118:HIS:CB	2.93	0.45
1:D:20:ARG:CD	1:D:110:ASP:OD2	2.65	0.44
1:D:221:ARG:CZ	1:D:227:THR:HG23	2.47	0.44
1:C:114:ILE:HG12	1:E:35:LEU:HD21	1.99	0.44
1:A:149:MET:O	1:A:153:THR:HG23	2.18	0.44
1:C:22:ARG:NH2	1:E:31:HIS:O	2.51	0.44
1:C:42:MET:HE1	1:E:118:HIS:CB	2.48	0.44
1:C:229:ARG:NH1	1:C:229:ARG:HB3	2.32	0.44
1:C:230:HIS:CE1	1:C:235:GLU:OE2	2.71	0.44
1:C:42:MET:HE1	1:E:118:HIS:HB2	2.00	0.44
1:E:36[B]:SER:OG	6:E:921:HOH:O	2.21	0.43
1:B:119:PRO:HB2	1:B:123[A]:MET:HG2	2.01	0.43
1:C:35:LEU:HD12	1:C:35:LEU:N	2.33	0.43
1:D:221:ARG:NH1	1:D:227:THR:HG21	2.34	0.42
1:E:221:ARG:HD2	1:F:308:GLY:HA2	2.01	0.42
1:C:20:ARG:HD2	1:C:23:GLU:OE2	2.18	0.42
1:C:42:MET:HB2	1:C:42:MET:HE3	1.71	0.42
1:D:4:LEU:HB2	1:D:136:ILE:HG13	2.02	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:119:PRO:HB2	1:A:123[A]:MET:HG2	2.02	0.42
1:B:32:LEU:HD22	1:D:110:ASP:O	2.20	0.42
1:D:118:HIS:ND1	6:D:677:HOH:O	2.26	0.42
1:E:31:HIS:O	1:E:31:HIS:CG	2.73	0.42
1:F:20:ARG:CZ	1:F:20:ARG:C	2.88	0.42
1:B:89:ARG:NH1	6:B:800:HOH:O	2.44	0.42
1:C:15:MET:SD	1:E:104:MET:HE1	2.60	0.41
1:F:19:GLY:CA	1:F:109:LEU:HD13	2.50	0.41
1:F:19:GLY:HA2	1:F:109:LEU:HD13	2.02	0.41
1:B:293:ALA:O	1:F:286:HIS:HE1	2.02	0.41
1:D:126:HIS:HD2	6:D:339:HOH:O	2.04	0.41
1:F:274:ARG:HB3	1:F:307:PHE:CE2	2.56	0.41
1:B:166:ASP:CG	1:B:256:ARG:HE	2.24	0.41
4:C:331:P33:H121	4:C:331:P33:H92	1.87	0.41
1:E:20:ARG:O	1:E:21:PHE:C	2.60	0.41
1:A:39:VAL:O	1:A:39:VAL:HG12	2.21	0.40
1:C:42:MET:CE	1:E:118:HIS:CG	3.04	0.40
1:A:33:ILE:HA	1:A:33:ILE:HD12	1.98	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles [i](#)

### 5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	301/326 (92%)	297 (99%)	4 (1%)	0	100	100
1	B	304/326 (93%)	300 (99%)	4 (1%)	0	100	100
1	C	302/326 (93%)	298 (99%)	3 (1%)	1 (0%)	41	24
1	D	301/326 (92%)	297 (99%)	4 (1%)	0	100	100
1	E	306/326 (94%)	300 (98%)	4 (1%)	2 (1%)	22	8
1	F	296/326 (91%)	291 (98%)	5 (2%)	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1810/1956 (92%)	1783 (98%)	24 (1%)	3 (0%)	47 30

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	231	ARG
1	E	231	ARG
1	E	22	ARG

### 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	234/255 (92%)	227 (97%)	7 (3%)	41 22
1	B	237/255 (93%)	225 (95%)	12 (5%)	24 8
1	C	235/255 (92%)	226 (96%)	9 (4%)	33 14
1	D	234/255 (92%)	221 (94%)	13 (6%)	21 7
1	E	239/255 (94%)	228 (95%)	11 (5%)	27 10
1	F	229/255 (90%)	219 (96%)	10 (4%)	28 11
All	All	1408/1530 (92%)	1346 (96%)	62 (4%)	29 11

All (62) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	ARG
1	A	78	TYR
1	A	104	MET
1	A	231	ARG
1	A	235	GLU
1	A	241	ARG
1	A	283	LYS
1	B	18	GLU
1	B	23	GLU

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Mol	Chain	Res	Type
1	B	24	HIS
1	B	31	HIS
1	B	33	ILE
1	B	41	THR
1	B	78	TYR
1	B	104	MET
1	B	135	ASP
1	B	137	LYS
1	B	198	LEU
1	B	283	LYS
1	C	20	ARG
1	C	34	ASN
1	C	44	ARG
1	C	78	TYR
1	C	110	ASP
1	C	135	ASP
1	C	241	ARG
1	C	283	LYS
1	C	300	ASP
1	D	35	LEU
1	D	42[A]	MET
1	D	42[B]	MET
1	D	78	TYR
1	D	114	ILE
1	D	134	LYS
1	D	135	ASP
1	D	158	GLN
1	D	173	LEU
1	D	197	LYS
1	D	198	LEU
1	D	231	ARG
1	D	283	LYS
1	E	18	GLU
1	E	35	LEU
1	E	78	TYR
1	E	173	LEU
1	E	194	TYR
1	E	197	LYS
1	E	198	LEU
1	E	223	GLU
1	E	231	ARG
1	E	283	LYS

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Mol	Chain	Res	Type
1	E	312	LYS
1	F	20	ARG
1	F	36	SER
1	F	44[A]	ARG
1	F	44[B]	ARG
1	F	78	TYR
1	F	113	GLN
1	F	114	ILE
1	F	235	GLU
1	F	283	LYS
1	F	287	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (24) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	ASN
1	A	112	ASN
1	A	113	GLN
1	A	118	HIS
1	A	128	ASN
1	A	230	HIS
1	A	287	GLN
1	B	112	ASN
1	B	113	GLN
1	B	158	GLN
1	B	265	HIS
1	B	287	GLN
1	C	34	ASN
1	C	112	ASN
1	C	113	GLN
1	C	230	HIS
1	D	126	HIS
1	D	230	HIS
1	D	236	GLN
1	E	112	ASN
1	F	112	ASN
1	F	113	GLN
1	F	158	GLN
1	F	236	GLN

### 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 ⓘ

Of 43 ligands modelled in this entry, 15 are monoatomic - leaving 28 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	ACT	E	329	-	1,3,3	1.15	0	0,3,3	0.00	-
2	NOS	A	401	-	17,21,21	1.47	3 (17%)	16,31,31	2.81	6 (37%)
3	ACT	F	328	-	1,3,3	2.56	1 (100%)	0,3,3	0.00	-
4	P33	E	332	-	21,21,21	0.63	0	20,20,20	1.03	1 (5%)
4	P33	C	331	-	21,21,21	0.52	0	20,20,20	0.59	0
3	ACT	A	330	-	1,3,3	2.62	1 (100%)	0,3,3	0.00	-
3	ACT	A	329	-	1,3,3	1.85	0	0,3,3	0.00	-
2	NOS	B	401	-	17,21,21	1.91	6 (35%)	16,31,31	1.98	3 (18%)
3	ACT	C	327	-	1,3,3	1.44	0	0,3,3	0.00	-
4	P33	B	329	-	13,13,21	0.54	0	12,12,20	0.51	0
2	NOS	D	401	-	17,21,21	1.90	5 (29%)	16,31,31	2.31	6 (37%)
2	NOS	F	401	-	17,21,21	1.62	4 (23%)	16,31,31	2.49	5 (31%)
4	P33	B	328	-	21,21,21	0.57	0	20,20,20	0.70	0
4	P33	A	331	-	21,21,21	0.60	0	20,20,20	1.30	3 (15%)
3	ACT	A	327	-	1,3,3	1.59	0	0,3,3	0.00	-
2	NOS	C	401	-	17,21,21	1.73	3 (17%)	16,31,31	2.12	4 (25%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
3	ACT	C	328	-	1,3,3	1.85	0	0,3,3	0.00	-
3	ACT	A	328	-	1,3,3	2.40	1 (100%)	0,3,3	0.00	-
3	ACT	E	328	-	1,3,3	1.58	0	0,3,3	0.00	-
3	ACT	B	327	-	1,3,3	2.19	1 (100%)	0,3,3	0.00	-
3	ACT	F	327	-	1,3,3	2.97	1 (100%)	0,3,3	0.00	-
3	ACT	C	329	-	1,3,3	2.44	1 (100%)	0,3,3	0.00	-
3	ACT	D	327	-	1,3,3	1.56	0	0,3,3	0.00	-
4	P33	C	330	-	18,18,21	0.53	0	17,17,20	1.40	3 (17%)
2	NOS	E	401	-	17,21,21	1.90	4 (23%)	16,31,31	2.65	5 (31%)
3	ACT	E	327	-	1,3,3	0.72	0	0,3,3	0.00	-
3	ACT	E	331	-	1,3,3	3.57	1 (100%)	0,3,3	0.00	-
3	ACT	E	330	-	1,3,3	2.28	1 (100%)	0,3,3	0.00	-

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	NOS	D	401	-	-	0/2/22/22	0/3/3/3
4	P33	E	332	-	-	11/19/19/19	-
4	P33	C	330	-	-	8/16/16/19	-
4	P33	B	328	-	-	12/19/19/19	-
4	P33	A	331	-	-	7/19/19/19	-
4	P33	C	331	-	-	12/19/19/19	-
2	NOS	A	401	-	-	0/2/22/22	0/3/3/3
2	NOS	C	401	-	-	0/2/22/22	0/3/3/3
2	NOS	E	401	-	-	0/2/22/22	0/3/3/3
2	NOS	F	401	-	-	0/2/22/22	0/3/3/3
4	P33	B	329	-	-	1/11/11/19	-
2	NOS	B	401	-	-	0/2/22/22	0/3/3/3

