



wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 22, 2023 – 11:47 PM EDT

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 wwPDB X-ray Structure Validation Summary Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtrriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

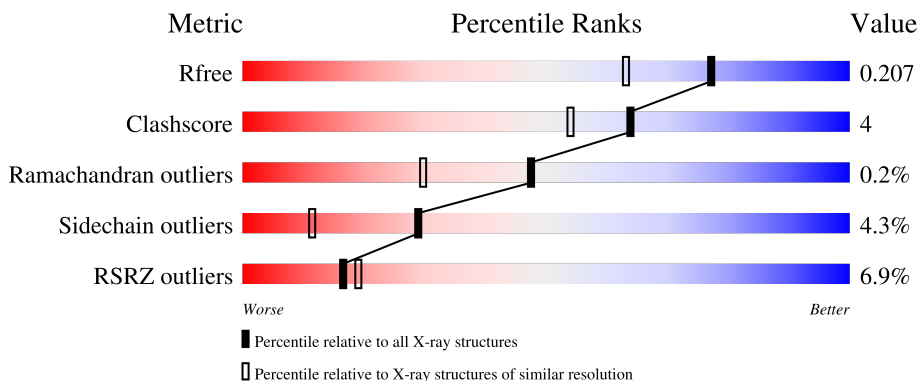
1 Overall quality at a glance

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.



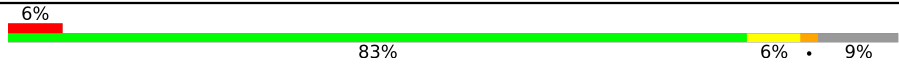
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (1.70-1.70)
RSRZ outliers	127900	4222 (1.70-1.70)

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 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	326	
1	B	326	
1	C	326	
1	D	326	
1	E	326	

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Mol	Chain	Length	Quality of chain
1	F	326	 <p>6% 83% 6% • 9%</p>

2 Entry composition [i](#)

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

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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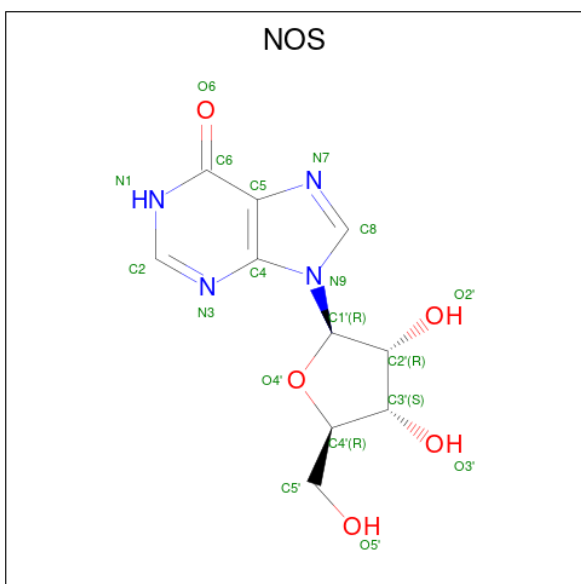
Chain	Residue	Modelled	Actual	Comment	Reference
B	316	LEU	-	expression tag	UNP Q2SZE4
B	317	ARG	-	expression tag	UNP Q2SZE4
B	318	SER	-	expression tag	UNP Q2SZE4
B	319	LEU	-	expression tag	UNP Q2SZE4
B	320	GLU	-	expression tag	UNP Q2SZE4
B	321	HIS	-	expression tag	UNP Q2SZE4
B	322	HIS	-	expression tag	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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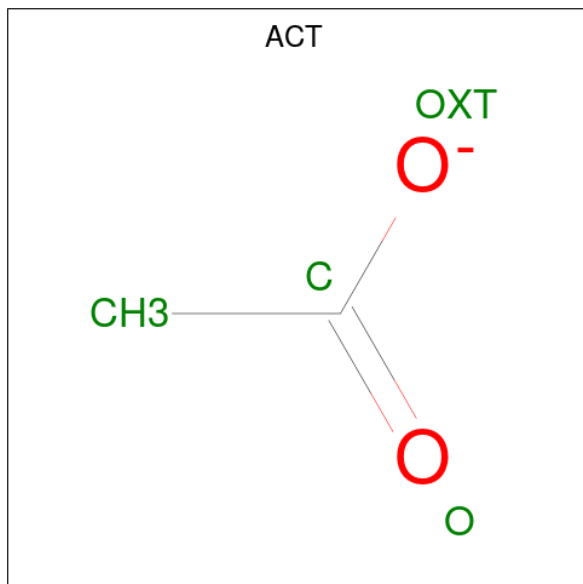
Chain	Residue	Modelled	Actual	Comment	Reference
E	316	LEU	-	expression tag	UNP Q2SZE4
E	317	ARG	-	expression tag	UNP Q2SZE4
E	318	SER	-	expression tag	UNP Q2SZE4
E	319	LEU	-	expression tag	UNP Q2SZE4
E	320	GLU	-	expression tag	UNP Q2SZE4
E	321	HIS	-	expression tag	UNP Q2SZE4
E	322	HIS	-	expression tag	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: C₁₀H₁₂N₄O₅).



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: C₂H₃O₂⁻).



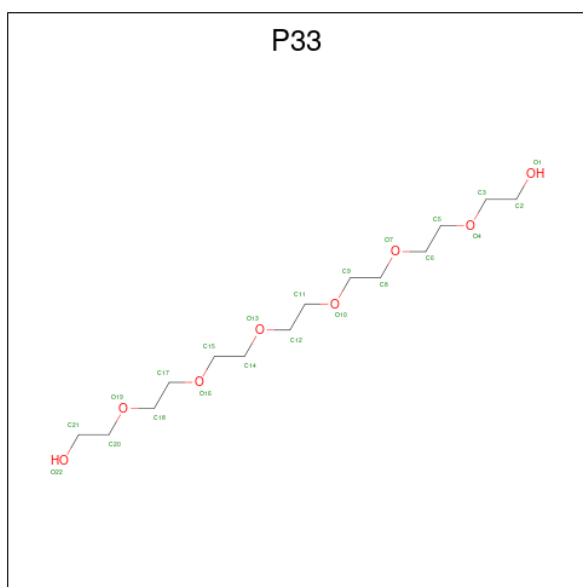
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	C O	0	0
			4	2 2		
3	A	1	Total	C O	0	0
			4	2 2		
3	A	1	Total	C O	0	0
			4	2 2		
3	A	1	Total	C O	0	0
			4	2 2		
3	B	1	Total	C O	0	0
			4	2 2		
3	C	1	Total	C O	0	0
			4	2 2		

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

- Molecule 4 is 3,6,9,12,15,18-HEXA-OXAICOSANE-1,20-DIOL (three-letter code: P33) (formula: C₁₄H₃₀O₈).



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

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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	A	3	Total	Na	0	0
			3	3		
5	B	3	Total	Na	0	0
			3	3		
5	C	2	Total	Na	0	0
			2	2		
5	D	1	Total	Na	0	0
			1	1		
5	E	4	Total	Na	0	0
			4	4		
5	F	2	Total	Na	0	0
			2	2		

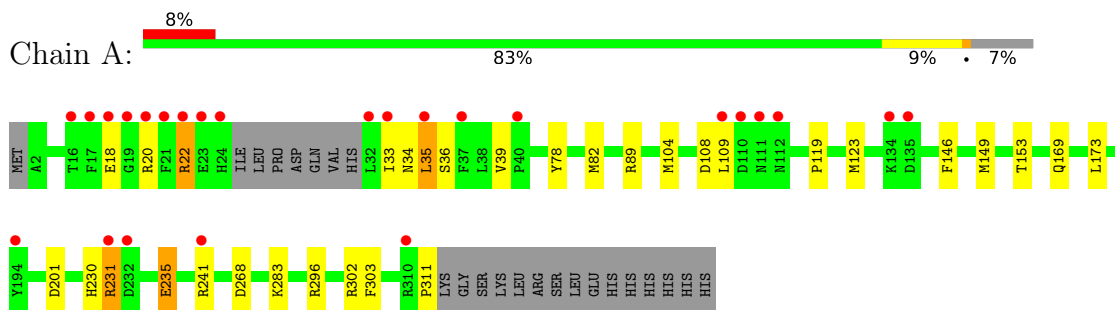
- Molecule 6 is water.

