



Full wwPDB X-ray Structure Validation Report ⓘ

Jul 14, 2021 – 08:05 AM EDT

PDB ID : 7KN1
Title : Crystal structure of UDP-glucose-4-epimerase (galE) from *Stenotrophomonas maltophilia* with bound NAD and formylated UDP-arabinopyranose
Authors : Seattle Structural Genomics Center for Infectious Disease (SSGCID)
Deposited on : 2020-11-03
Resolution : 1.45 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

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	:	2.22
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)	:	2.22

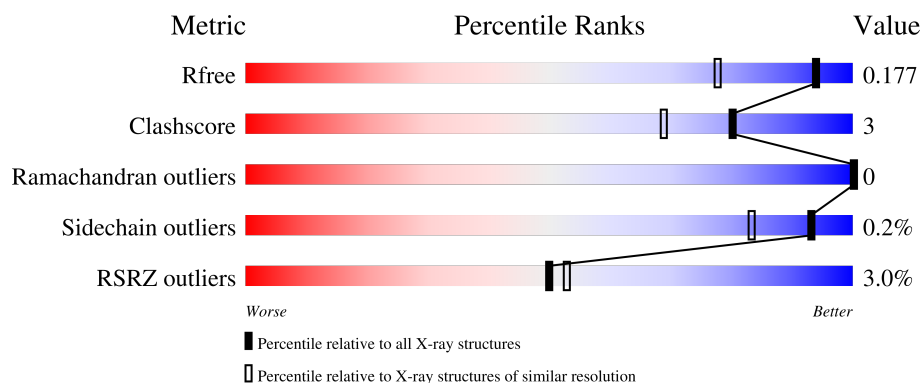
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

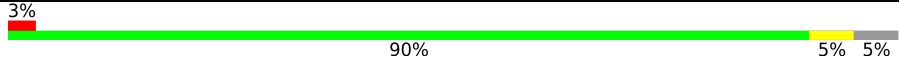

The reported resolution of this entry is 1.45 Å.

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	1156 (1.46-1.46)
Clashscore	141614	1202 (1.46-1.46)
Ramachandran outliers	138981	1178 (1.46-1.46)
Sidechain outliers	138945	1178 (1.46-1.46)
RSRZ outliers	127900	1139 (1.46-1.46)

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	354	
1	B	354	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	EDO	B	409	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6382 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 UDP-glucose 4-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	336	Total	C	N	O	S	0	17	0
			2642	1664	473	490	15			
1	B	336	Total	C	N	O	S	0	17	0
			2632	1663	469	485	15			

There are 16 discrepancies between the modelled and reference sequences:

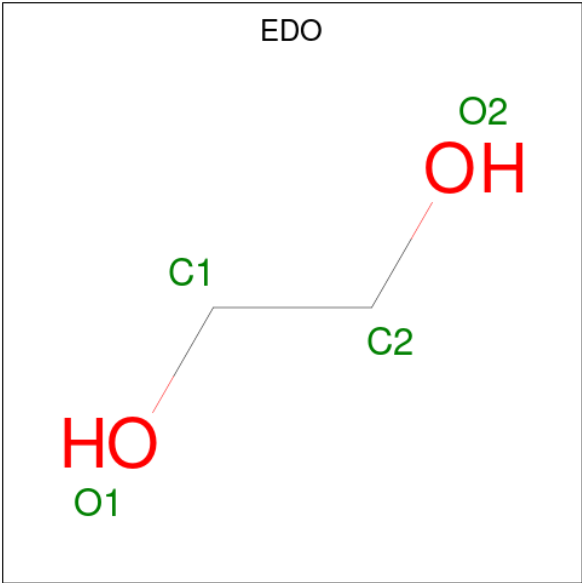
Chain	Residue	Modelled	Actual	Comment	Reference
A	-7	MET	-	initiating methionine	UNP B2FNY6
A	-6	ALA	-	expression tag	UNP B2FNY6
A	-5	HIS	-	expression tag	UNP B2FNY6
A	-4	HIS	-	expression tag	UNP B2FNY6
A	-3	HIS	-	expression tag	UNP B2FNY6
A	-2	HIS	-	expression tag	UNP B2FNY6
A	-1	HIS	-	expression tag	UNP B2FNY6
A	0	HIS	-	expression tag	UNP B2FNY6
B	-7	MET	-	initiating methionine	UNP B2FNY6
B	-6	ALA	-	expression tag	UNP B2FNY6
B	-5	HIS	-	expression tag	UNP B2FNY6
B	-4	HIS	-	expression tag	UNP B2FNY6
B	-3	HIS	-	expression tag	UNP B2FNY6
B	-2	HIS	-	expression tag	UNP B2FNY6
B	-1	HIS	-	expression tag	UNP B2FNY6
B	0	HIS	-	expression tag	UNP B2FNY6

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 44	C 21	N 7	O 14	P 2	0	0
2	B	1	Total 44	C 21	N 7	O 14	P 2	0	0

- Molecule 3 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: C₂H₆O₂).