All (33) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NOS	O6-C6	4.44	1.35	1.24
2	E	401	NOS	C6-C5	4.34	1.48	1.41
2	E	401	NOS	O6-C6	4.24	1.35	1.24
2	F	401	NOS	C6-C5	3.78	1.47	1.41

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	NOS	C6-C5	3.64	1.47	1.41
2	C	401	NOS	C6-C5	3.61	1.47	1.41
2	C	401	NOS	O6-C6	3.57	1.33	1.24
3	E	331	ACT	CH3-C	3.57	1.53	1.48
2	D	401	NOS	C2-N3	3.48	1.37	1.32
2	B	401	NOS	O6-C6	3.42	1.33	1.24
2	A	401	NOS	O6-C6	3.40	1.33	1.24
2	F	401	NOS	O6-C6	3.24	1.32	1.24
2	E	401	NOS	O4'-C1'	2.99	1.45	1.41
2	B	401	NOS	O4'-C1'	2.99	1.45	1.41
3	F	327	ACT	CH3-C	2.97	1.52	1.48
2	B	401	NOS	C2-N3	2.79	1.36	1.32
3	A	330	ACT	CH3-C	2.62	1.52	1.48
2	D	401	NOS	C5-C4	2.58	1.47	1.40
3	F	328	ACT	CH3-C	2.56	1.52	1.48
2	F	401	NOS	O4'-C1'	2.53	1.44	1.41
3	C	329	ACT	CH3-C	2.44	1.51	1.48
3	A	328	ACT	CH3-C	2.40	1.51	1.48
2	D	401	NOS	C6-N1	2.33	1.37	1.33
2	A	401	NOS	C6-C5	2.32	1.45	1.41
2	D	401	NOS	C6-C5	2.32	1.45	1.41
2	A	401	NOS	C5-C4	2.31	1.47	1.40
3	E	330	ACT	CH3-C	2.28	1.51	1.48
2	B	401	NOS	C5-C4	2.28	1.47	1.40
2	C	401	NOS	C6-N1	2.20	1.36	1.33
3	B	327	ACT	CH3-C	2.19	1.51	1.48
2	F	401	NOS	C5-C4	2.06	1.46	1.40
2	B	401	NOS	O3'-C3'	2.01	1.47	1.43
2	E	401	NOS	C5-C4	2.00	1.46	1.40

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	F	401	NOS	C6-C5-C4	-7.32	113.81	120.80
2	A	401	NOS	C6-C5-C4	-6.72	114.38	120.80
2	E	401	NOS	C6-C5-C4	-6.56	114.54	120.80
2	E	401	NOS	N3-C2-N1	-5.85	119.54	128.68
2	B	401	NOS	C6-C5-C4	-5.26	115.78	120.80
2	C	401	NOS	C6-C5-C4	-5.15	115.88	120.80
2	D	401	NOS	C6-C5-C4	-4.77	116.24	120.80
2	A	401	NOS	N3-C2-N1	-4.68	121.37	128.68
2	C	401	NOS	N3-C2-N1	-4.47	121.69	128.68

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	401	NOS	C2-N1-C6	4.34	123.14	115.88
2	B	401	NOS	N3-C2-N1	-3.84	122.67	128.68
2	A	401	NOS	C2-N1-C6	3.74	122.14	115.88
2	D	401	NOS	O4'-C1'-C2'	-3.59	101.68	106.93
2	D	401	NOS	N3-C2-N1	-3.55	123.12	128.68
4	C	330	P33	C12-O13-C14	3.39	127.96	113.29
2	F	401	NOS	C2-N1-C6	3.21	121.26	115.88
2	A	401	NOS	O4'-C1'-C2'	-3.10	102.39	106.93
2	A	401	NOS	C3'-C2'-C1'	3.02	105.52	100.98
2	F	401	NOS	O4'-C1'-C2'	-2.95	102.61	106.93
2	C	401	NOS	C2-N1-C6	2.92	120.77	115.88
2	D	401	NOS	C2-N1-C6	2.89	120.72	115.88
4	A	331	P33	O16-C17-C18	2.88	123.39	110.39
2	B	401	NOS	C2-N1-C6	2.76	120.50	115.88
4	C	330	P33	O10-C11-C12	2.73	122.71	110.39
2	A	401	NOS	C1'-N9-C4	-2.70	121.89	126.64
2	F	401	NOS	N3-C2-N1	-2.46	124.83	128.68
2	F	401	NOS	O4'-C4'-C3'	-2.37	100.43	105.11
2	E	401	NOS	O4'-C1'-C2'	-2.34	103.51	106.93
2	D	401	NOS	C4-C5-N7	-2.27	107.03	109.40
4	A	331	P33	C9-O10-C11	-2.23	103.62	113.29
2	D	401	NOS	O2'-C2'-C1'	-2.17	102.84	110.85
4	A	331	P33	O4-C3-C2	-2.17	100.55	110.07
2	C	401	NOS	C1'-N9-C4	-2.14	122.88	126.64
4	E	332	P33	O16-C15-C14	2.13	119.99	110.39
4	C	330	P33	O13-C12-C11	-2.07	101.04	110.39
2	E	401	NOS	C1'-N9-C4	-2.01	123.11	126.64

There are no chirality outliers.

All (51) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	331	P33	C12-C11-O10-C9
4	C	331	P33	O1-C2-C3-O4
4	E	332	P33	O10-C11-C12-O13
4	C	331	P33	O4-C5-C6-O7
4	C	330	P33	O10-C11-C12-O13
4	B	328	P33	O7-C8-C9-O10
4	A	331	P33	O16-C17-C18-O19
4	E	332	P33	O19-C20-C21-O22
4	C	331	P33	O19-C20-C21-O22
4	B	328	P33	O19-C20-C21-O22

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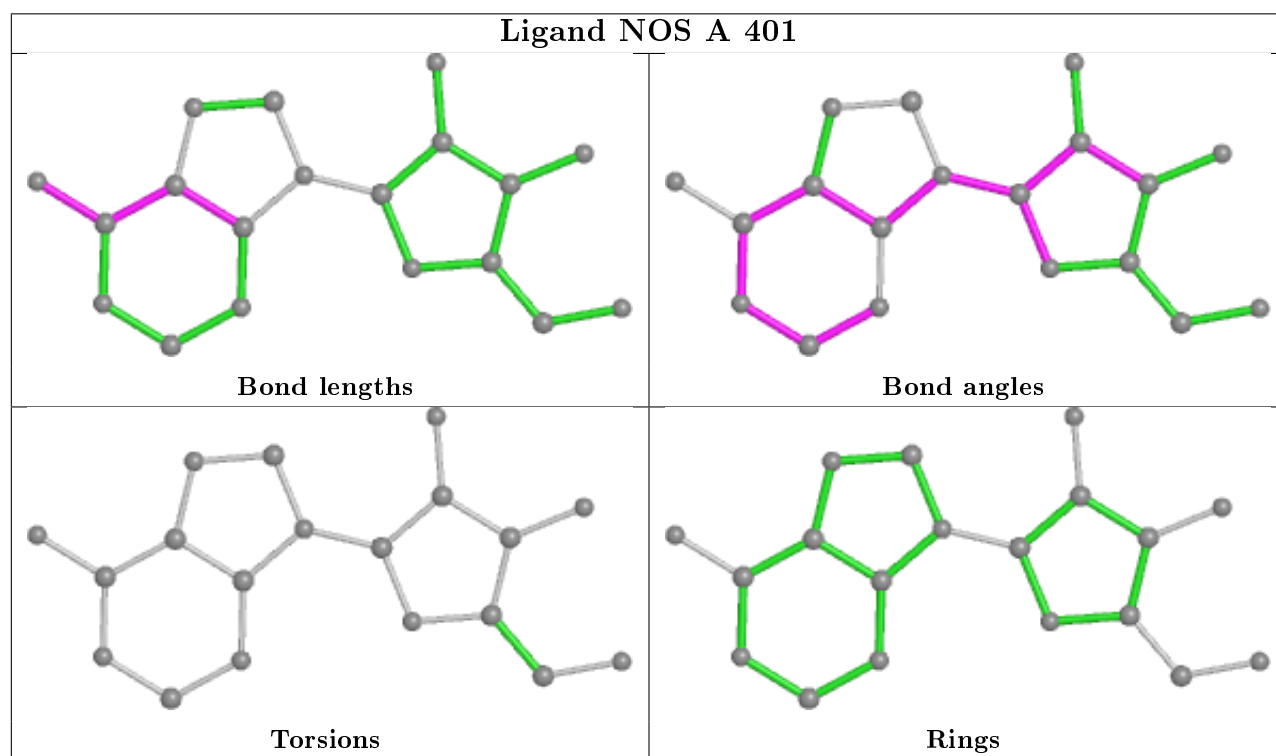
Mol	Chain	Res	Type	Atoms
4	C	331	P33	O13-C14-C15-O16
4	C	331	P33	O7-C8-C9-O10
4	E	332	P33	O4-C5-C6-O7
4	B	328	P33	C6-C5-O4-C3
4	C	331	P33	O16-C17-C18-O19
4	C	331	P33	O10-C11-C12-O13
4	E	332	P33	O16-C17-C18-O19
4	B	328	P33	O1-C2-C3-O4
4	B	329	P33	O16-C17-C18-O19
4	A	331	P33	C17-C18-O19-C20
4	C	330	P33	C8-C9-O10-C11
4	C	331	P33	C6-C5-O4-C3
4	E	332	P33	C6-C5-O4-C3
4	C	331	P33	C15-C14-O13-C12
4	C	330	P33	C11-C12-O13-C14
4	C	331	P33	C9-C8-O7-C6
4	A	331	P33	C8-C9-O10-C11
4	C	330	P33	C17-C18-O19-C20
4	E	332	P33	C5-C6-O7-C8
4	B	328	P33	C14-C15-O16-C17
4	B	328	P33	C17-C18-O19-C20
4	A	331	P33	C14-C15-O16-C17
4	C	331	P33	C5-C6-O7-C8
4	A	331	P33	C18-C17-O16-C15
4	B	328	P33	O13-C14-C15-O16
4	B	328	P33	C21-C20-O19-C18
4	C	330	P33	C5-C6-O7-C8
4	B	328	P33	O16-C17-C18-O19
4	A	331	P33	O10-C11-C12-O13
4	E	332	P33	C21-C20-O19-C18
4	E	332	P33	C11-C12-O13-C14
4	E	332	P33	C2-C3-O4-C5
4	E	332	P33	C17-C18-O19-C20
4	E	332	P33	C9-C8-O7-C6
4	B	328	P33	C18-C17-O16-C15
4	C	330	P33	O4-C5-C6-O7
4	C	330	P33	C9-C8-O7-C6
4	B	328	P33	O4-C5-C6-O7
4	C	330	P33	C14-C15-O16-C17
4	B	328	P33	C9-C8-O7-C6
4	A	331	P33	O13-C14-C15-O16