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		

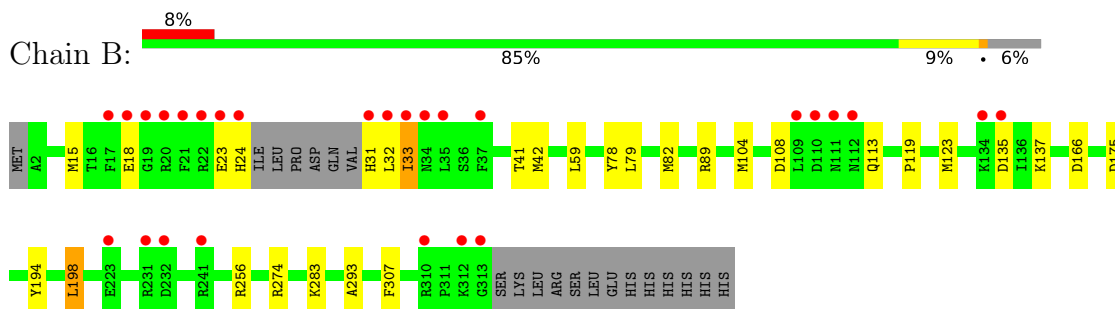
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

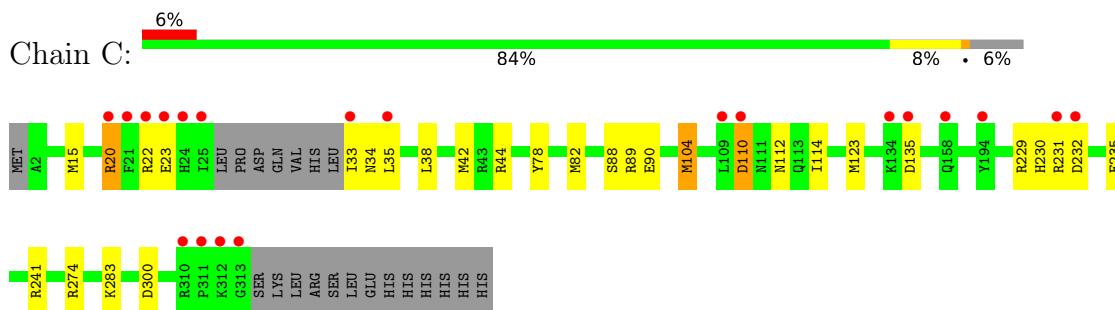
- Molecule 1: Ribokinase, putative



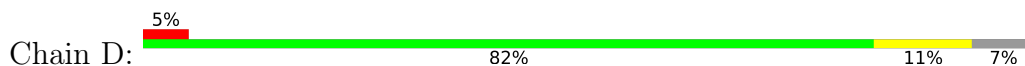
- Molecule 1: Ribokinase, putative

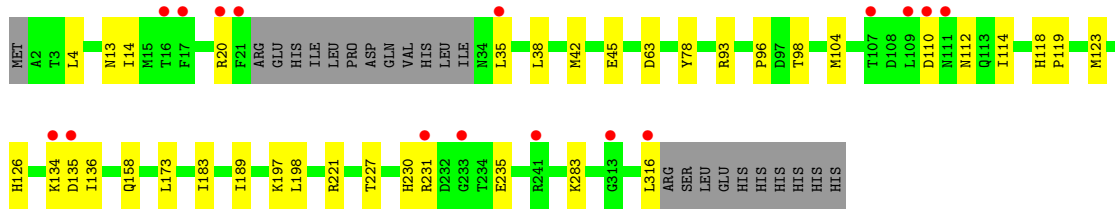


- Molecule 1: Ribokinase, putative

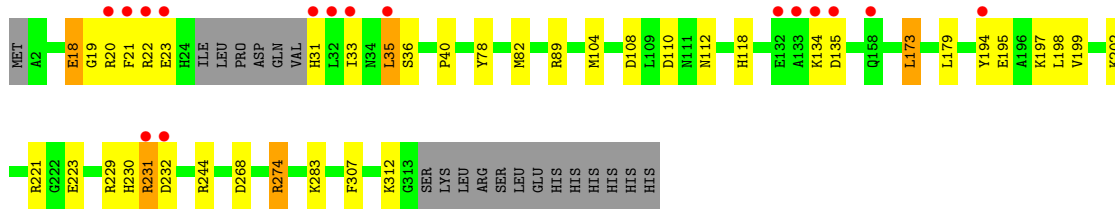
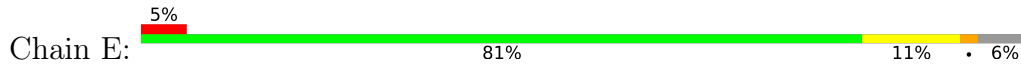


- Molecule 1: Ribokinase, putative

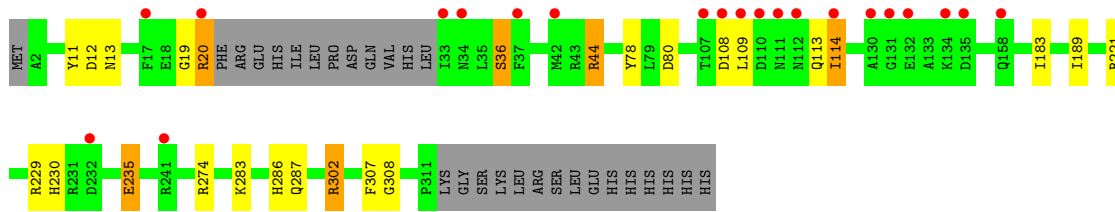
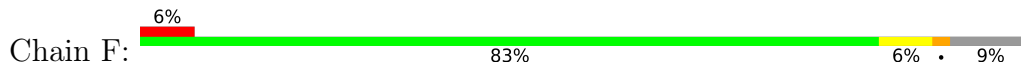




• Molecule 1: Ribokinase, putative



• Molecule 1: Ribokinase, putative



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	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
$\langle I/\sigma(I) \rangle$ ¹	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 ²)	20.3	Xtriage
Anisotropy	0.023	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.40 , 53.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	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 ²)	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.*

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: P33, ACT, NOS, NA

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

The worst 5 of 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

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	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
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.

The worst 5 of 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:HH11	1:F:44[A]:ARG:HB2	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

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
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 [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	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

5 of 62 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	35	LEU
1	F	44[B]	ARG
1	D	158	GLN
1	F	44[A]	ARG
1	F	235	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	C	113	GLN
1	D	230	HIS
1	D	126	HIS
1	D	236	GLN
1	A	287	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 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
4	P33	E	332	-	21,21,21	0.63	0	20,20,20	1.03	1 (5%)
2	NOS	A	401	-	17,21,21	1.56	2 (11%)	17,31,31	2.07	5 (29%)
3	ACT	E	328	-	3,3,3	0.77	0	3,3,3	0.69	0
3	ACT	C	329	-	3,3,3	0.73	0	3,3,3	0.98	0
3	ACT	E	331	-	3,3,3	0.98	0	3,3,3	1.80	2 (66%)
4	P33	B	328	-	21,21,21	0.57	0	20,20,20	0.70	0
2	NOS	C	401	-	17,21,21	1.71	2 (11%)	17,31,31	1.68	4 (23%)
3	ACT	E	329	-	3,3,3	0.56	0	3,3,3	1.67	1 (33%)
3	ACT	F	328	-	3,3,3	0.78	0	3,3,3	0.89	0
3	ACT	C	327	-	3,3,3	0.67	0	3,3,3	0.67	0
4	P33	C	330	-	18,18,21	0.53	0	17,17,20	1.40	3 (17%)
3	ACT	C	328	-	3,3,3	0.63	0	3,3,3	1.62	1 (33%)
2	NOS	E	401	-	17,21,21	1.96	4 (23%)	17,31,31	1.81	6 (35%)
3	ACT	E	327	-	3,3,3	1.03	0	3,3,3	0.19	0
3	ACT	A	328	-	3,3,3	0.69	0	3,3,3	1.28	0
3	ACT	A	330	-	3,3,3	1.55	1 (33%)	3,3,3	0.99	0
4	P33	C	331	-	21,21,21	0.52	0	20,20,20	0.59	0
3	ACT	D	327	-	3,3,3	0.90	0	3,3,3	1.03	0
2	NOS	B	401	-	17,21,21	1.85	4 (23%)	17,31,31	1.66	4 (23%)
3	ACT	B	327	-	3,3,3	0.68	0	3,3,3	1.09	0
3	ACT	A	329	-	3,3,3	0.92	0	3,3,3	1.34	0
3	ACT	F	327	-	3,3,3	1.33	1 (33%)	3,3,3	0.23	0
3	ACT	A	327	-	3,3,3	0.77	0	3,3,3	1.09	0
4	P33	A	331	-	21,21,21	0.60	0	20,20,20	1.30	3 (15%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
4	P33	B	329	-	13,13,21	0.54	0	12,12,20	0.51	0
2	NOS	F	401	-	17,21,21	1.60	2 (11%)	17,31,31	1.55	3 (17%)
2	NOS	D	401	-	17,21,21	2.03	2 (11%)	17,31,31	1.83	5 (29%)
3	ACT	E	330	-	3,3,3	0.87	0	3,3,3	0.62	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	P33	E	332	-	-	11/19/19/19	-
2	NOS	A	401	-	-	0/2/22/22	0/3/3/3
2	NOS	E	401	-	-	0/2/22/22	0/3/3/3
4	P33	B	329	-	-	1/11/11/19	-
4	P33	C	331	-	-	12/19/19/19	-
4	P33	B	328	-	-	12/19/19/19	-
2	NOS	C	401	-	-	0/2/22/22	0/3/3/3
2	NOS	F	401	-	-	0/2/22/22	0/3/3/3
2	NOS	D	401	-	-	0/2/22/22	0/3/3/3
2	NOS	B	401	-	-	0/2/22/22	0/3/3/3
4	P33	A	331	-	-	7/19/19/19	-
4	P33	C	330	-	-	8/16/16/19	-

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

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	401	NOS	O6-C6	6.11	1.35	1.23
2	E	401	NOS	O6-C6	5.86	1.35	1.23
2	C	401	NOS	O6-C6	5.03	1.33	1.23
2	B	401	NOS	O6-C6	4.84	1.33	1.23
2	A	401	NOS	O6-C6	4.83	1.33	1.23

The worst 5 of 38 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	401	NOS	O6-C6-C5	-3.68	117.19	124.37
2	B	401	NOS	O6-C6-C5	-3.63	117.28	124.37
2	D	401	NOS	O4'-C1'-C2'	-3.59	101.68	106.93
2	A	401	NOS	O6-C6-C5	-3.53	117.47	124.37
2	A	401	NOS	C5-C6-N1	3.53	120.18	113.95

There are no chirality outliers.