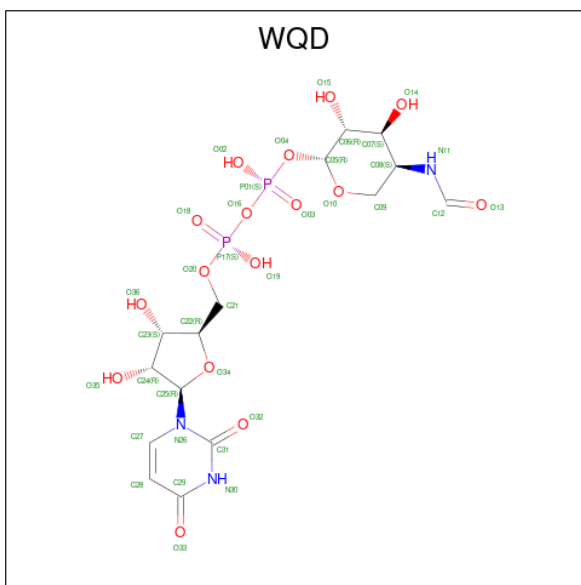
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	A	1	Total	C	O	0	0
			4	2	2		

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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	A	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		
3	B	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is UDP-4-deoxy-4-formamido-beta-L-arabinopyranose (three-letter code: WQD) (formula: C₁₅H₂₃N₃O₁₆P₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 36	C 15	N 3	O 16	P 2	0	0
4	B	1	Total 36	C 15	N 3	O 16	P 2	0	0

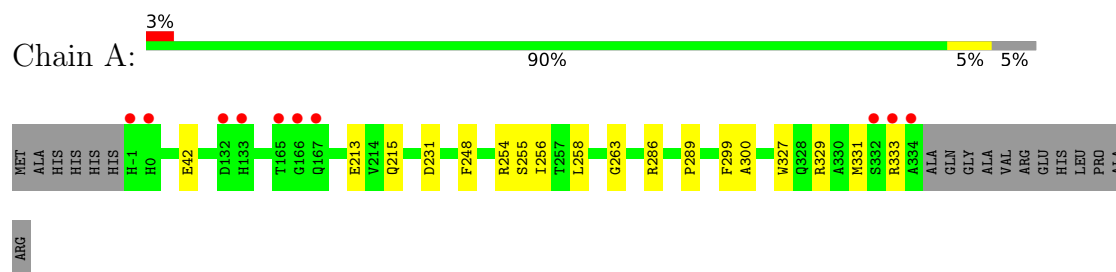
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	451	Total O 462 462	0	11
5	B	415	Total O 426 426	0	12

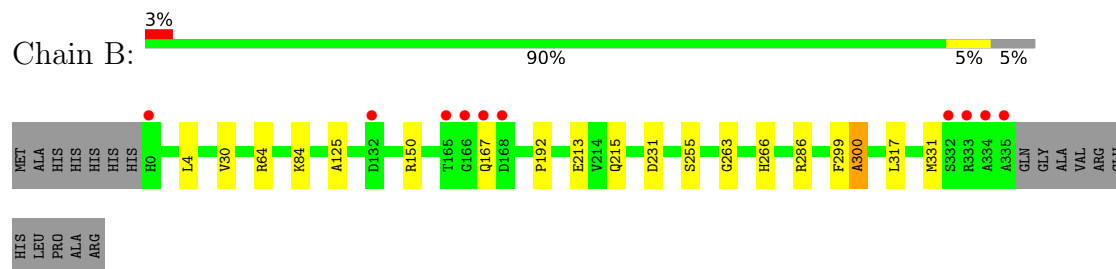
3 Residue-property plots [i](#)

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: UDP-glucose 4-epimerase



- Molecule 1: UDP-glucose 4-epimerase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	72.27Å 79.42Å 153.85Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.08 – 1.45 43.90 – 1.45	Depositor EDS
% Data completeness (in resolution range)	99.8 (43.08-1.45) 99.8 (43.90-1.45)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.46 (at 1.45Å)	Xtriage
Refinement program	PHENIX 1.19rc-4022	Depositor
R, R_{free}	0.159 , 0.177 0.159 , 0.177	Depositor DCC
R_{free} test set	2017 reflections (1.29%)	wwPDB-VP
Wilson B-factor (Å ²)	10.4	Xtriage
Anisotropy	0.193	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 48.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6382	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.72% 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: NAD, WQD, EDO

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	0.32	0/2746	0.55	0/3731
1	B	0.31	0/2733	0.56	0/3715
All	All	0.31	0/5479	0.55	0/7446

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	300	ALA	Peptide

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	2642	0	2667	15	0
1	B	2632	0	2672	12	0
2	A	44	0	26	0	0
2	B	44	0	26	0	0
3	A	32	0	48	1	0
3	B	28	0	42	5	0
4	A	36	0	0	0	0
4	B	36	0	0	1	0
5	A	462	0	0	5	0
5	B	426	0	0	4	1
All	All	6382	0	5481	30	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 3.