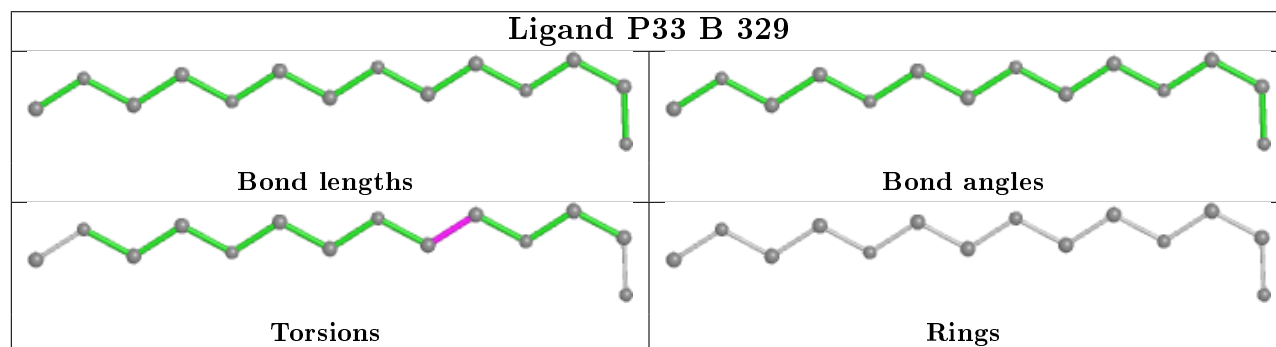
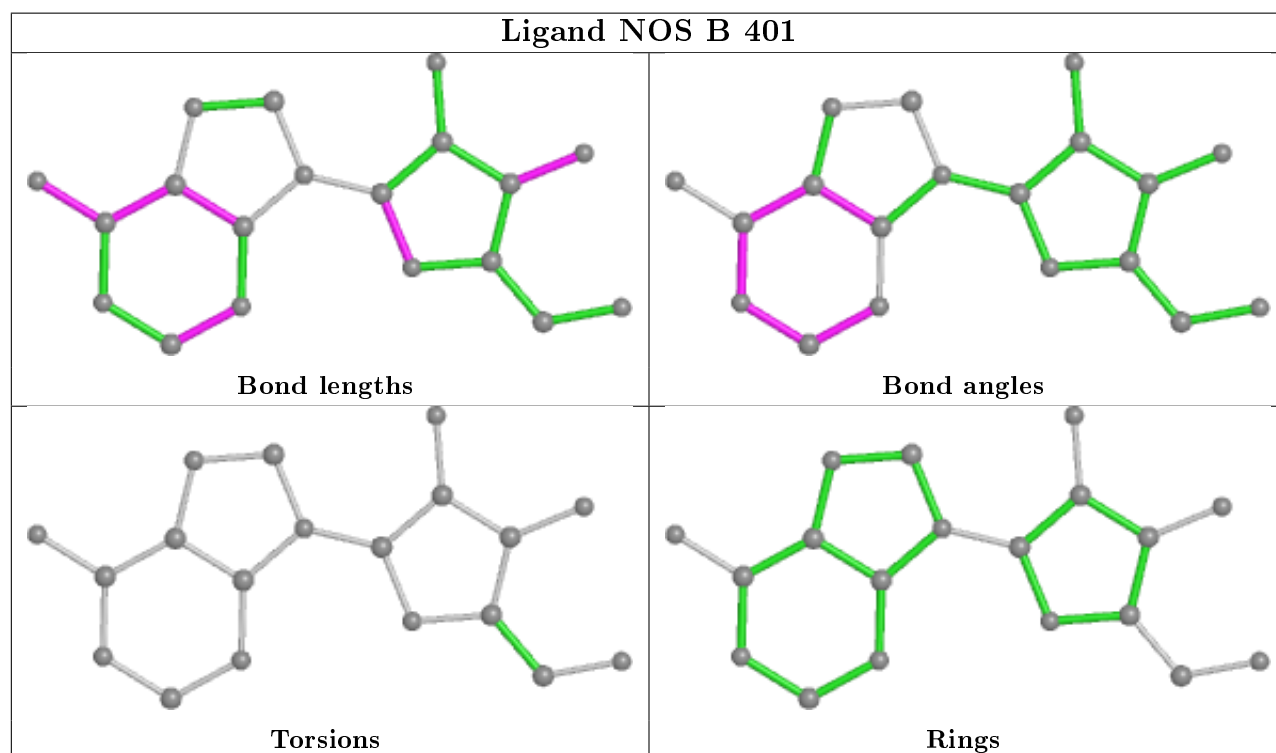
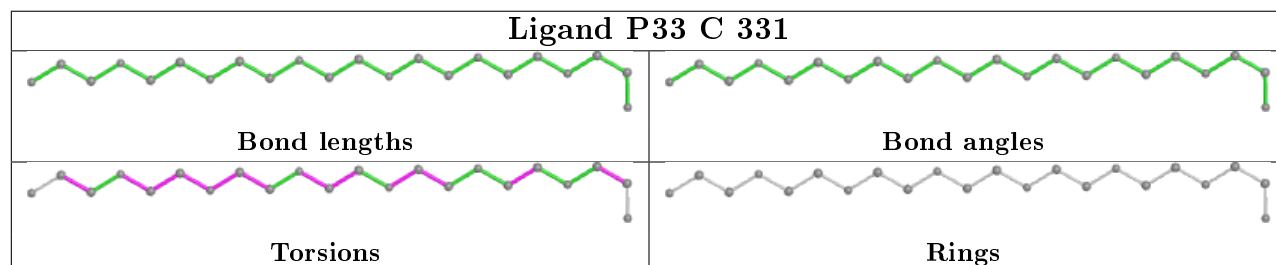
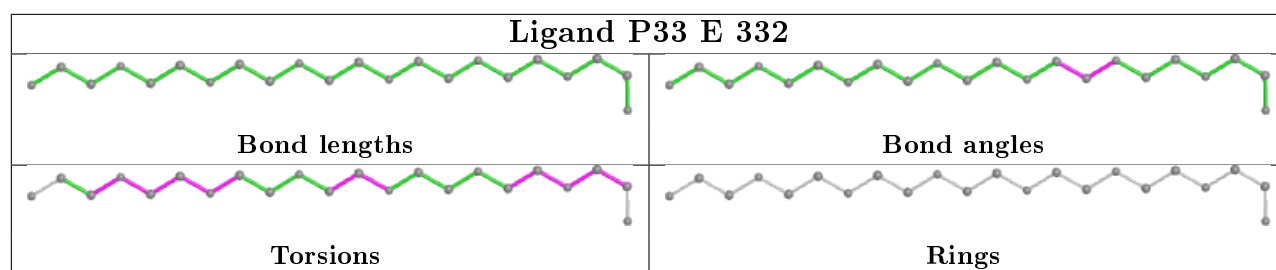
There are no ring outliers.

6 monomers are involved in 10 short contacts:

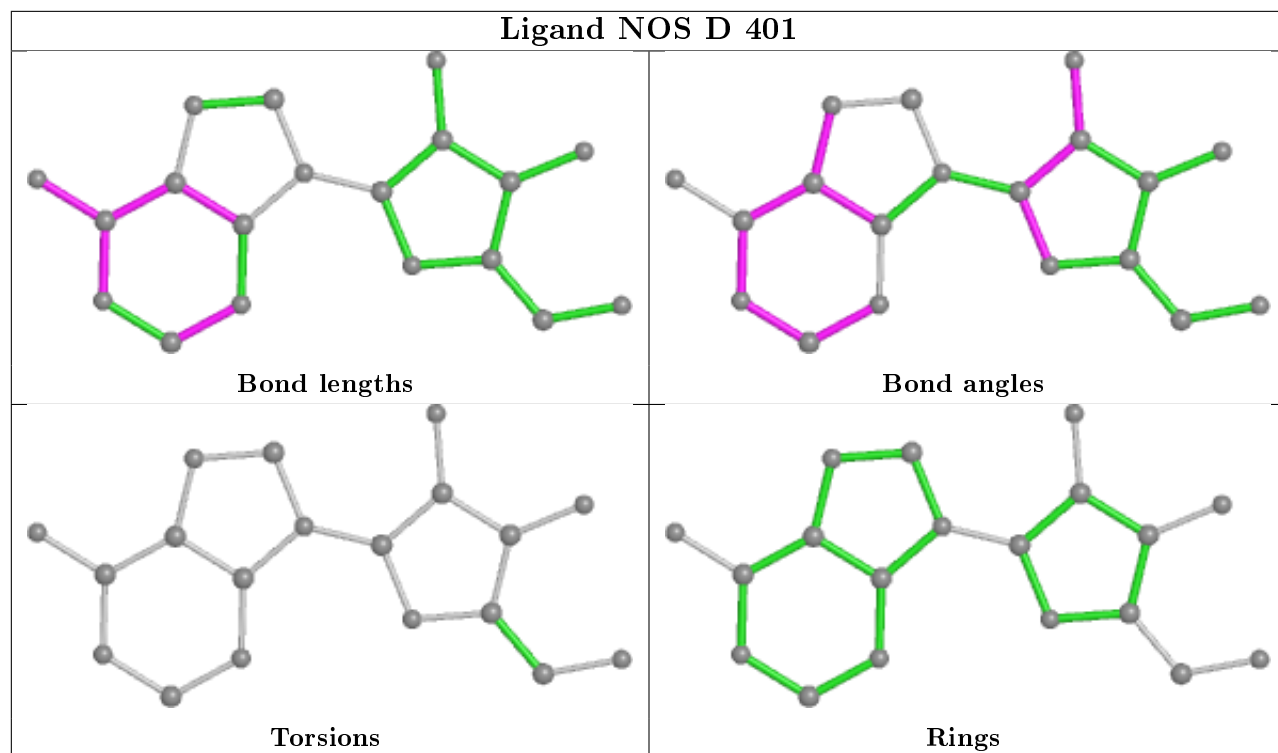
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	328	ACT	1	0
4	E	332	P33	2	0
4	C	331	P33	1	0
3	A	330	ACT	1	0
4	A	331	P33	4	0
3	F	327	ACT	1	0

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.

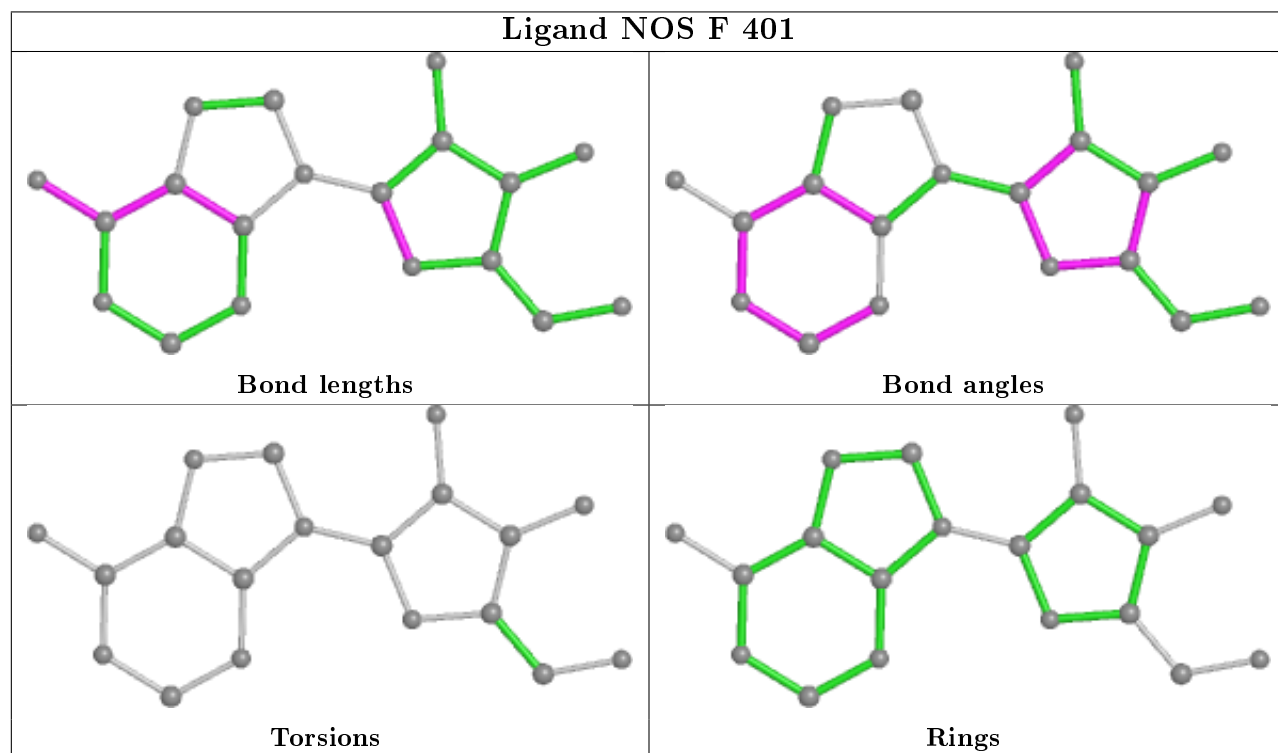




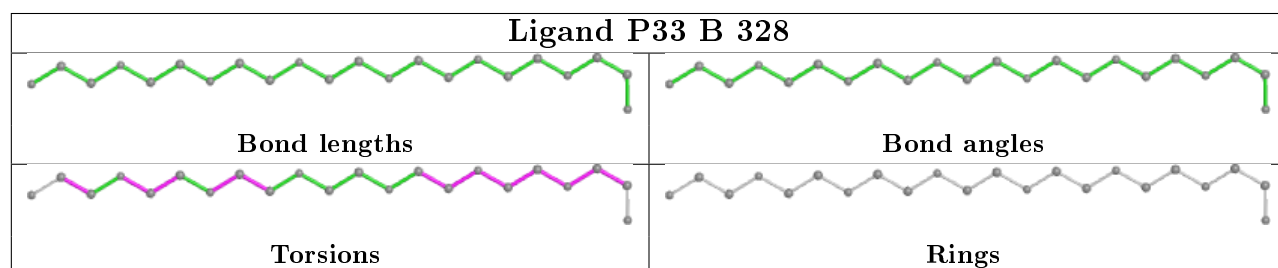
## Ligand NOS D 401

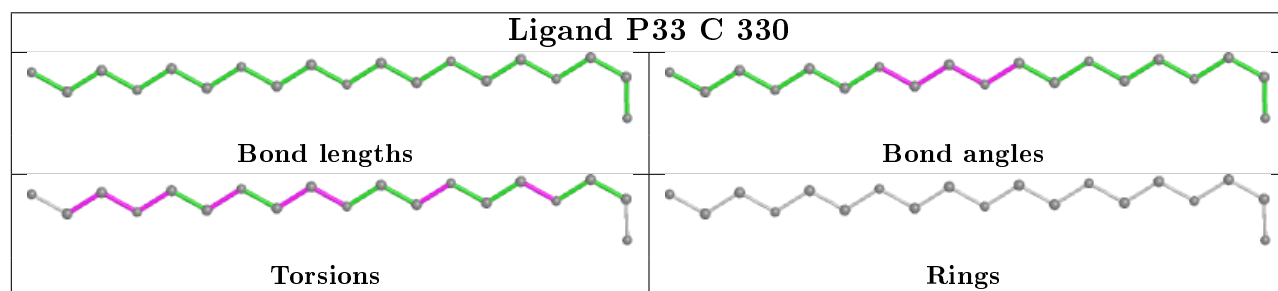
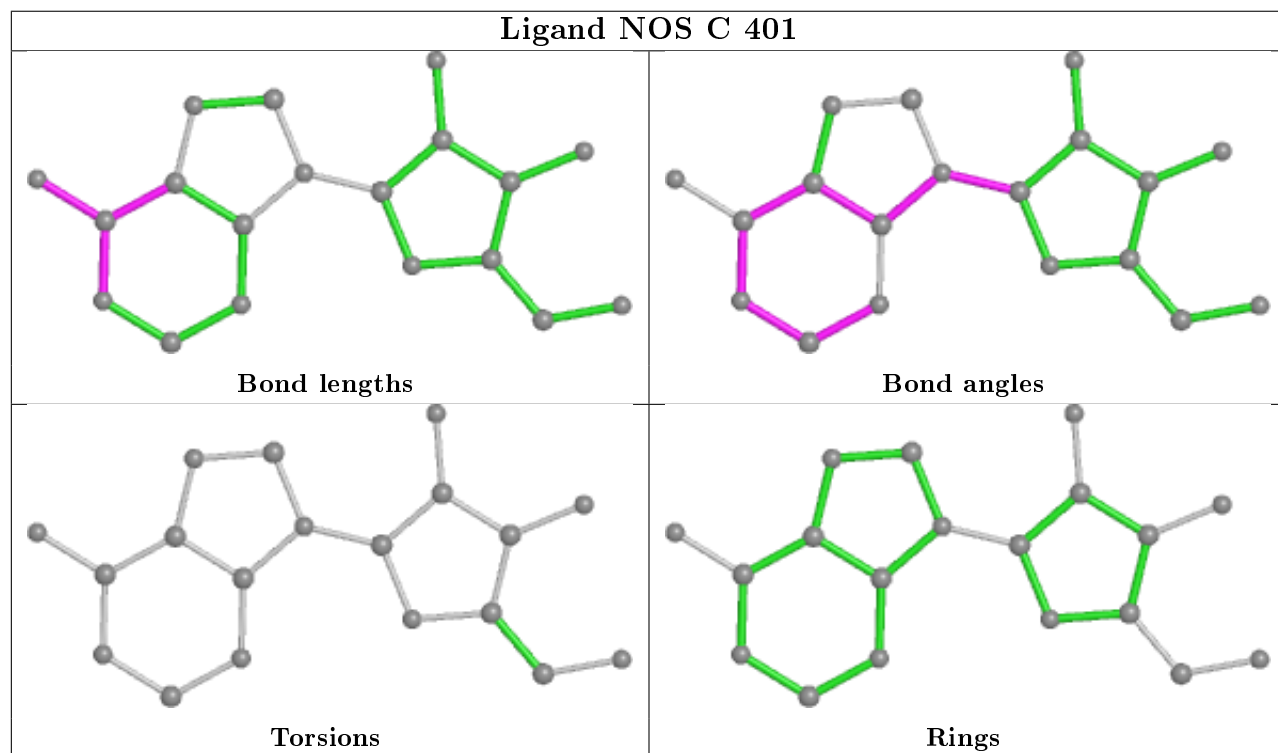
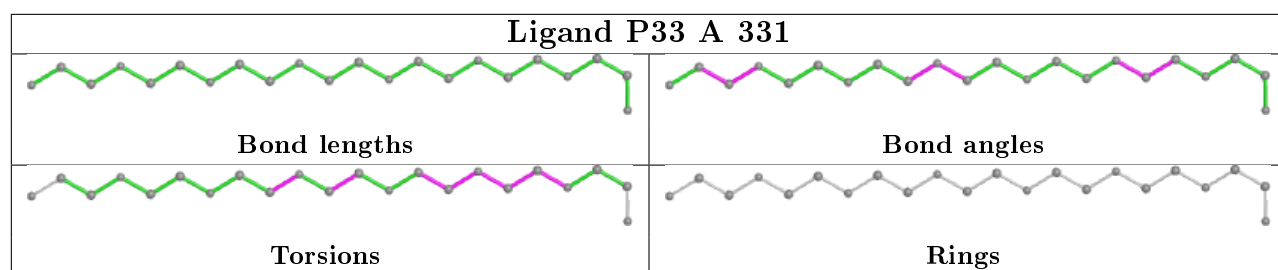