5 of 51 torsion outliers are listed below:

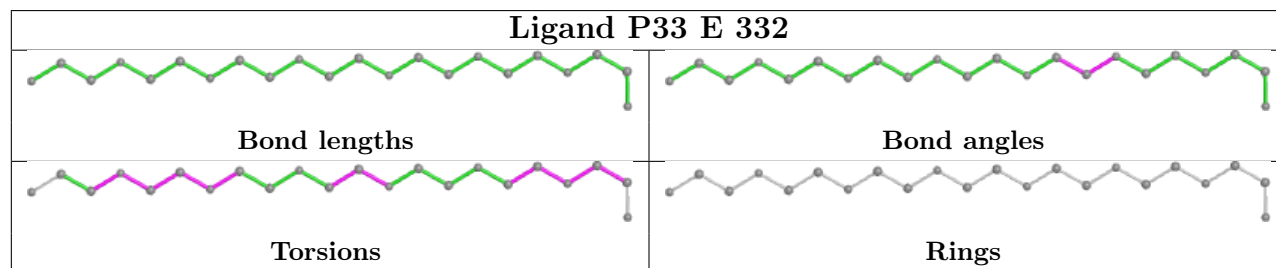
Mol	Chain	Res	Type	Atoms
4	C	331	P33	C12-C11-O10-C9
4	C	331	P33	O1-C2-C3-O4
4	C	331	P33	O4-C5-C6-O7
4	E	332	P33	O10-C11-C12-O13
4	C	330	P33	O10-C11-C12-O13

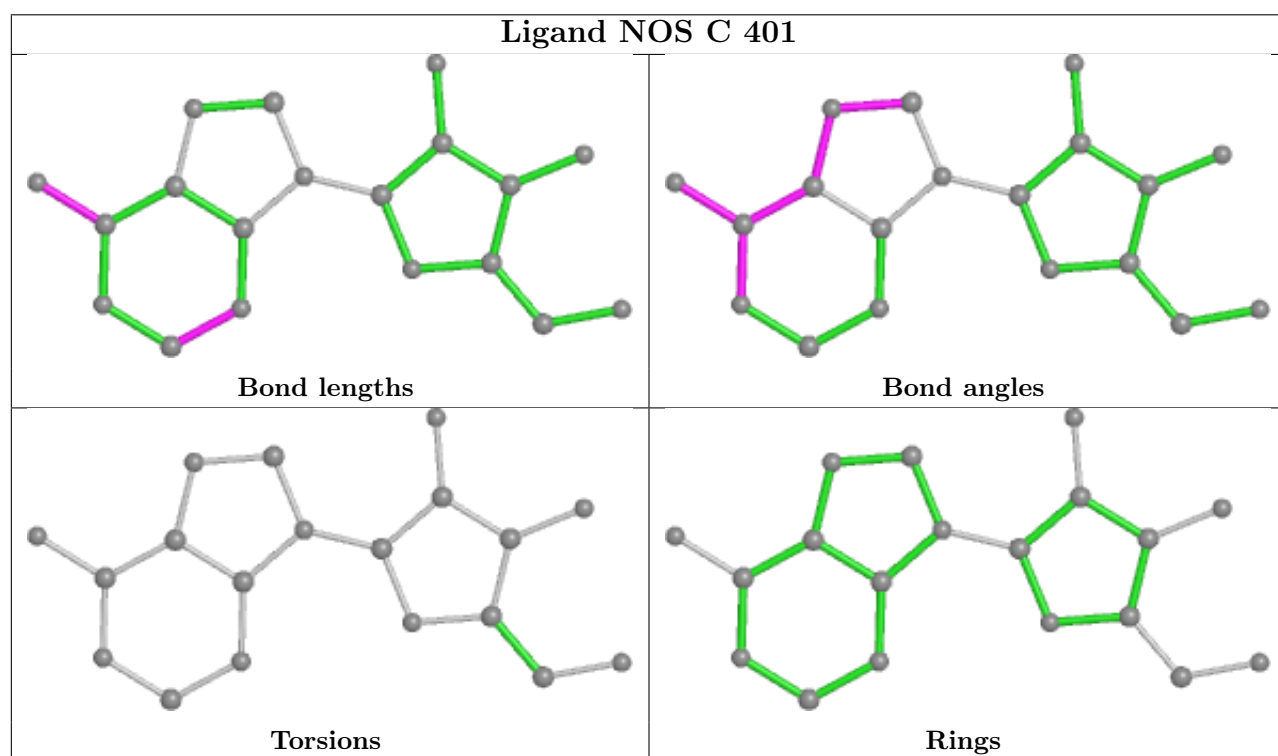
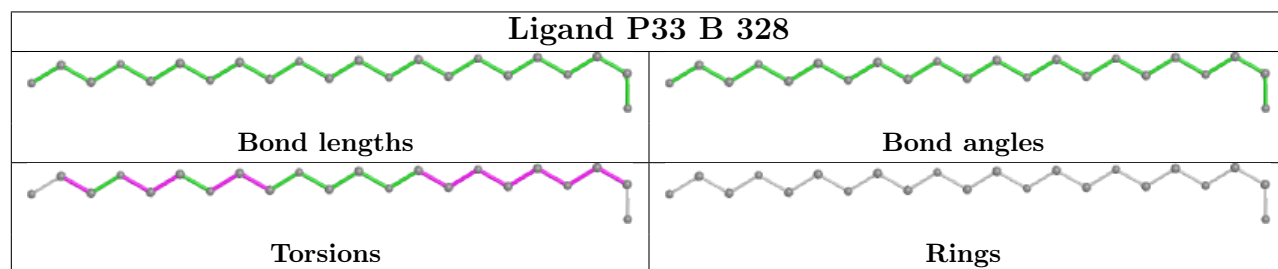
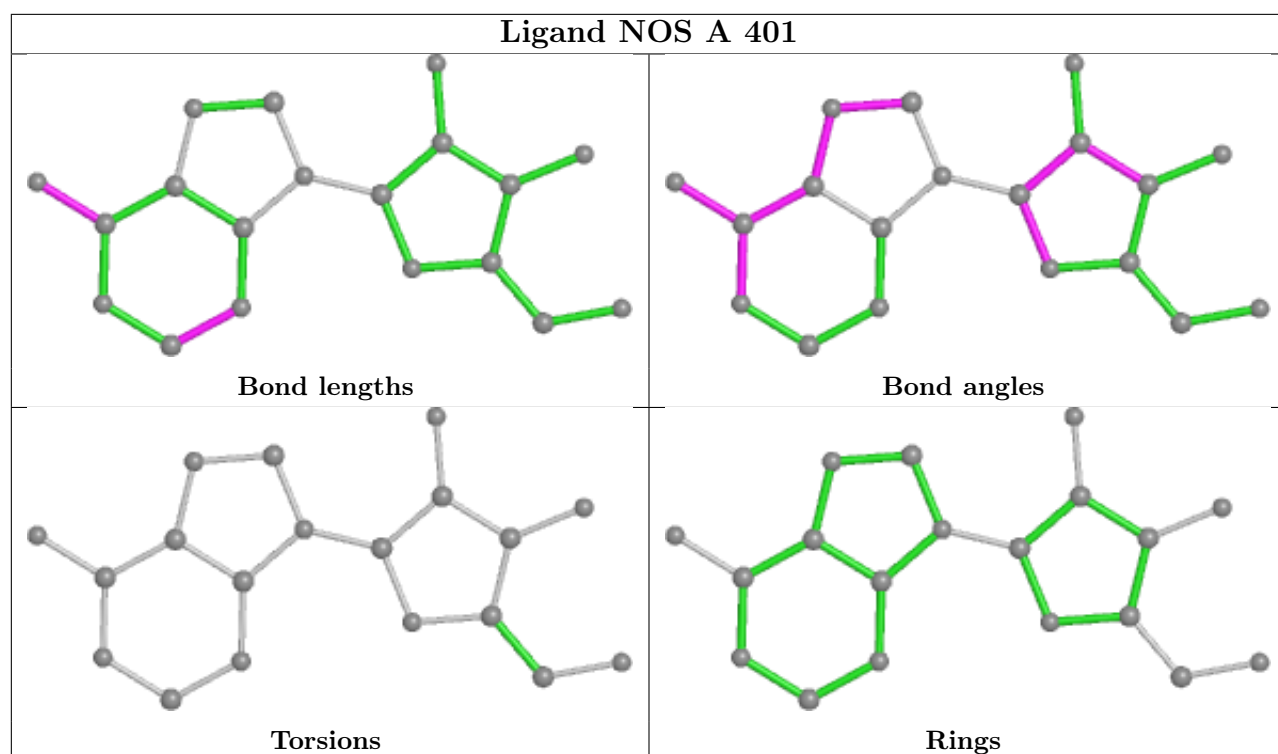
There are no ring outliers.