All (30) 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:B:64[A]:ARG:NH1	5:B:501:HOH:O	2.08	0.86
1:A:329[A]:ARG:NH1	5:A:501:HOH:O	2.19	0.76
3:B:409:EDO:H22	5:B:550:HOH:O	1.92	0.70
1:B:4[B]:LEU:HD11	1:B:30:VAL:HG23	1.76	0.66
4:B:408:WQD:N11	3:B:409:EDO:H12	2.11	0.66
1:B:150:ARG:NH1	5:B:502:HOH:O	2.17	0.63
1:A:215[A]:GLN:OE1	1:A:286:ARG:NH1	2.34	0.60
1:A:329[B]:ARG:NH2	5:A:508:HOH:O	2.38	0.55
1:B:167[A]:GLN:HG2	5:B:614:HOH:O	2.08	0.54
1:A:333:ARG:NH1	5:A:510:HOH:O	2.42	0.53
1:B:231:ASP:HB2	1:B:299:PHE:HA	1.91	0.52
1:B:255:SER:H	3:B:403:EDO:H11	1.75	0.52
1:A:231:ASP:HB2	1:A:299:PHE:HA	1.92	0.52
1:A:255:SER:O	1:A:256[B]:ILE:HG12	2.11	0.51
1:A:256[A]:ILE:HD12	1:A:258:LEU:HD11	1.95	0.48
1:A:289:PRO:HG3	3:A:408:EDO:H22	1.96	0.47
1:A:333:ARG:NH1	5:A:501:HOH:O	2.19	0.46
1:A:213:GLU:HG3	1:A:215[A]:GLN:NE2	2.31	0.46
1:A:263:GLY:HA2	1:A:300:ALA:O	2.15	0.45
1:B:213:GLU:HG3	1:B:215[B]:GLN:NE2	2.32	0.45
1:B:266:HIS:CG	1:B:317[A]:LEU:HD11	2.53	0.44
1:B:192:PRO:HD3	1:B:331:MET:SD	2.58	0.44
1:B:263:GLY:HA2	1:B:300:ALA:O	2.17	0.44
1:B:215[B]:GLN:OE1	1:B:286:ARG:NH2	2.52	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:GLU:HB2	5:A:640:HOH:O	2.18	0.43
1:A:248:PHE:CE1	1:A:256[B]:ILE:HG13	2.55	0.42
1:A:254:ARG:NH1	1:A:256[B]:ILE:HD11	2.35	0.42
1:B:125:ALA:HB3	3:B:405:EDO:H22	2.01	0.42
1:A:327:TRP:O	1:A:331:MET:HG3	2.21	0.40

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)
5:B:809:HOH:O	5:B:859:HOH:O[3_555]	2.14	0.06

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	352/354 (99%)	345 (98%)	7 (2%)	0	100	100
1	B	351/354 (99%)	343 (98%)	8 (2%)	0	100	100
All	All	703/708 (99%)	688 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	286/282 (101%)	286 (100%)	0	100	100
1	B	285/282 (101%)	283 (99%)	2 (1%)	84	65
All	All	571/564 (101%)	569 (100%)	2 (0%)	93	80

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	84[A]	LYS
1	B	84[B]	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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](#)

19 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	$\# Z > 2$
4	WQD	B	408	-	31,38,38	1.30	3 (9%)	37,57,57	1.25	2 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	EDO	B	407	-	3,3,3	0.49	0	2,2,2	0.28	0
2	NAD	B	401	-	42,48,48	0.56	0	50,73,73	0.69	1 (2%)
3	EDO	A	404	-	3,3,3	0.48	0	2,2,2	0.35	0
3	EDO	A	408	-	3,3,3	0.47	0	2,2,2	0.30	0
3	EDO	A	403	-	3,3,3	0.52	0	2,2,2	0.17	0
3	EDO	A	407	-	3,3,3	0.47	0	2,2,2	0.30	0
3	EDO	A	405	-	3,3,3	0.59	0	2,2,2	0.16	0
3	EDO	B	403	-	3,3,3	0.44	0	2,2,2	0.37	0
2	NAD	A	401	-	42,48,48	0.55	0	50,73,73	0.67	1 (2%)
4	WQD	A	410	-	31,38,38	1.26	3 (9%)	37,57,57	1.36	3 (8%)
3	EDO	B	409	-	3,3,3	0.27	0	2,2,2	0.45	0
3	EDO	A	409	-	3,3,3	0.41	0	2,2,2	0.43	0
3	EDO	B	402	-	3,3,3	0.52	0	2,2,2	0.30	0
3	EDO	A	406	-	3,3,3	0.49	0	2,2,2	0.22	0
3	EDO	B	404	-	3,3,3	0.56	0	2,2,2	0.23	0
3	EDO	A	402	-	3,3,3	0.44	0	2,2,2	0.41	0
3	EDO	B	405	-	3,3,3	0.48	0	2,2,2	0.29	0
3	EDO	B	406	-	3,3,3	0.47	0	2,2,2	0.23	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	WQD	B	408	-	-	2/22/57/57	0/3/3/3
3	EDO	B	407	-	-	0/1/1/1	-
2	NAD	B	401	-	-	7/26/62/62	0/5/5/5
3	EDO	A	404	-	-	0/1/1/1	-
3	EDO	A	408	-	-	0/1/1/1	-
3	EDO	A	403	-	-	0/1/1/1	-
3	EDO	A	407	-	-	0/1/1/1	-
3	EDO	A	405	-	-	0/1/1/1	-
3	EDO	B	403	-	-	0/1/1/1	-
2	NAD	A	401	-	-	7/26/62/62	0/5/5/5
4	WQD	A	410	-	-	2/22/57/57	0/3/3/3
3	EDO	B	409	-	-	0/1/1/1	-
3	EDO	A	409	-	-	0/1/1/1	-
3	EDO	B	402	-	-	0/1/1/1	-
3	EDO	A	406	-	-	0/1/1/1	-
3	EDO	B	404	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	EDO	A	402	-	-	0/1/1/1	-
3	EDO	B	405	-	-	0/1/1/1	-
3	EDO	B	406	-	-	0/1/1/1	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	408	WQD	C29-N30	4.88	1.41	1.33
4	A	410	WQD	C29-N30	4.68	1.41	1.33
4	A	410	WQD	C27-N26	2.67	1.39	1.35
4	B	408	WQD	C27-N26	2.25	1.38	1.35
4	B	408	WQD	P01-O04	2.19	1.66	1.60
4	A	410	WQD	P01-O04	2.07	1.65	1.60