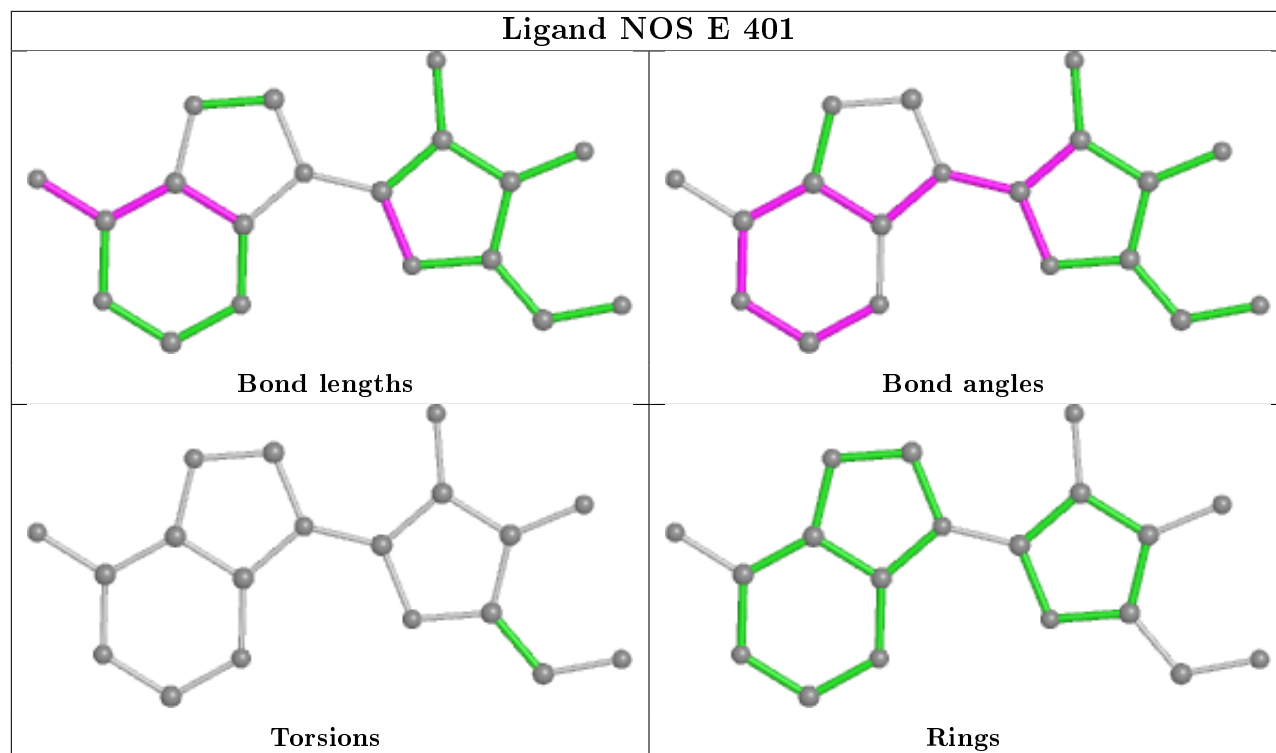
## Ligand NOS F 401



## Ligand P33 B 328







## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	303/326 (92%)	0.13	25 (8%)	11 13	11, 18, 46, 78	0
1	B	306/326 (93%)	0.20	27 (8%)	10 11	13, 22, 47, 80	0
1	C	305/326 (93%)	0.16	20 (6%)	18 20	11, 21, 46, 70	0
1	D	303/326 (92%)	0.13	16 (5%)	26 29	14, 23, 43, 55	0
1	E	306/326 (93%)	0.15	16 (5%)	27 30	12, 20, 40, 80	0
1	F	298/326 (91%)	0.16	21 (7%)	16 18	15, 24, 45, 65	0
All	All	1821/1956 (93%)	0.15	125 (6%)	16 19	11, 22, 46, 80	0

All (125) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	109	LEU	11.3
1	B	22	ARG	7.0
1	D	109	LEU	6.8
1	A	33	ILE	6.4
1	B	21	PHE	6.2
1	A	21	PHE	6.2
1	B	17	PHE	6.1
1	C	25	ILE	6.0
1	E	232	ASP	5.7
1	A	22	ARG	5.7
1	D	134	LYS	5.6
1	F	135	ASP	5.4
1	E	194	TYR	5.3
1	C	313	GLY	5.3
1	A	35	LEU	5.3
1	C	231	ARG	5.2
1	B	31	HIS	5.2
1	E	33	ILE	5.2
1	B	32	LEU	5.1

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Mol	Chain	Res	Type	RSRZ
1	B	110	ASP	4.8
1	A	109	LEU	4.7
1	D	231	ARG	4.7
1	A	232	ASP	4.7
1	F	33	ILE	4.7
1	C	312	LYS	4.7
1	A	17	PHE	4.5
1	B	109	LEU	4.5
1	E	31	HIS	4.5
1	D	316	LEU	4.4
1	F	114	ILE	4.3
1	A	20	ARG	4.3
1	D	135	ASP	4.2
1	F	134	LYS	4.2
1	C	109	LEU	4.2
1	C	22	ARG	4.1
1	F	110	ASP	4.1
1	E	35	LEU	4.0
1	D	35	LEU	4.0
1	A	231	ARG	4.0
1	C	23	GLU	4.0
1	E	231	ARG	3.8
1	B	20	ARG	3.8
1	A	310	ARG	3.7
1	B	33	ILE	3.7
1	F	20	ARG	3.7
1	B	37	PHE	3.7
1	C	33	ILE	3.6
1	F	108	ASP	3.6
1	F	34	ASN	3.5
1	A	24	HIS	3.5
1	A	23	GLU	3.5
1	C	24	HIS	3.5
1	F	111	ASN	3.4
1	D	107	THR	3.4
1	C	232	ASP	3.3
1	C	135	ASP	3.3
1	D	21	PHE	3.3
1	E	22	ARG	3.3
1	C	134	LYS	3.3
1	A	16	THR	3.2
1	D	110	ASP	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	24	HIS	3.1
1	E	135	ASP	3.0
1	F	158	GLN	3.0
1	A	110	ASP	3.0
1	B	134	LYS	3.0
1	D	20	ARG	3.0
1	A	134	LYS	2.9
1	C	20	ARG	2.9
1	C	310	ARG	2.9
1	C	194	TYR	2.9
1	B	241	ARG	2.9
1	F	107	THR	2.9
1	B	111	ASN	2.8
1	B	23	GLU	2.8
1	A	37	PHE	2.8
1	E	32	LEU	2.8
1	F	37	PHE	2.8
1	E	21	PHE	2.8
1	D	17	PHE	2.7
1	F	232	ASP	2.7
1	C	158	GLN	2.7
1	D	313	GLY	2.6
1	D	111	ASN	2.6
1	A	135	ASP	2.6
1	B	135	ASP	2.6
1	A	194	TYR	2.6
1	C	21	PHE	2.6
1	B	112	ASN	2.5
1	B	223	GLU	2.5
1	B	34	ASN	2.5
1	B	19	GLY	2.5
1	B	232	ASP	2.4
1	E	134	LYS	2.4
1	E	132	GLU	2.4
1	D	241	ARG	2.4
1	B	18	GLU	2.3
1	E	133	ALA	2.3
1	E	23	GLU	2.3
1	E	158	GLN	2.3
1	D	233	GLY	2.3
1	A	112	ASN	2.3
1	C	35	LEU	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	241	ARG	2.2
1	F	132	GLU	2.2
1	A	40	PRO	2.2
1	B	312	LYS	2.2
1	A	32	LEU	2.2
1	B	310	ARG	2.2
1	F	17	PHE	2.2
1	F	42	MET	2.2
1	C	110	ASP	2.2
1	F	112	ASN	2.1
1	B	231	ARG	2.1
1	E	20	ARG	2.1
1	F	241	ARG	2.1
1	C	311	PRO	2.1
1	A	18	GLU	2.1
1	B	313	GLY	2.1
1	A	19	GLY	2.1
1	F	131	GLY	2.1
1	D	16	THR	2.0
1	B	35	LEU	2.0
1	F	130	ALA	2.0
1	A	111	ASN	2.0

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

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

## 6.3 Carbohydrates [i](#)

There are no carbohydrates 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, 95<sup>th</sup> 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.