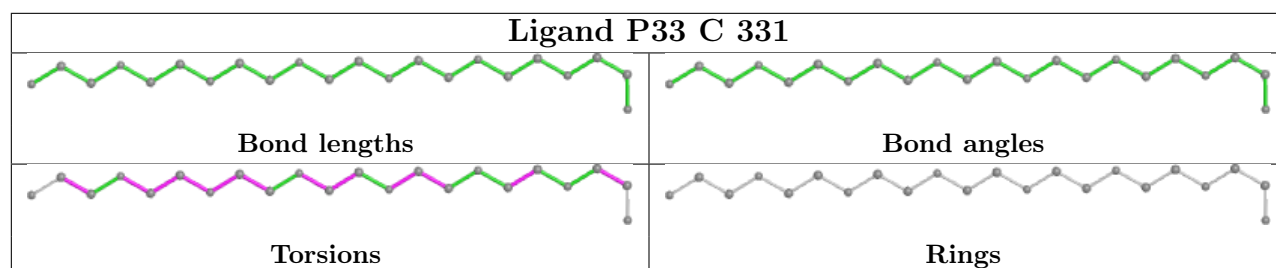
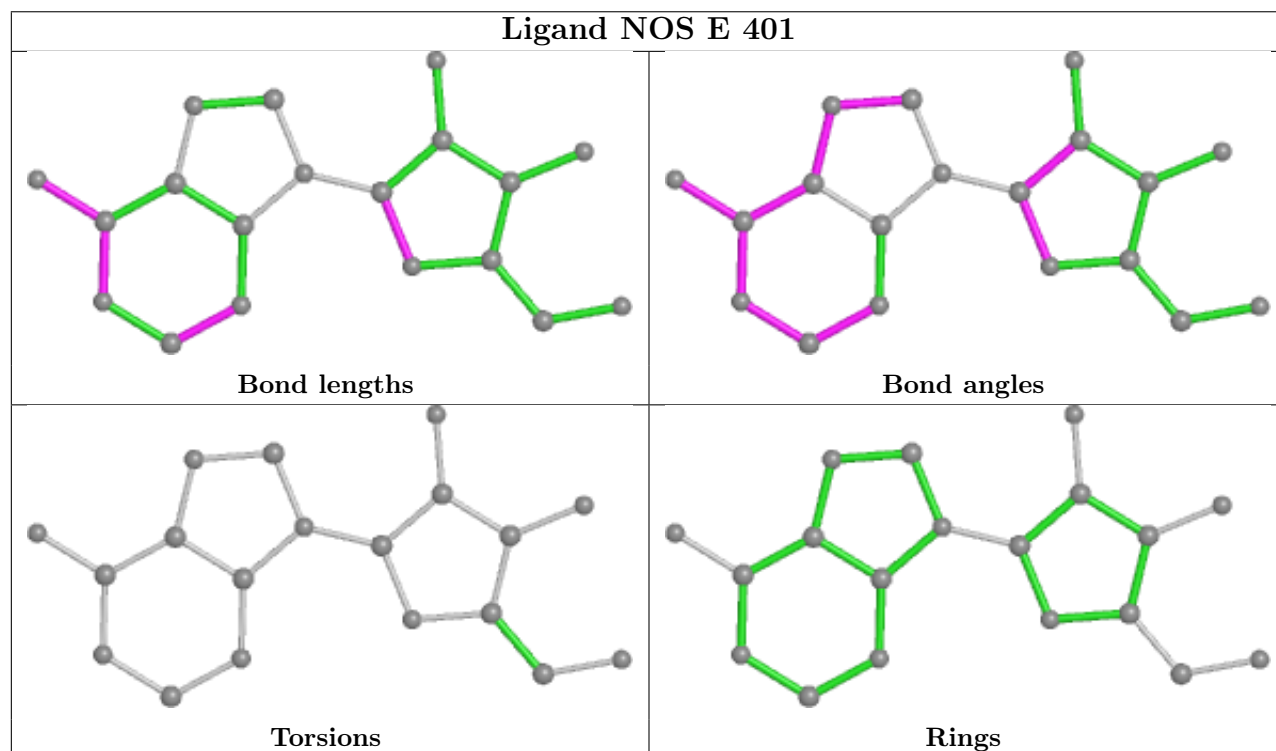
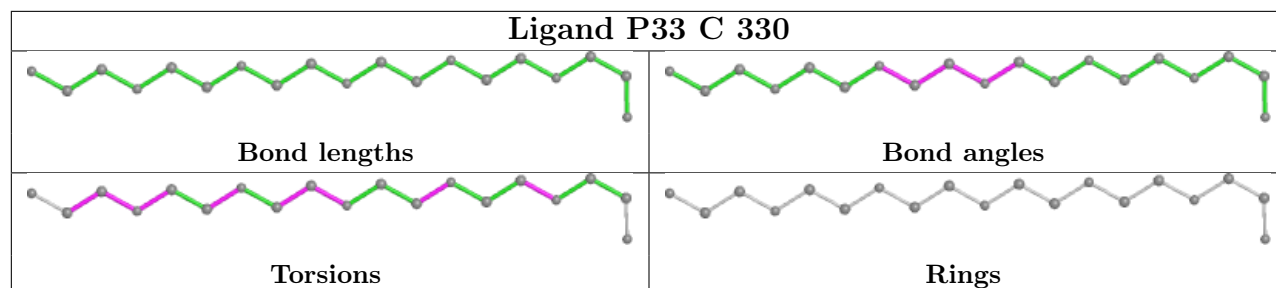
6 monomers are involved in 10 short contacts:

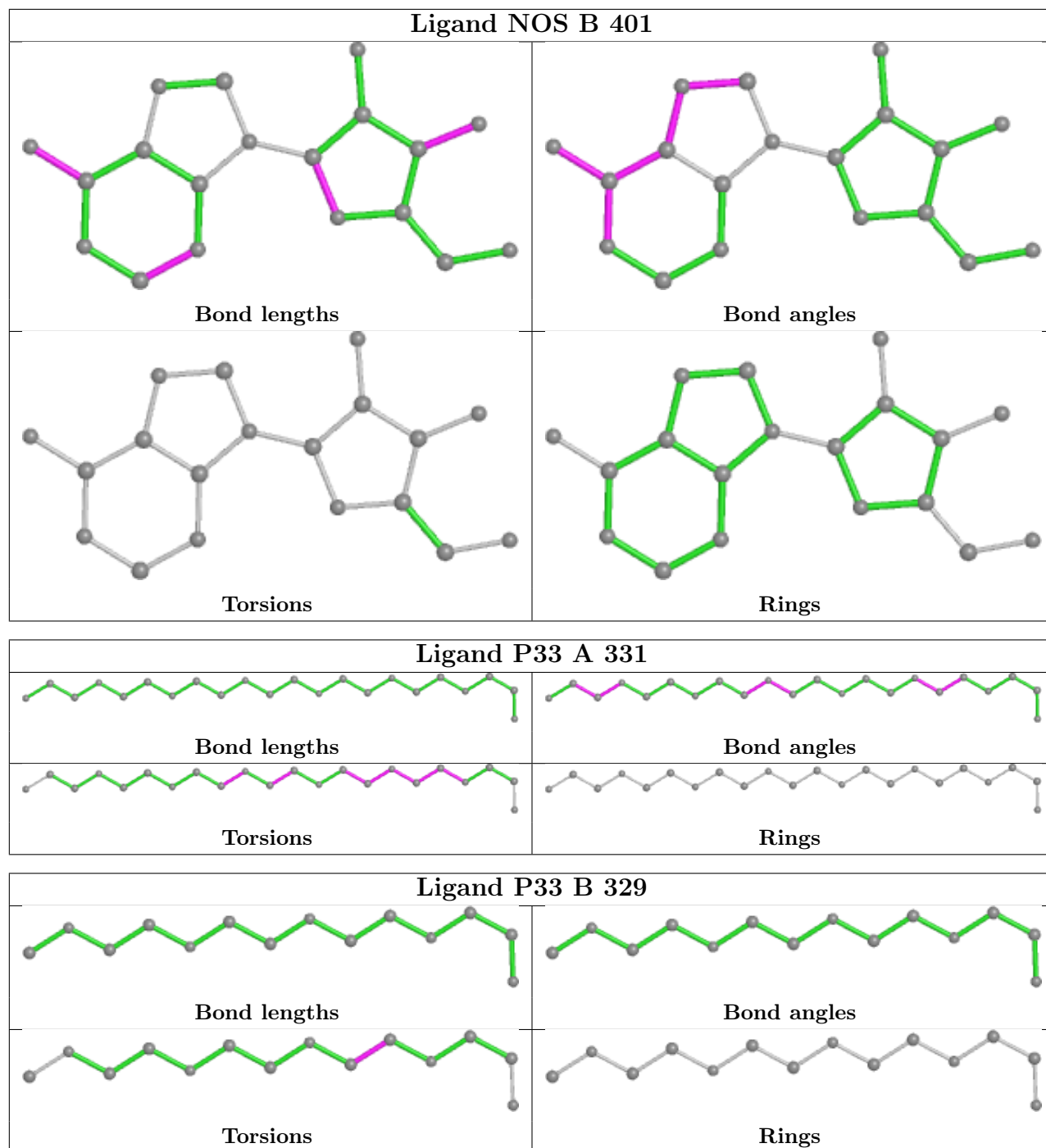
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	E	332	P33	2	0
3	F	328	ACT	1	0
3	A	330	ACT	1	0
4	C	331	P33	1	0
3	F	327	ACT	1	0
4	A	331	P33	4	0