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	410	WQD	C28-C29-N30	-4.82	112.72	123.31
4	B	408	WQD	C28-C29-N30	-4.49	113.42	123.31
4	A	410	WQD	O10-C05-O04	-3.81	106.39	111.36
4	B	408	WQD	O10-C05-O04	-2.87	107.62	111.36
4	A	410	WQD	O10-C09-C08	-2.43	107.45	111.29
2	B	401	NAD	C5A-C6A-N6A	2.31	123.86	120.35
2	A	401	NAD	C5A-C6A-N6A	2.30	123.84	120.35

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	NAD	C5D-O5D-PN-O2N
2	A	401	NAD	O4D-C1D-N1N-C2N
2	B	401	NAD	C5D-O5D-PN-O2N
2	B	401	NAD	O4D-C1D-N1N-C2N
4	A	410	WQD	P01-O16-P17-O20
4	B	408	WQD	P01-O16-P17-O20
2	A	401	NAD	C5D-O5D-PN-O3
2	B	401	NAD	C5D-O5D-PN-O3
2	A	401	NAD	C5D-O5D-PN-O1N
2	B	401	NAD	C5D-O5D-PN-O1N
2	A	401	NAD	PA-O3-PN-O1N
2	A	401	NAD	PA-O3-PN-O2N

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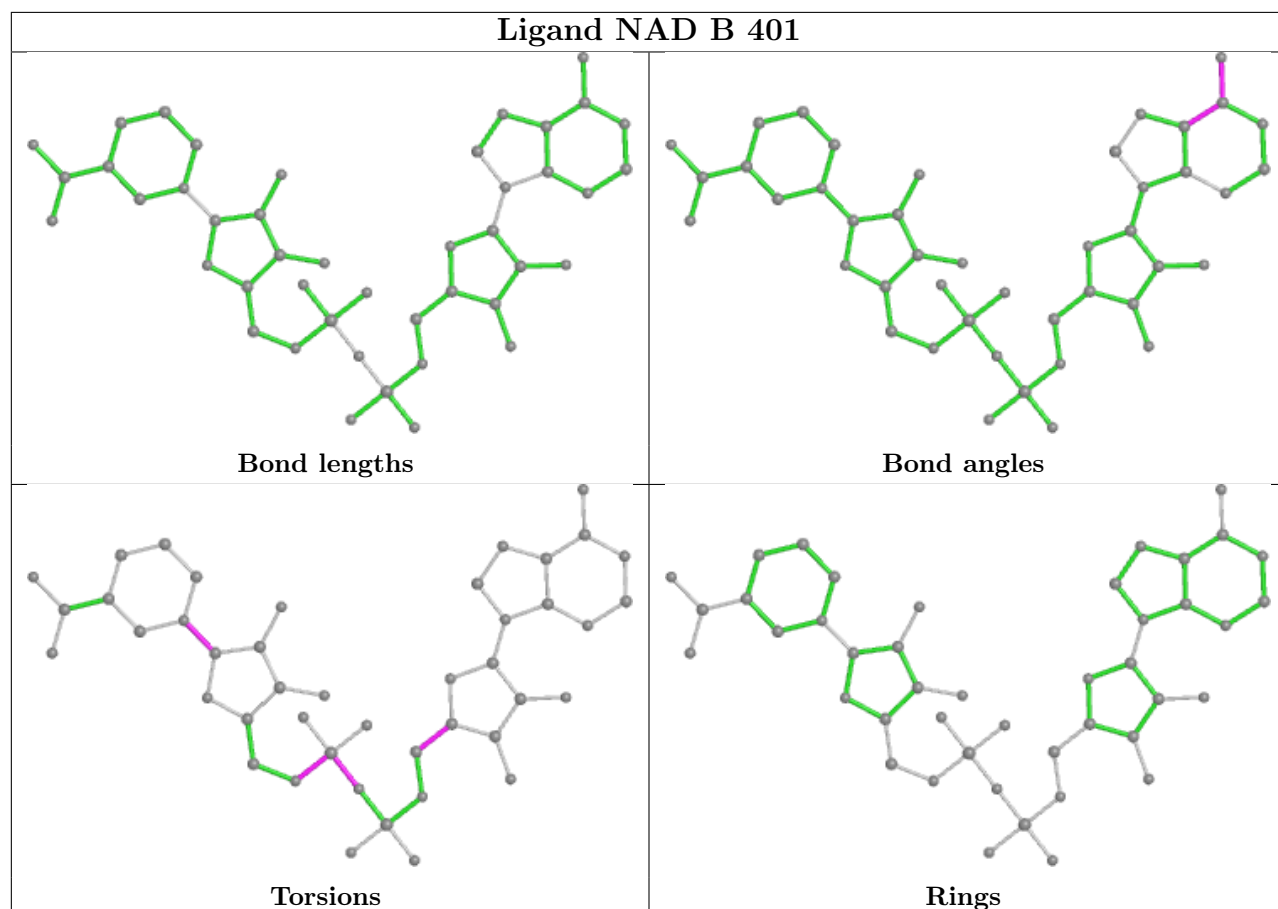
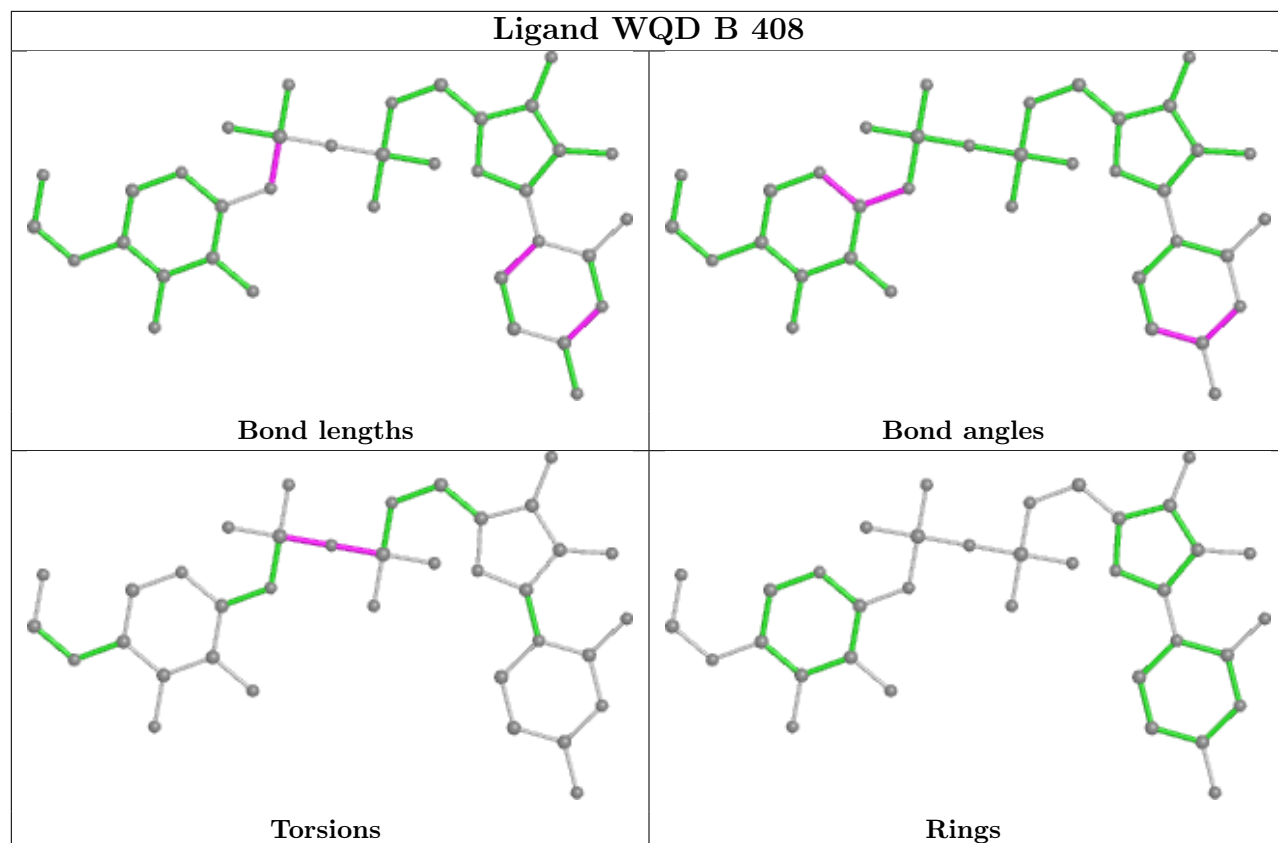
Mol	Chain	Res	Type	Atoms
2	B	401	NAD	PA-O3-PN-O2N
2	B	401	NAD	O4B-C4B-C5B-O5B
2	A	401	NAD	O4B-C4B-C5B-O5B
2	B	401	NAD	PA-O3-PN-O1N
4	A	410	WQD	P17-O16-P01-O03
4	B	408	WQD	P17-O16-P01-O03