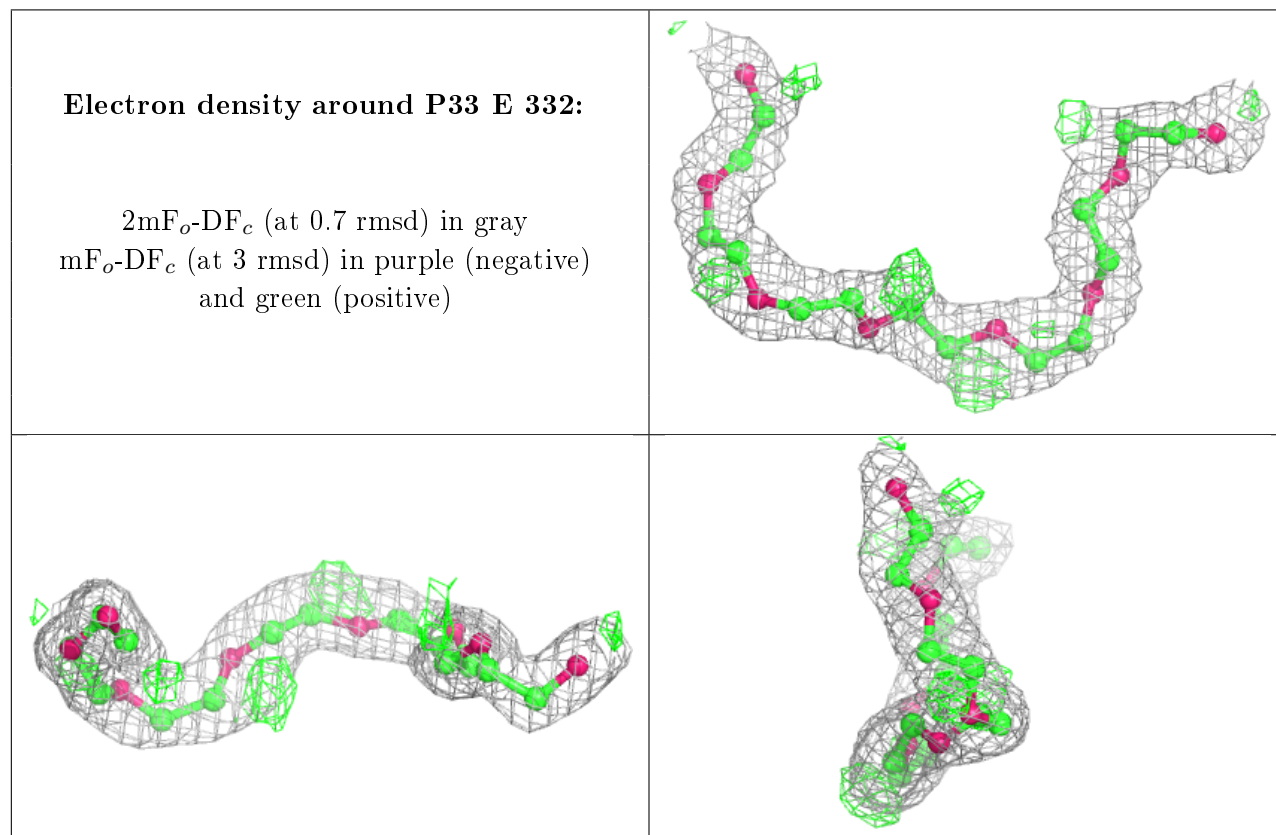
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	ACT	F	327	4/4	0.73	0.20	27,29,29,31	0

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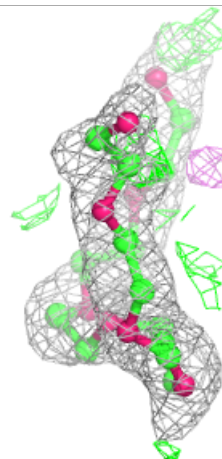
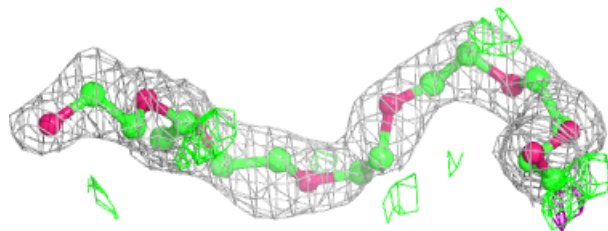
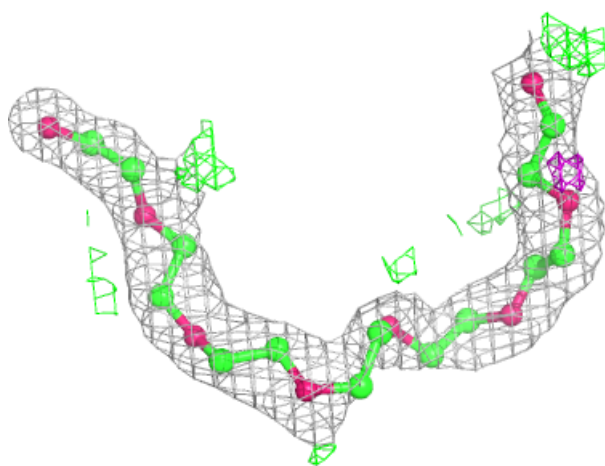
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	ACT	A	330	4/4	0.78	0.20	23,24,25,26	0
3	ACT	E	329	4/4	0.79	0.16	43,43,44,44	0
4	P33	E	332	22/22	0.87	0.18	30,35,40,41	0
4	P33	C	331	22/22	0.87	0.13	39,44,48,49	0
3	ACT	F	328	4/4	0.90	0.14	26,28,29,29	0
4	P33	B	328	22/22	0.91	0.14	31,39,43,45	0
3	ACT	E	331	4/4	0.91	0.12	27,28,29,30	0
3	ACT	E	328	4/4	0.92	0.10	18,21,21,22	0
3	ACT	B	327	4/4	0.92	0.11	30,31,32,33	0
5	NA	F	330	1/1	0.92	0.11	31,31,31,31	0
4	P33	C	330	19/22	0.92	0.13	20,26,45,48	0
4	P33	A	331	22/22	0.92	0.11	20,25,33,35	0
3	ACT	D	327	4/4	0.93	0.15	33,34,34,35	0
3	ACT	C	328	4/4	0.93	0.09	33,34,34,34	0
3	ACT	C	329	4/4	0.93	0.12	27,29,30,32	0
3	ACT	E	330	4/4	0.93	0.10	22,22,23,23	0
5	NA	E	335	1/1	0.94	0.13	29,29,29,29	0
3	ACT	A	328	4/4	0.94	0.09	23,25,25,26	0
5	NA	F	329	1/1	0.95	0.11	25,25,25,25	0
3	ACT	A	327	4/4	0.95	0.11	20,23,23,24	0
3	ACT	A	329	4/4	0.95	0.09	22,23,23,23	0
4	P33	B	329	14/22	0.96	0.09	25,29,32,34	0
5	NA	E	333	1/1	0.96	0.23	26,26,26,26	0
3	ACT	C	327	4/4	0.97	0.11	20,22,22,23	0
2	NOS	D	401	19/19	0.97	0.07	16,18,21,21	0
5	NA	E	336	1/1	0.97	0.05	31,31,31,31	0
3	ACT	E	327	4/4	0.97	0.09	15,19,19,19	0
5	NA	A	334	1/1	0.97	0.05	29,29,29,29	0
2	NOS	F	401	19/19	0.97	0.07	14,18,21,23	0
5	NA	D	328	1/1	0.97	0.12	31,31,31,31	0
5	NA	B	332	1/1	0.98	0.05	21,21,21,21	0
2	NOS	E	401	19/19	0.98	0.08	11,14,17,17	0
5	NA	A	333	1/1	0.98	0.05	18,18,18,18	0
2	NOS	A	401	19/19	0.98	0.07	12,14,17,17	0
2	NOS	C	401	19/19	0.98	0.08	11,13,15,16	0
2	NOS	B	401	19/19	0.98	0.07	13,15,16,19	0
5	NA	C	333	1/1	0.99	0.06	17,17,17,17	0
5	NA	B	330	1/1	0.99	0.04	22,22,22,22	0
5	NA	C	332	1/1	0.99	0.07	26,26,26,26	0
5	NA	A	332	1/1	0.99	0.06	21,21,21,21	0
5	NA	E	334	1/1	0.99	0.06	14,14,14,14	0
5	NA	B	331	1/1	0.99	0.06	18,18,18,18	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.