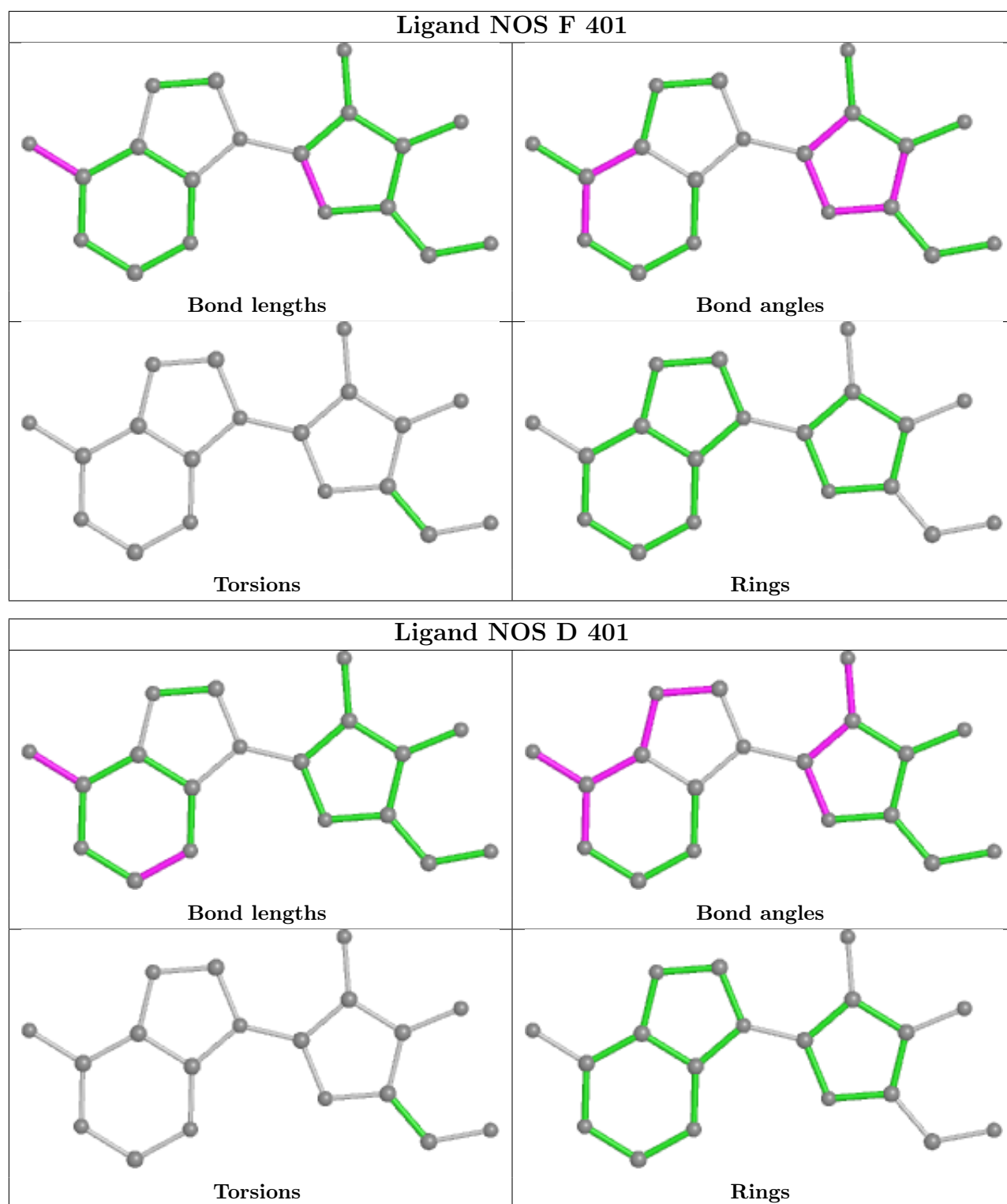
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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

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	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

The worst 5 of 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

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 i

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

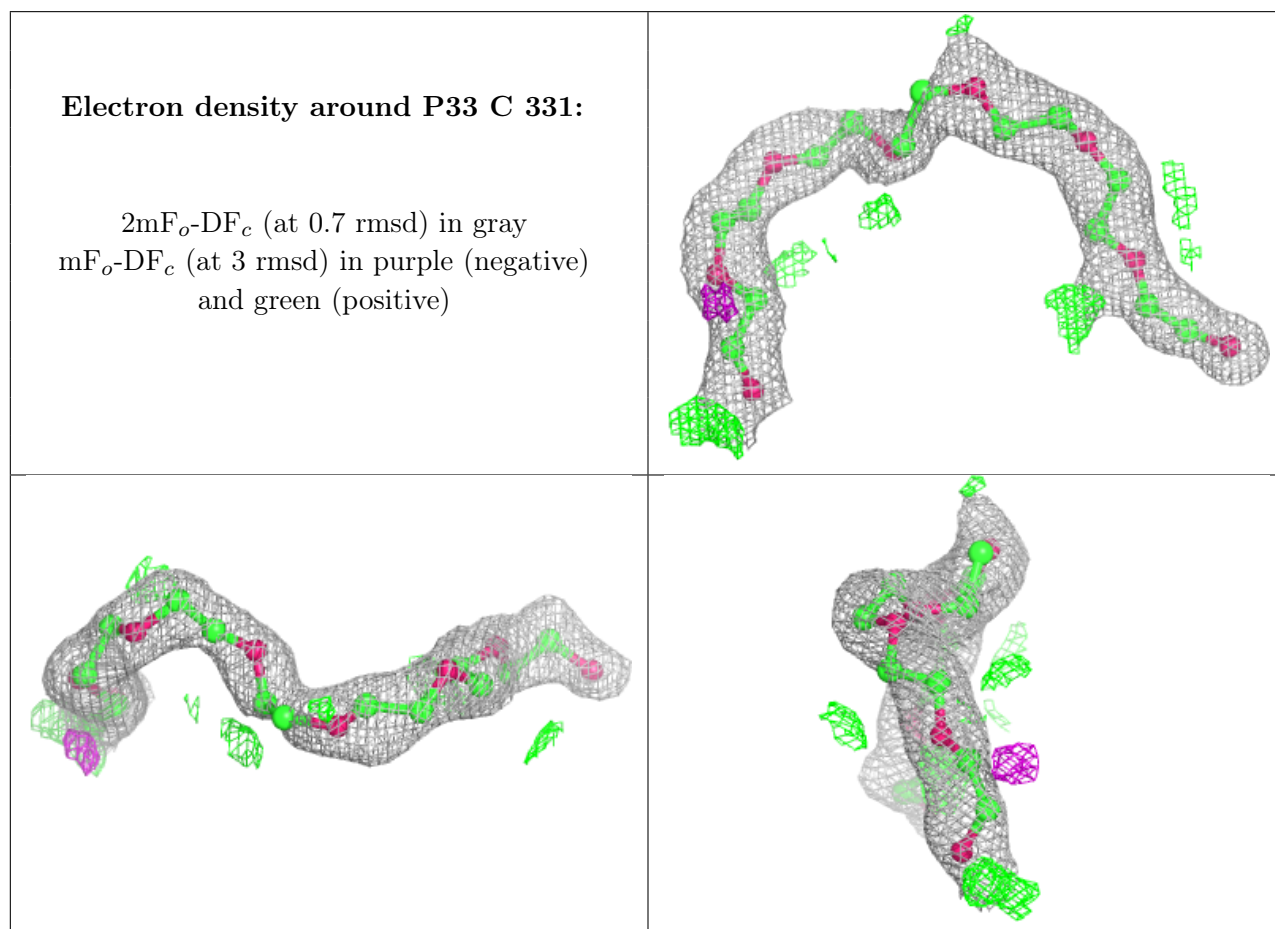
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ACT	F	327	4/4	0.73	0.20	27,29,29,31	0
3	ACT	A	330	4/4	0.78	0.20	23,24,25,26	0
3	ACT	E	329	4/4	0.79	0.16	43,43,44,44	0
4	P33	C	331	22/22	0.87	0.13	39,44,48,49	0
4	P33	E	332	22/22	0.87	0.18	30,35,40,41	0
3	ACT	F	328	4/4	0.90	0.14	26,28,29,29	0
3	ACT	E	331	4/4	0.91	0.12	27,28,29,30	0
4	P33	B	328	22/22	0.91	0.14	31,39,43,45	0
3	ACT	B	327	4/4	0.92	0.11	30,31,32,33	0
4	P33	C	330	19/22	0.92	0.13	20,26,45,48	0
3	ACT	E	328	4/4	0.92	0.10	18,21,21,22	0
4	P33	A	331	22/22	0.92	0.11	20,25,33,35	0
5	NA	F	330	1/1	0.92	0.11	31,31,31,31	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
3	ACT	D	327	4/4	0.93	0.15	33,34,34,35	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
3	ACT	A	327	4/4	0.95	0.11	20,23,23,24	0
5	NA	F	329	1/1	0.95	0.11	25,25,25,25	0
3	ACT	A	329	4/4	0.95	0.09	22,23,23,23	0
5	NA	E	333	1/1	0.96	0.23	26,26,26,26	0
4	P33	B	329	14/22	0.96	0.09	25,29,32,34	0
5	NA	A	334	1/1	0.97	0.05	29,29,29,29	0
5	NA	D	328	1/1	0.97	0.12	31,31,31,31	0
2	NOS	F	401	19/19	0.97	0.07	14,18,21,23	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	C	327	4/4	0.97	0.11	20,22,22,23	0
3	ACT	E	327	4/4	0.97	0.09	15,19,19,19	0
2	NOS	B	401	19/19	0.98	0.07	13,15,16,19	0
2	NOS	C	401	19/19	0.98	0.08	11,13,15,16	0
2	NOS	A	401	19/19	0.98	0.07	12,14,17,17	0
5	NA	A	333	1/1	0.98	0.05	18,18,18,18	0
2	NOS	E	401	19/19	0.98	0.08	11,14,17,17	0
5	NA	B	332	1/1	0.98	0.05	21,21,21,21	0