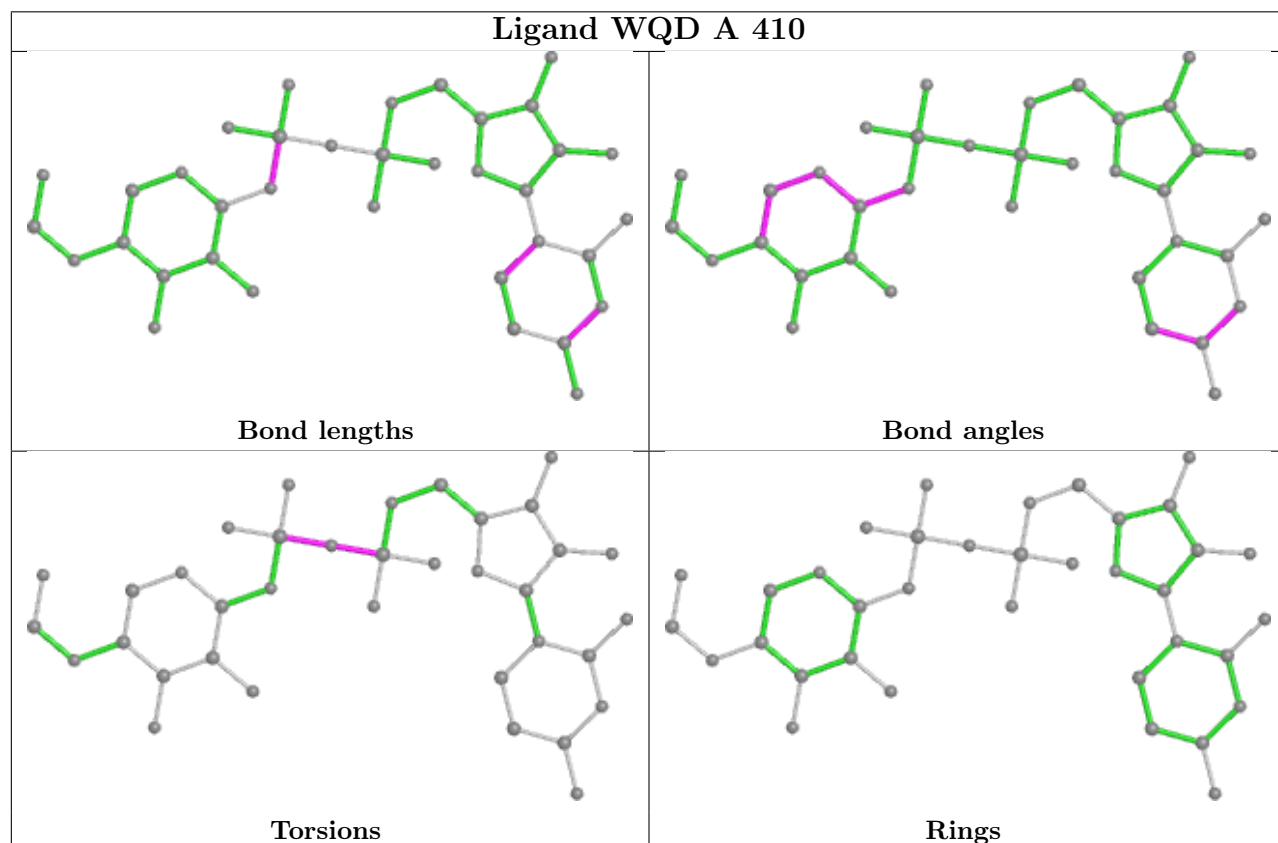
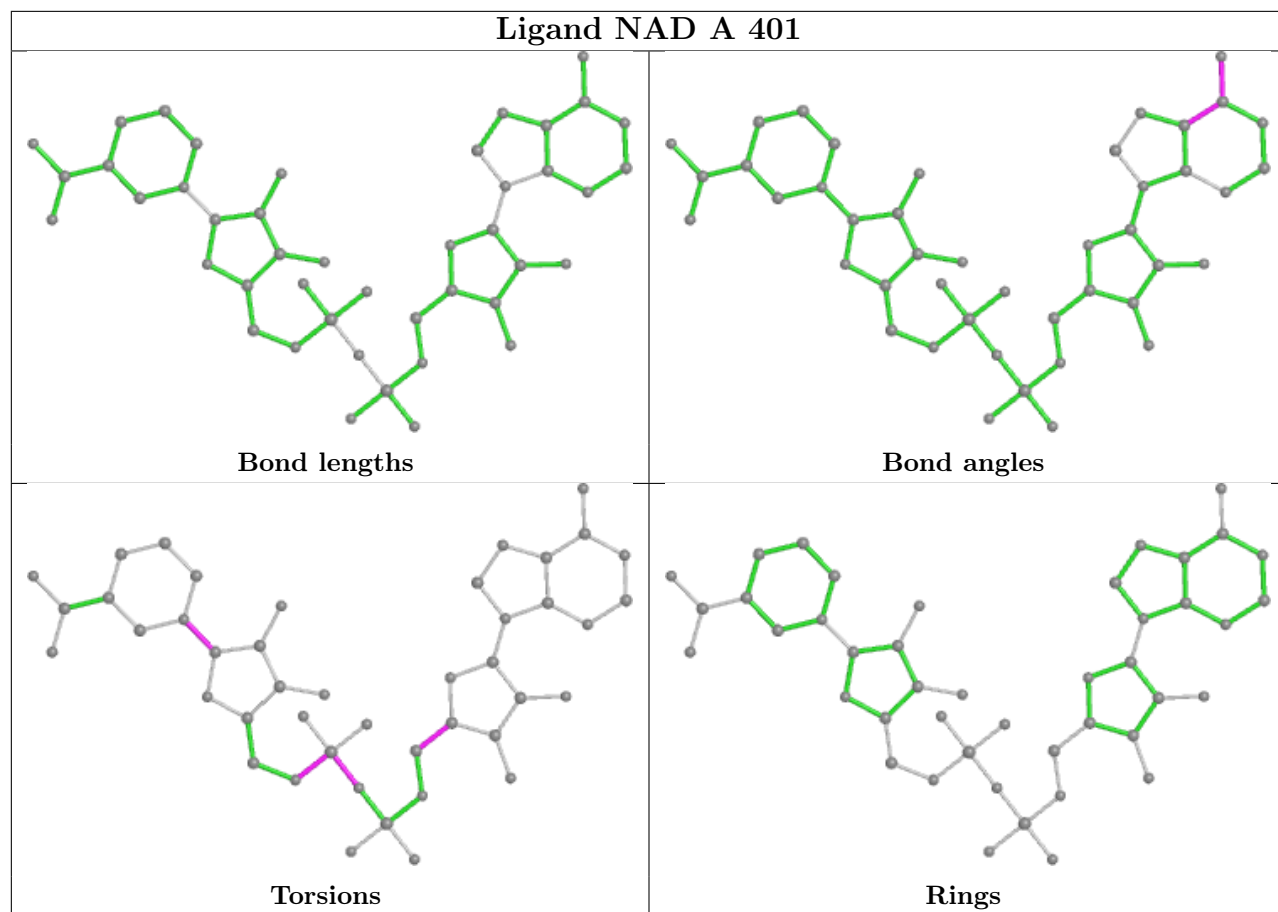
There are no ring outliers.