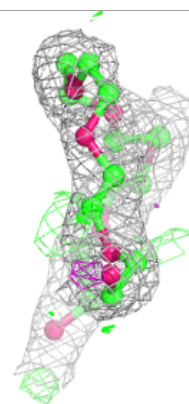
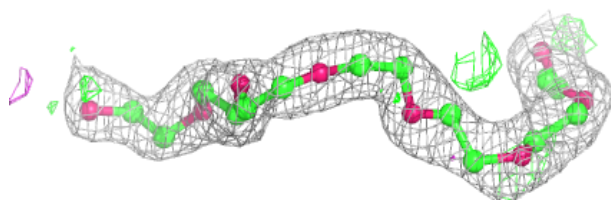
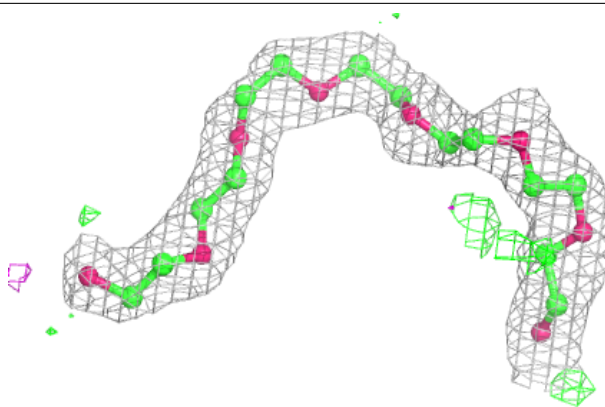
**Electron density around P33 C 331:**

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

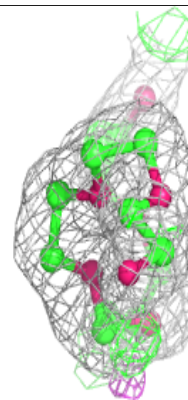
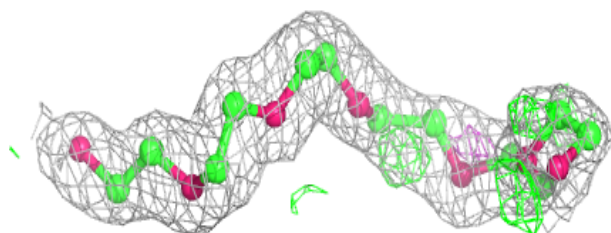
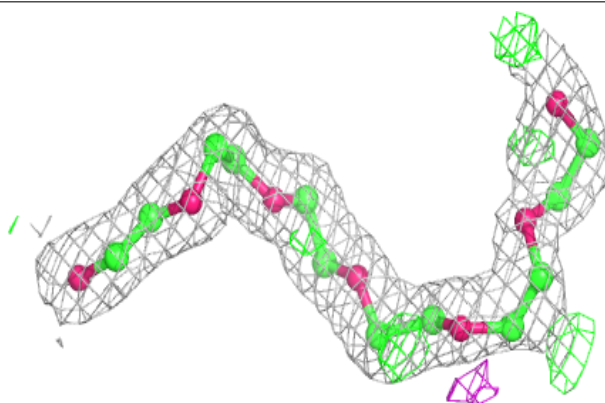


**Electron density around P33 B 328:**

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

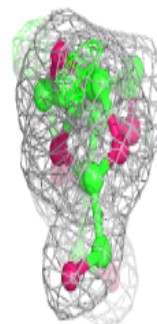
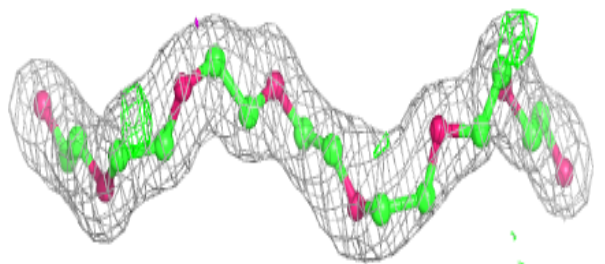
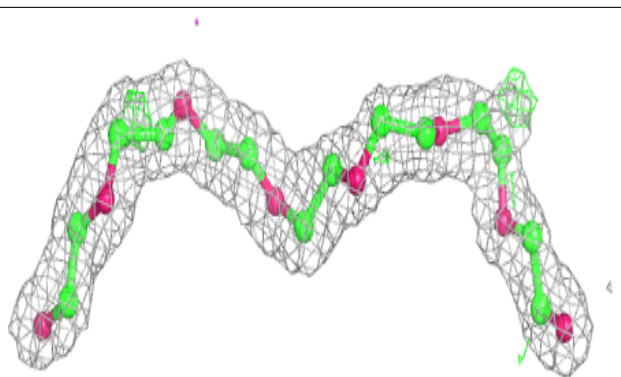
**Electron density around P33 C 330:**

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

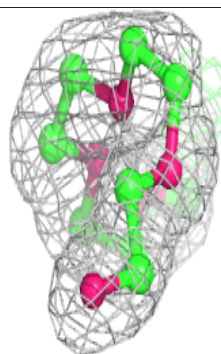
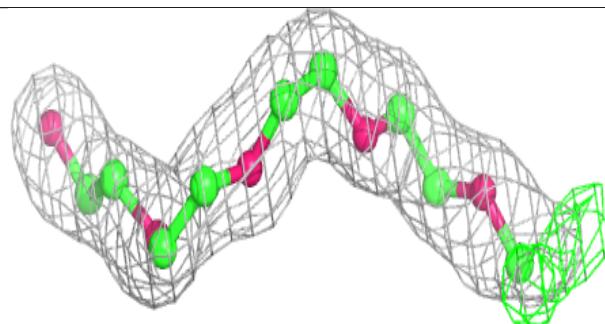
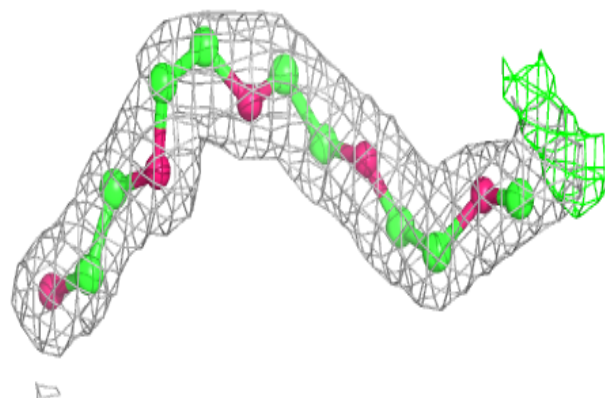


**Electron density around P33 A 331:**

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

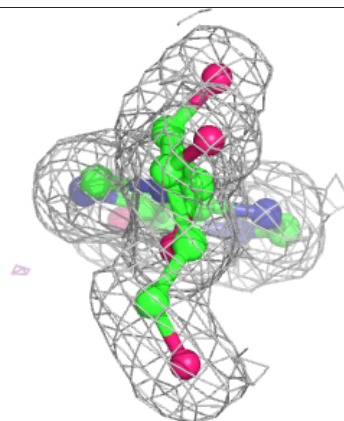
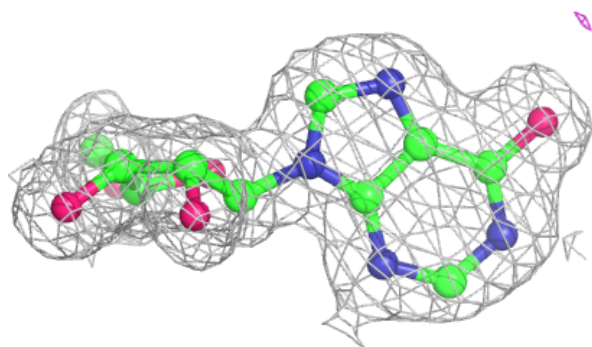
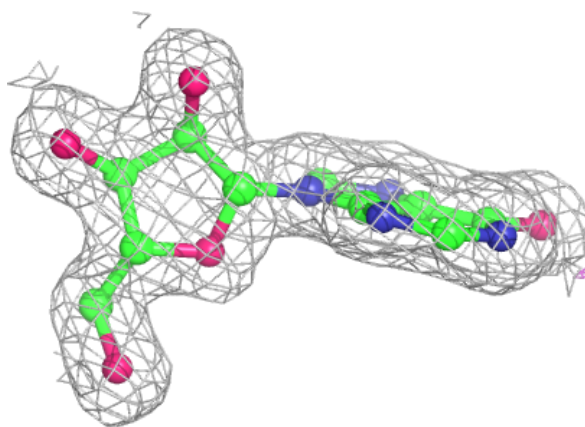
**Electron density around P33 B 329:**

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

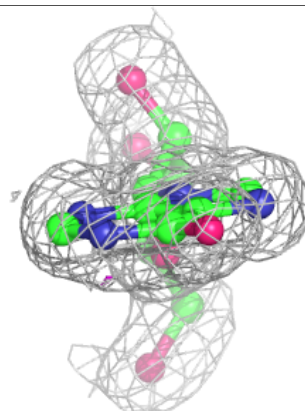
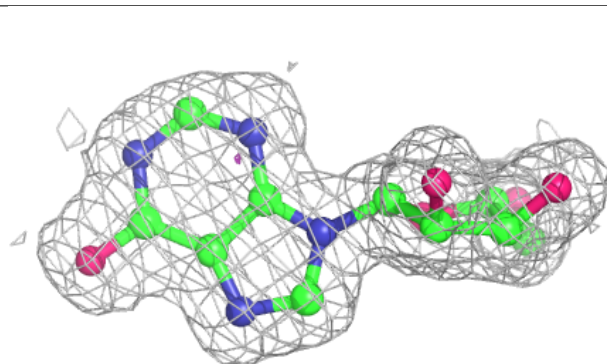
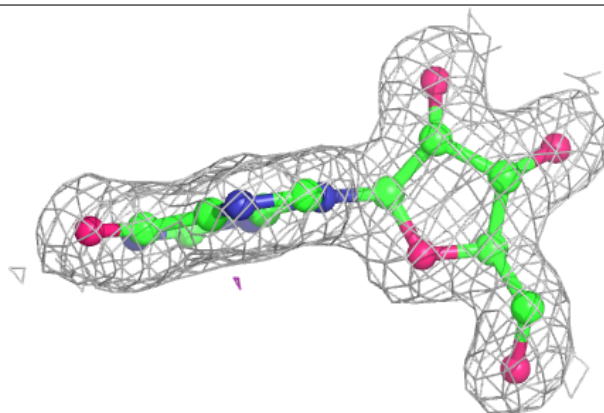