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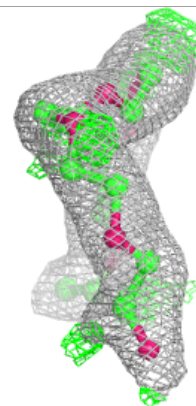
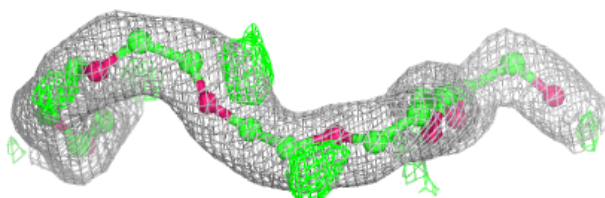
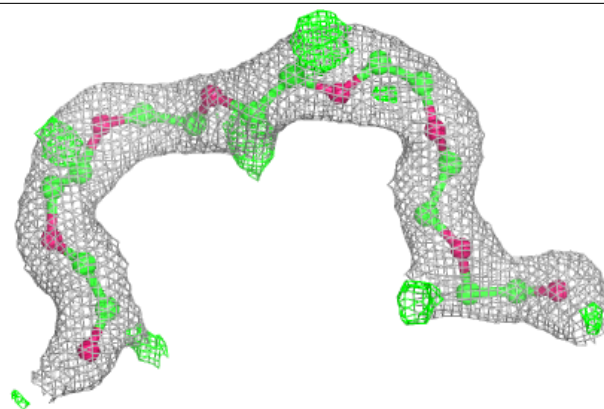
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	NA	B	331	1/1	0.99	0.06	18,18,18,18	0
5	NA	E	334	1/1	0.99	0.06	14,14,14,14	0
5	NA	A	332	1/1	0.99	0.06	21,21,21,21	0
5	NA	C	332	1/1	0.99	0.07	26,26,26,26	0
5	NA	C	333	1/1	0.99	0.06	17,17,17,17	0
5	NA	B	330	1/1	0.99	0.04	22,22,22,22	0

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.

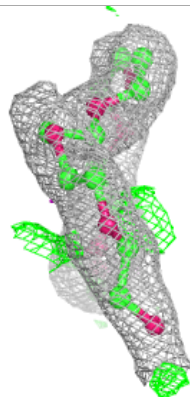
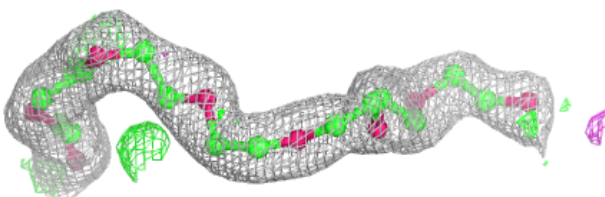
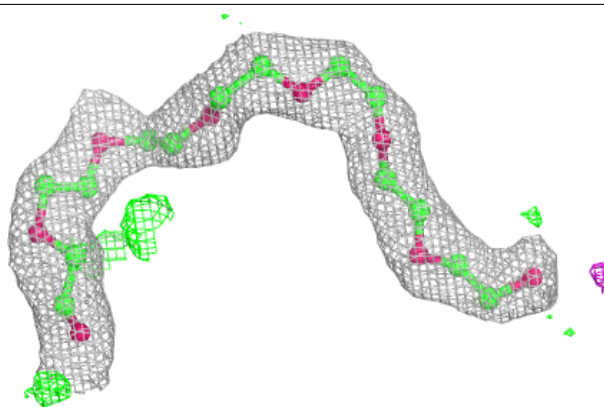


Electron density around P33 E 332:

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

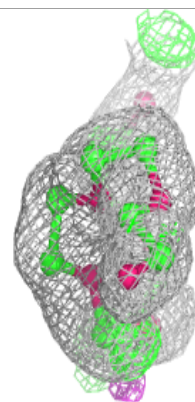
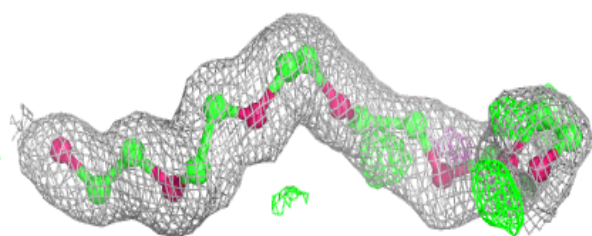
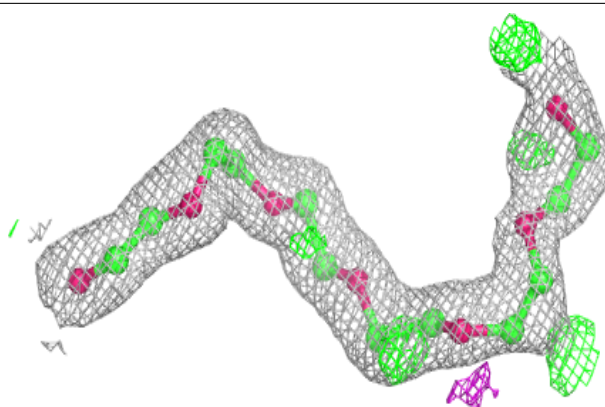
**Electron density around P33 B 328:**

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

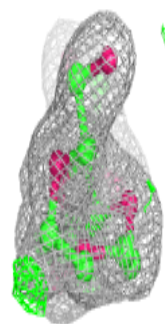
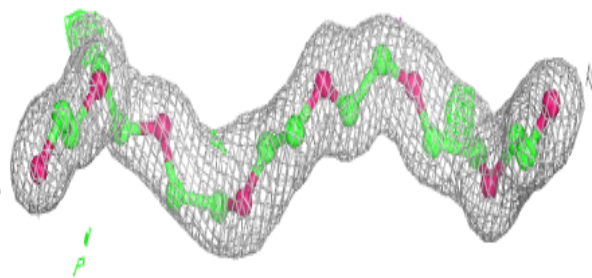
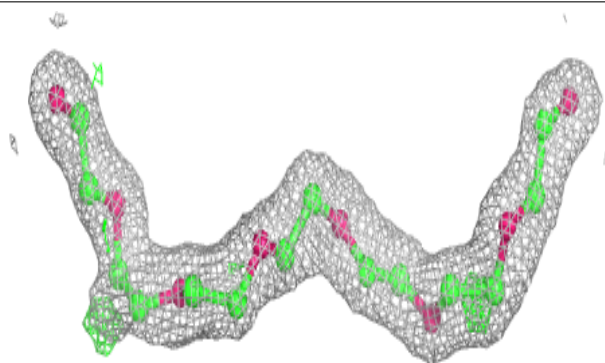


Electron density around P33 C 330:

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 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

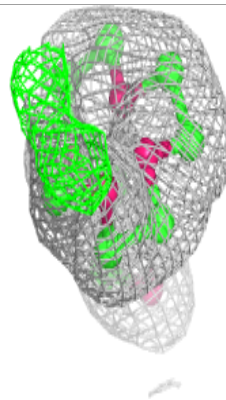
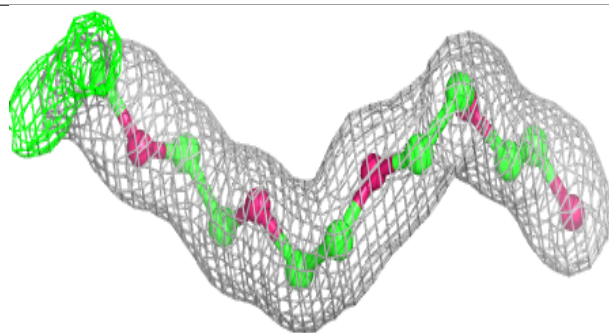
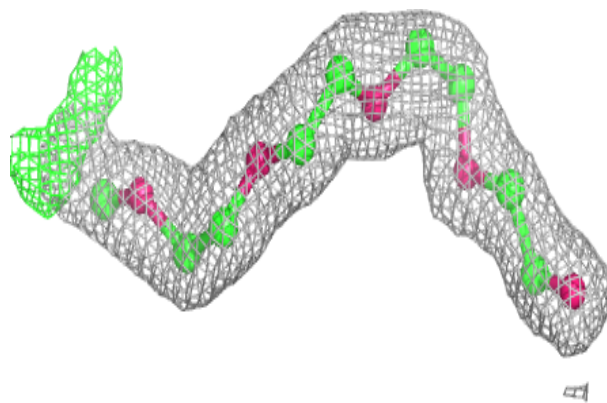
**Electron density around P33 A 331:**