5 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	408	WQD	1	0
3	A	408	EDO	1	0
3	B	403	EDO	1	0
3	B	409	EDO	3	0
3	B	405	EDO	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	336/354 (94%)	-0.22	10 (2%) 50 53	6, 11, 25, 49	0
1	B	336/354 (94%)	-0.20	10 (2%) 50 53	6, 12, 29, 51	0
All	All	672/708 (94%)	-0.21	20 (2%) 50 53	6, 11, 29, 51	0

All (20) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	334	ALA	6.6
1	B	335	ALA	3.9
1	A	333	ARG	3.7
1	A	133	HIS	3.6
1	A	332	SER	3.4
1	B	334	ALA	3.3
1	B	132	ASP	3.1
1	A	-1	HIS	2.9
1	A	167	GLN	2.9
1	B	167[A]	GLN	2.9
1	B	166	GLY	2.7
1	A	132	ASP	2.4
1	B	168	ASP	2.4
1	B	332	SER	2.4
1	A	166	GLY	2.4
1	A	0	HIS	2.2
1	B	0	HIS	2.2
1	B	333	ARG	2.2
1	B	165	THR	2.1
1	A	165	THR	2.1

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](#)

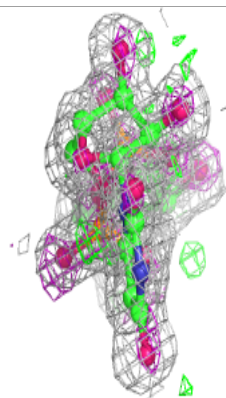
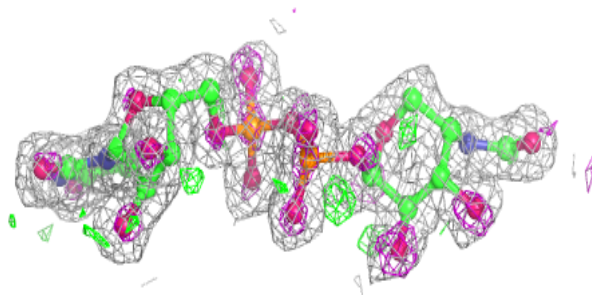
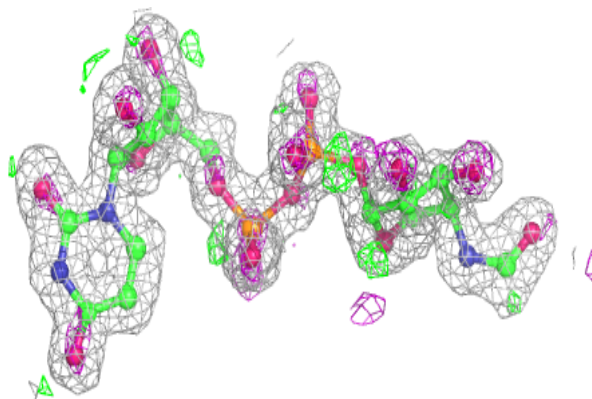
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	EDO	B	409	4/4	0.50	0.59	42,42,42,43	0
3	EDO	A	407	4/4	0.53	0.26	43,43,43,44	0
3	EDO	B	407	4/4	0.62	0.25	44,44,44,44	0
3	EDO	A	404	4/4	0.66	0.17	31,31,31,32	0
3	EDO	A	408	4/4	0.67	0.35	52,52,52,52	0
3	EDO	B	406	4/4	0.72	0.19	36,36,36,36	0
3	EDO	A	409	4/4	0.78	0.26	39,39,39,39	0
3	EDO	A	402	4/4	0.81	0.14	33,34,34,34	0
3	EDO	B	403	4/4	0.83	0.20	38,38,38,38	0
3	EDO	B	405	4/4	0.84	0.18	23,24,24,25	0
3	EDO	A	406	4/4	0.86	0.16	23,23,23,24	0
3	EDO	A	405	4/4	0.92	0.12	16,16,17,18	0
3	EDO	A	403	4/4	0.95	0.07	11,12,12,13	0
3	EDO	B	404	4/4	0.95	0.08	13,14,14,14	0
3	EDO	B	402	4/4	0.95	0.07	11,11,12,12	0
4	WQD	B	408	36/36	0.97	0.07	11,13,17,18	0
4	WQD	A	410	36/36	0.98	0.06	10,11,14,15	0
2	NAD	B	401	44/44	0.98	0.06	5,6,8,9	0
2	NAD	A	401	44/44	0.99	0.07	6,7,8,9	0

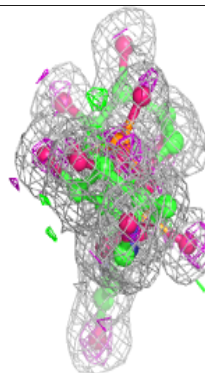
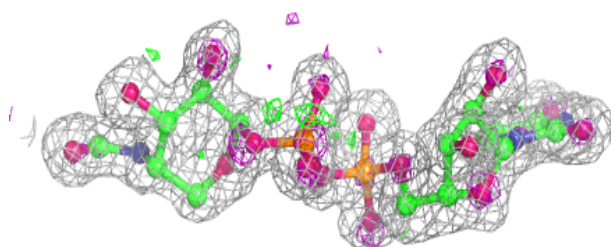
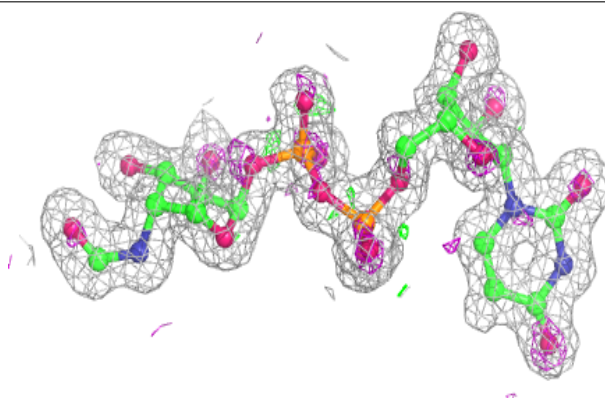
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around WQD B 408:

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

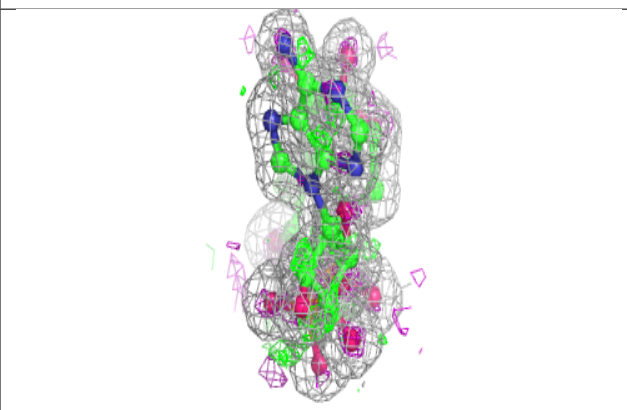
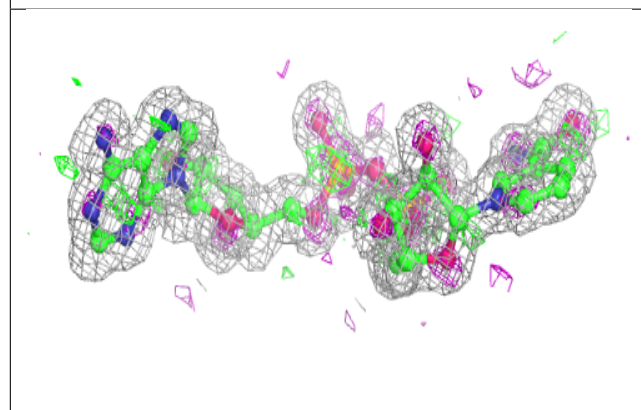
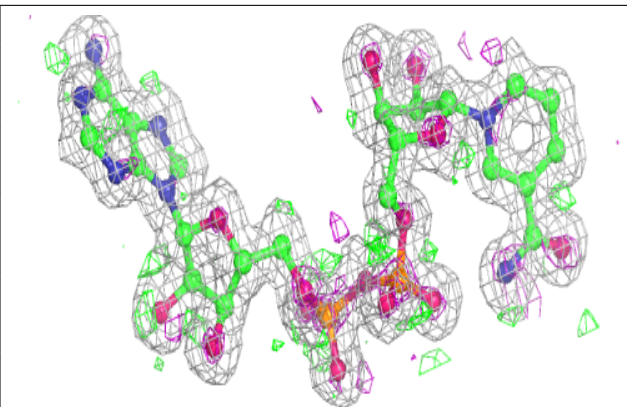
**Electron density around WQD A 410:**

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

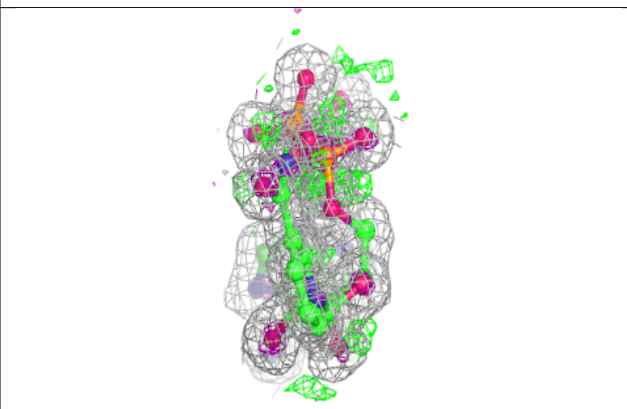
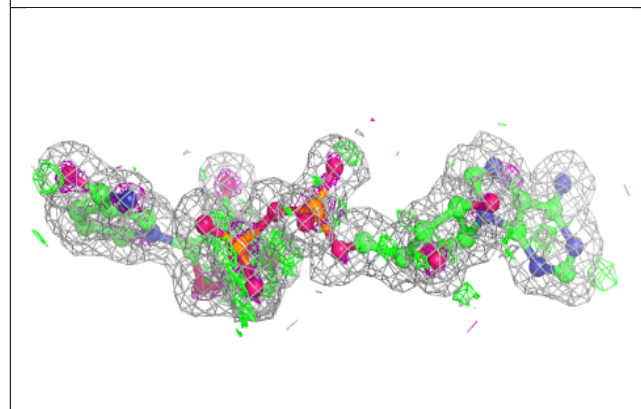
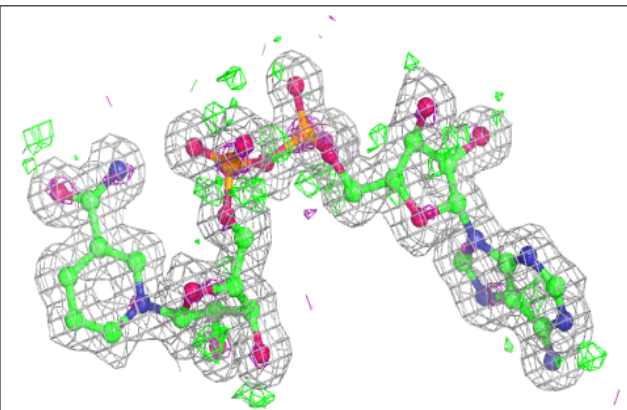


Electron density around NAD B 401:

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

**Electron density around NAD 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)



6.5 Other polymers [i](#)

There are no such residues in this entry.