**Electron density around NOS D 401:**

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

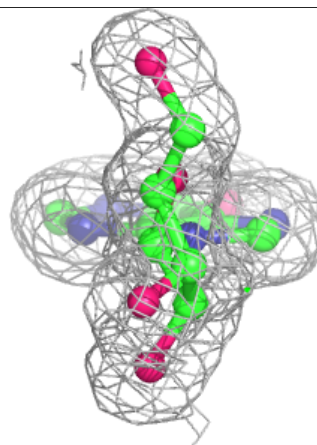
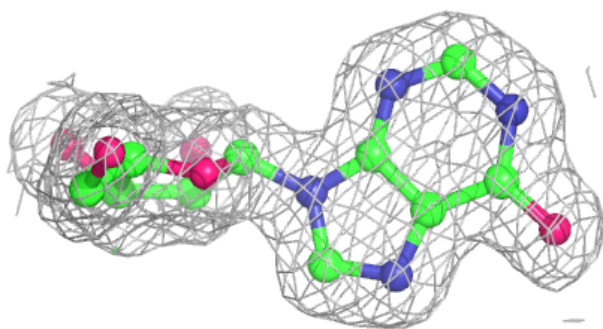
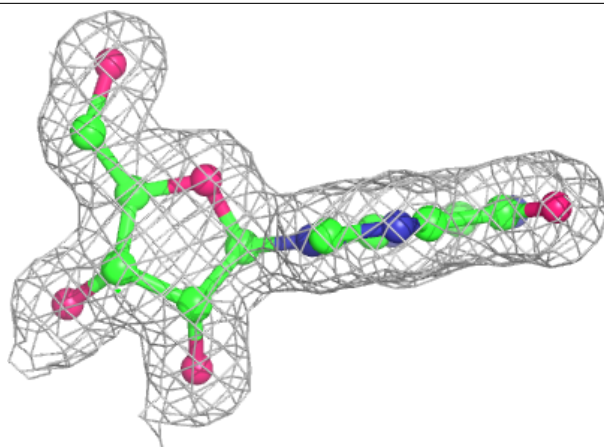
**Electron density around NOS F 401:**

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



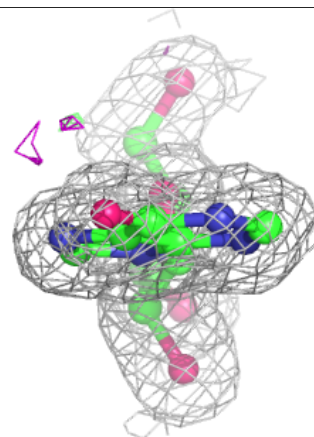
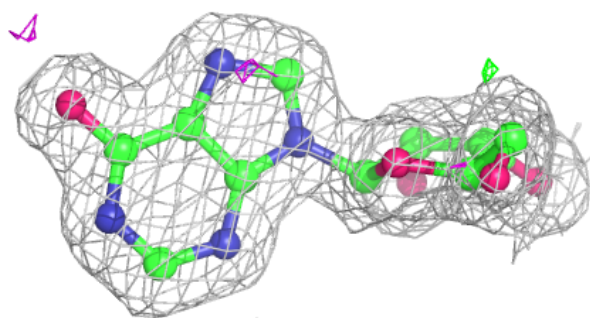
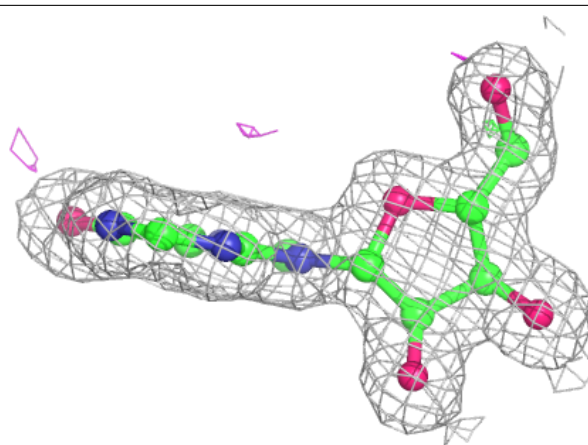
**Electron density around NOS E 401:**

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



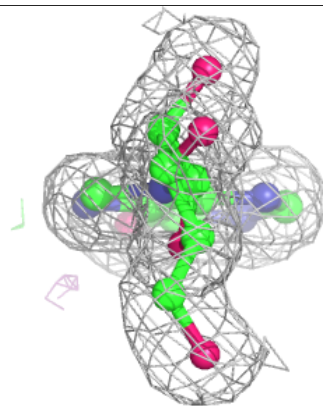
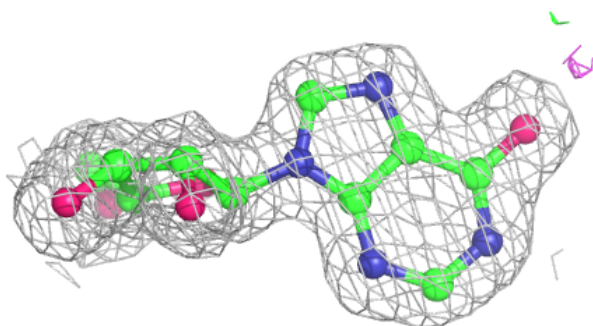
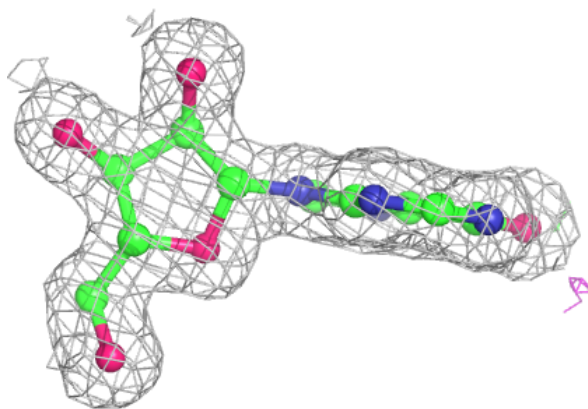
**Electron density around NOS A 401:**

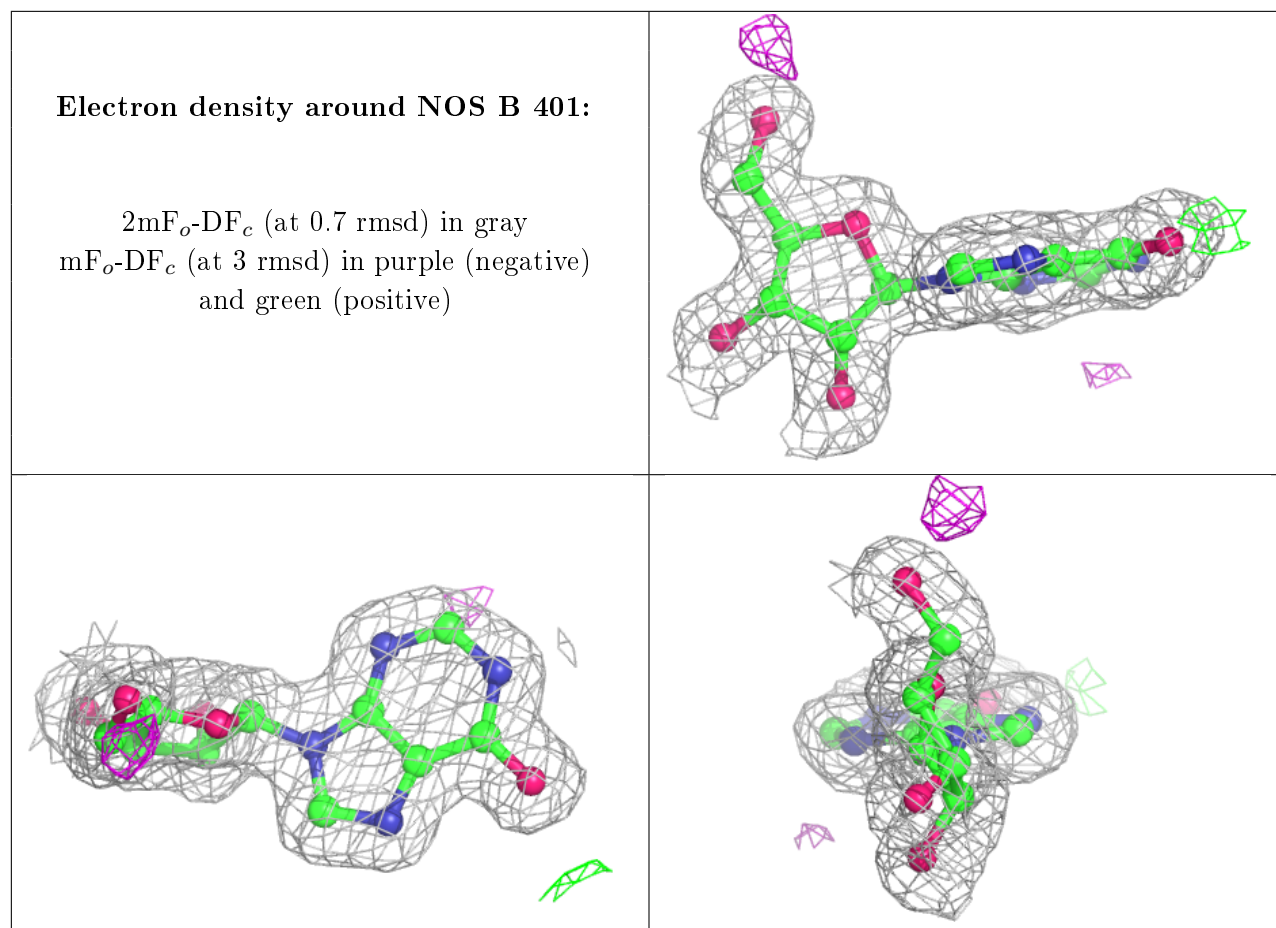
$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around NOS C 401:**

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





## 6.5 Other polymers ⓘ

There are no such residues in this entry.