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

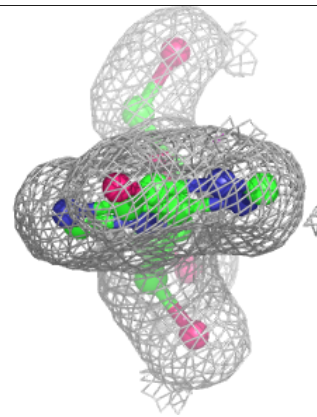
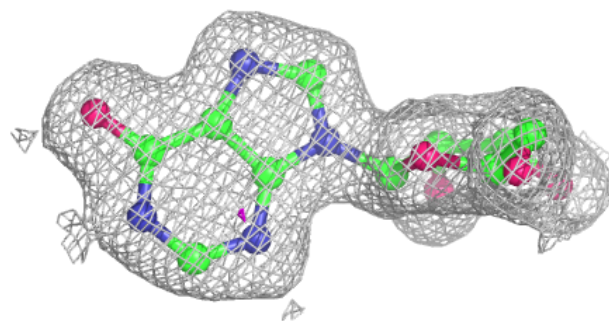
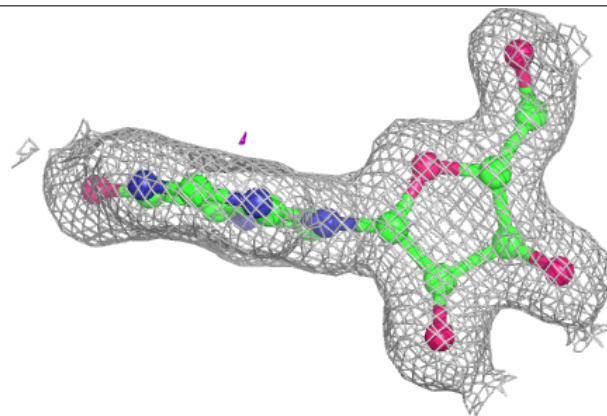


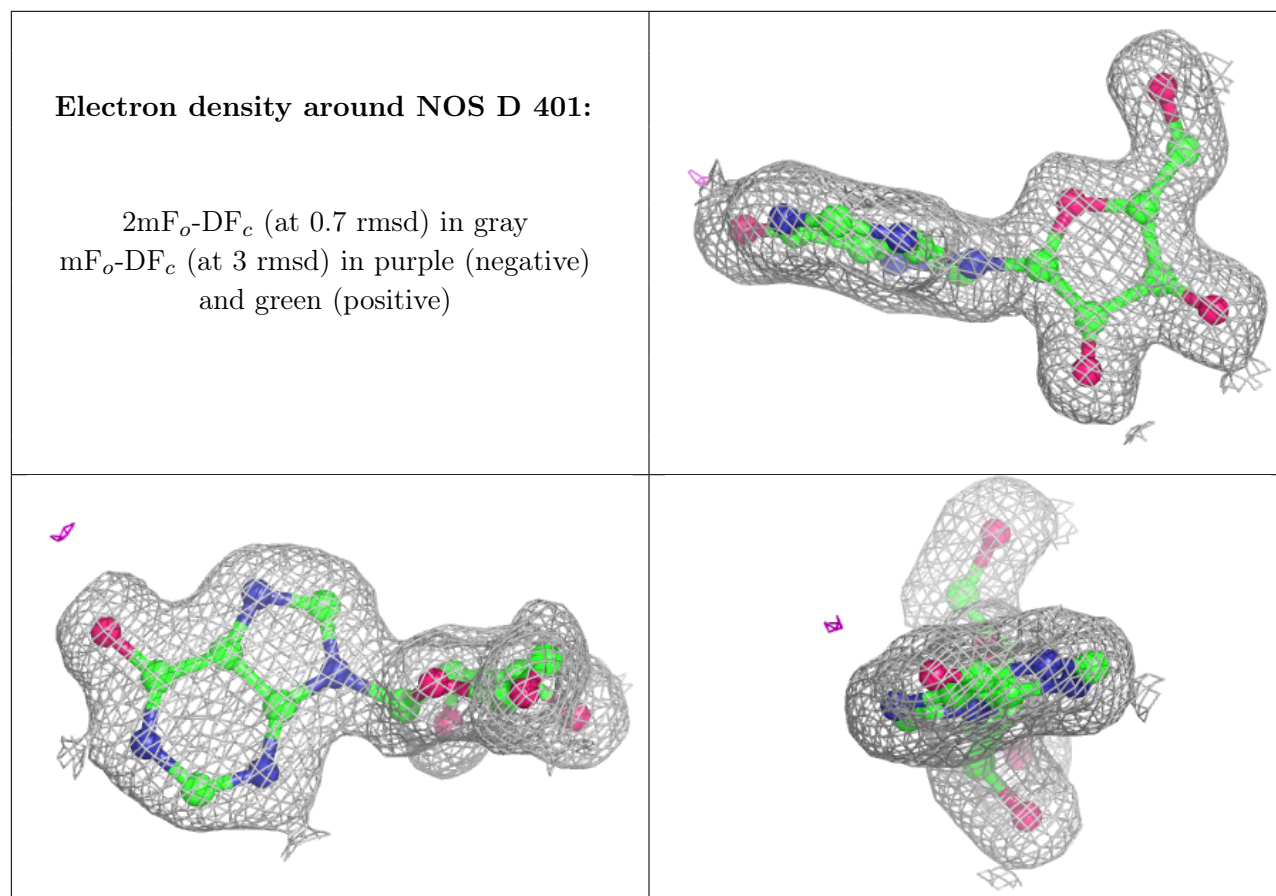
Electron density around P33 B 329:

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

**Electron density around NOS F 401:**

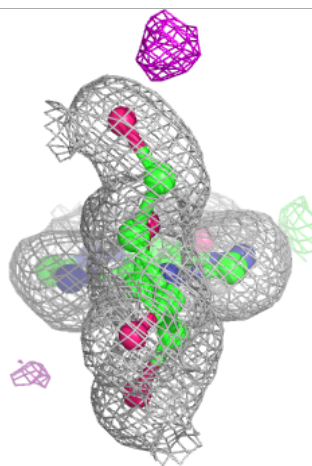
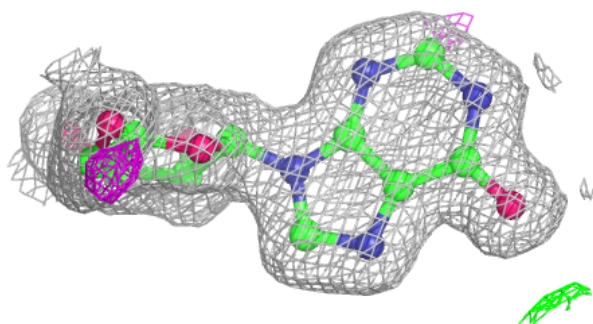
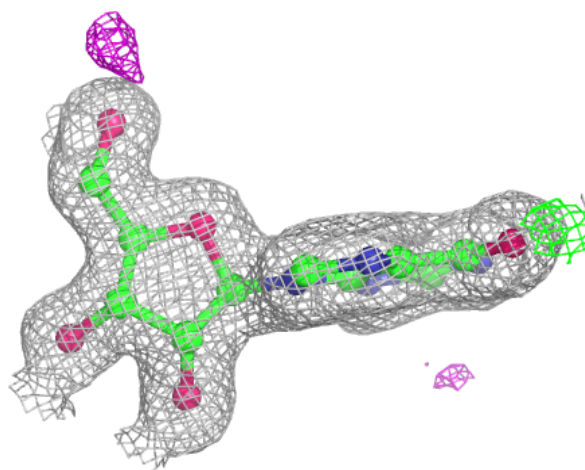
$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

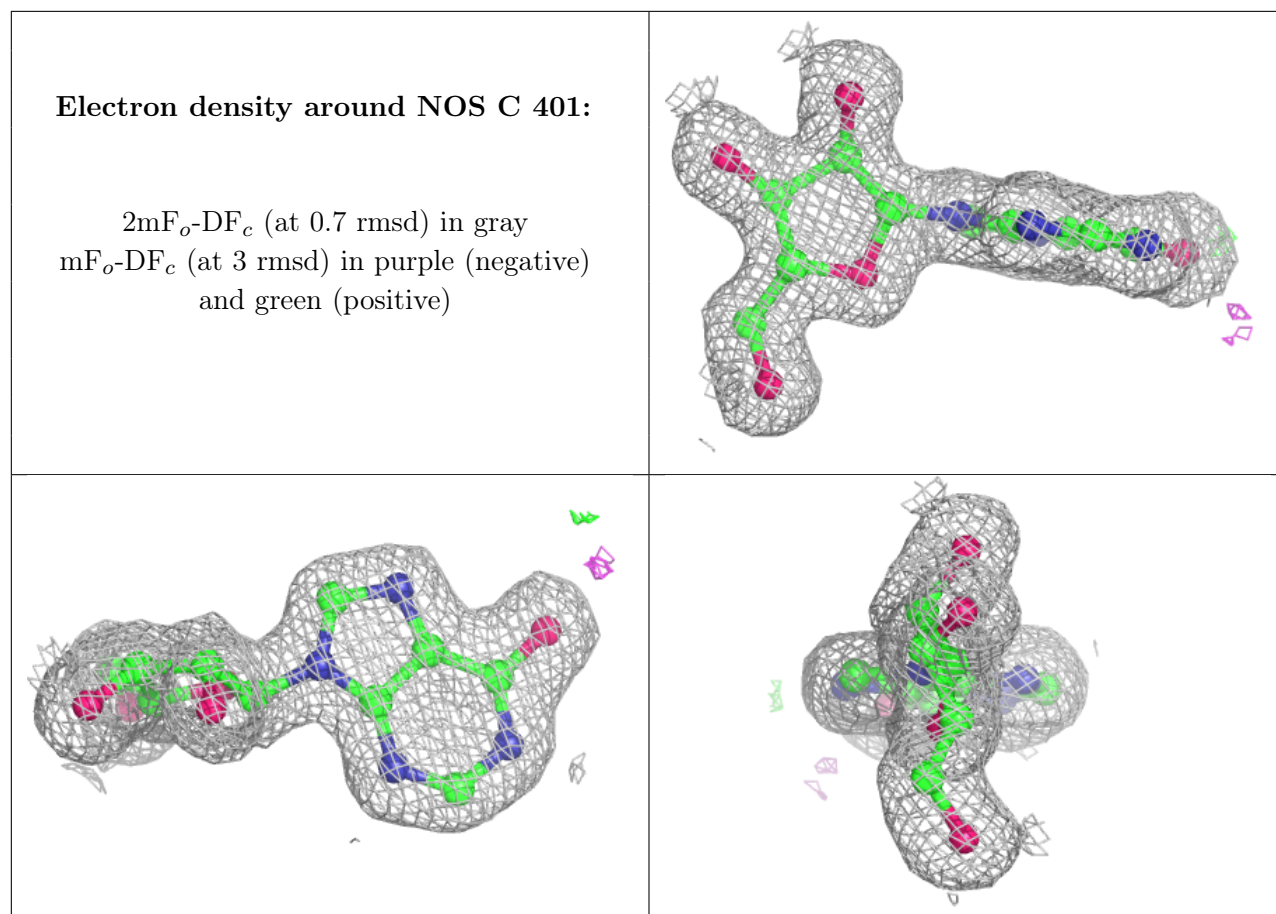


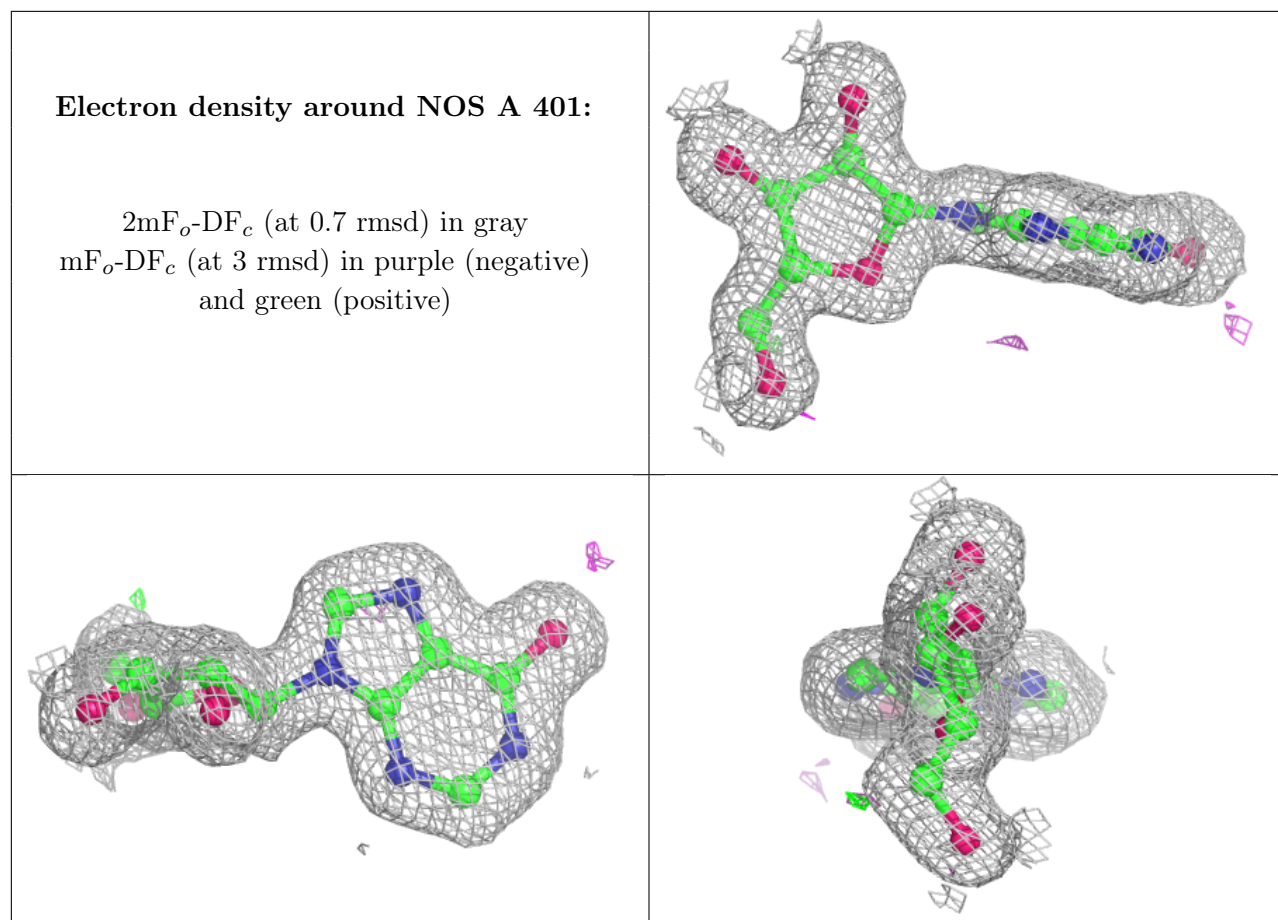


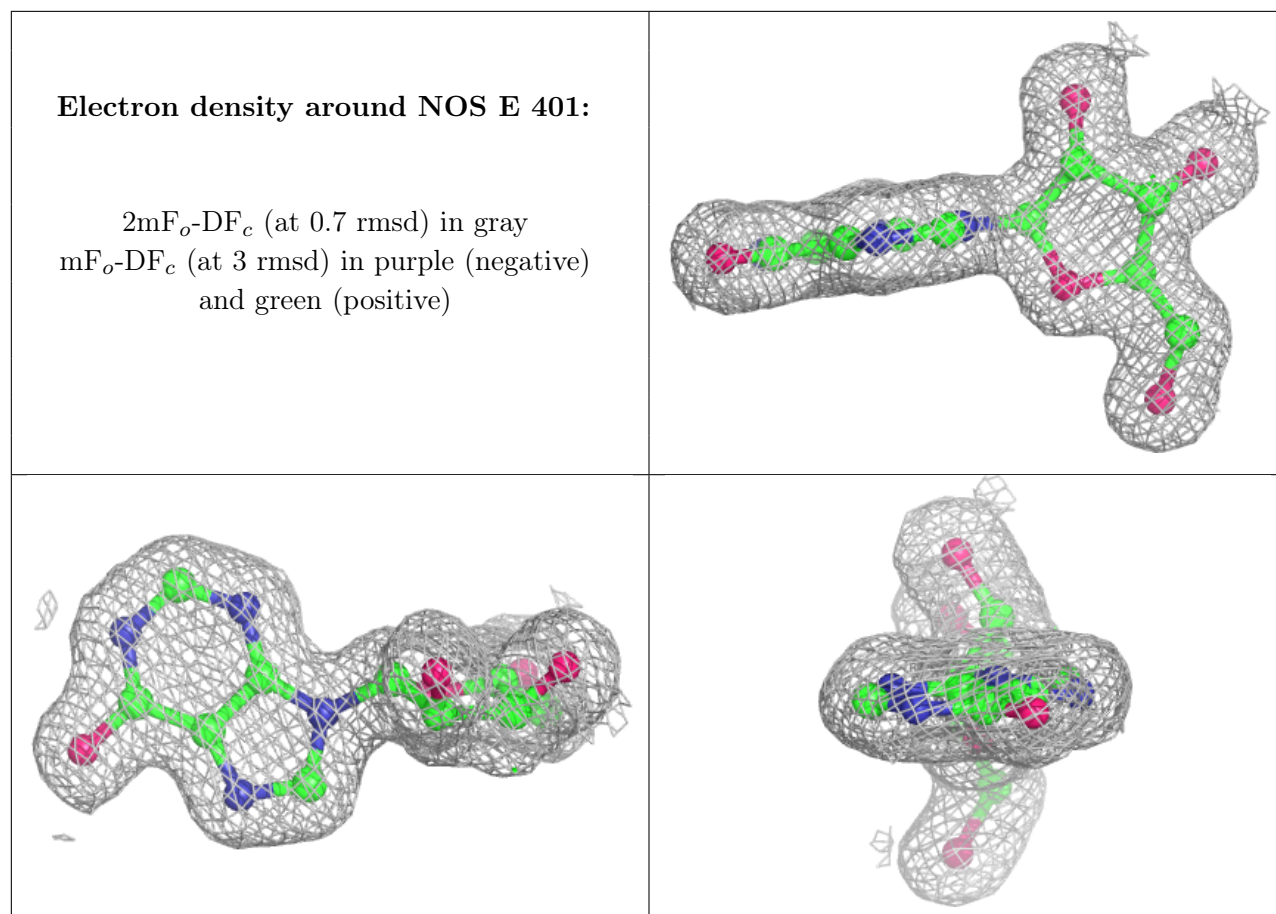
Electron density around NOS B 401:

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









6.5 Other polymers [i](#)

There are no such residues in this entry.