wwPDB X-ray Structure Validation Summary Report (i)

May 27, 2025 – 10:50 AM EDT

PDB ID	:	9C36 / pdb_00009c36
Title	:	Proline utilization A complexed with the substrate L-glutamate gamma-semialdehyde in the aldehyde dehydrogenase active site
Authors	:	Tanner, J.J.; Buckley, D.P.
Deposited on	:	2024-05-31
Resolution	:	1.47 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 (i) 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 (i)) were used in the production of this report:

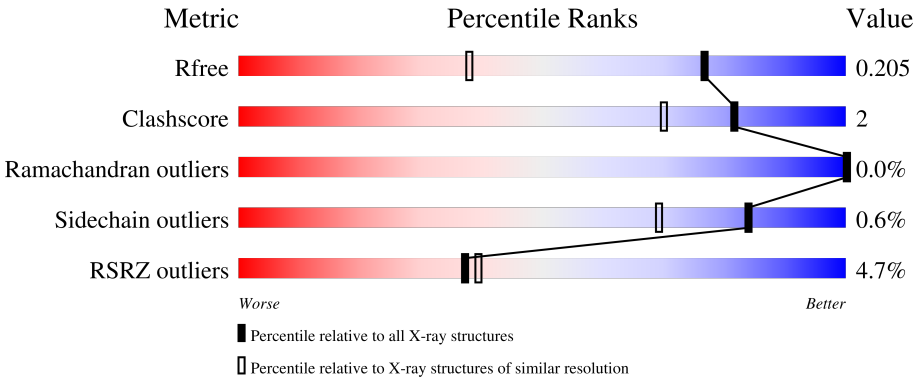
MolProbity	:	4-5-2 with Phenix2.0rc1
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0rc1
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.006 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.43.1

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 1.47 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}	164625	6131 (1.50-1.46)
Clashscore	180529	6623 (1.50-1.46)
Ramachandran outliers	177936	6521 (1.50-1.46)
Sidechain outliers	177891	6518 (1.50-1.46)
RSRZ outliers	164620	6132 (1.50-1.46)

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 <=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	1235	4% 93% 5%
1	B	1235	5% 92% 5%

2 Entry composition (i)

There are 10 unique types of molecules in this entry. The entry contains 37779 atoms, of which 17914 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.

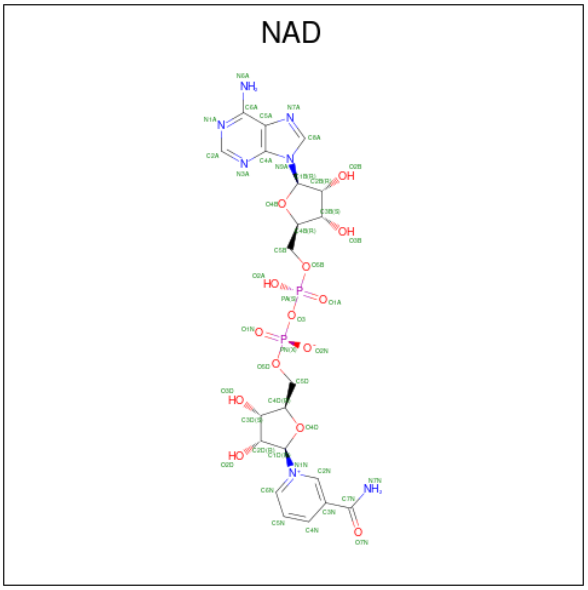
- Molecule 1 is a protein called Bifunctional protein PutA.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	1210	Total	C	H	N	O	S	0	7	0
			17790	5616	8877	1591	1674	32			
1	B	1209	Total	C	H	N	O	S	0	9	0
			17734	5603	8839	1586	1674	32			

There are 6 discrepancies between the modelled and reference sequences:

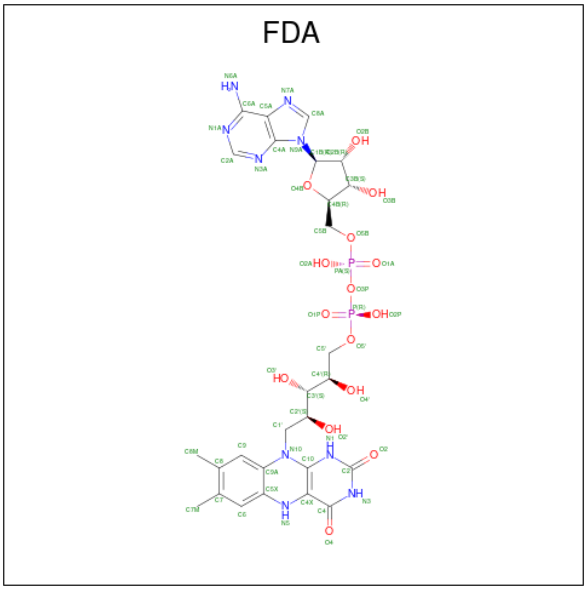
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	SER	-	expression tag	UNP F7X6I3
A	0	MET	-	expression tag	UNP F7X6I3
A	844	SER	CYS	engineered mutation	UNP F7X6I3
B	-1	SER	-	expression tag	UNP F7X6I3
B	0	MET	-	expression tag	UNP F7X6I3
B	844	SER	CYS	engineered mutation	UNP F7X6I3

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$) (labeled as "Ligand of Interest" by depositor).



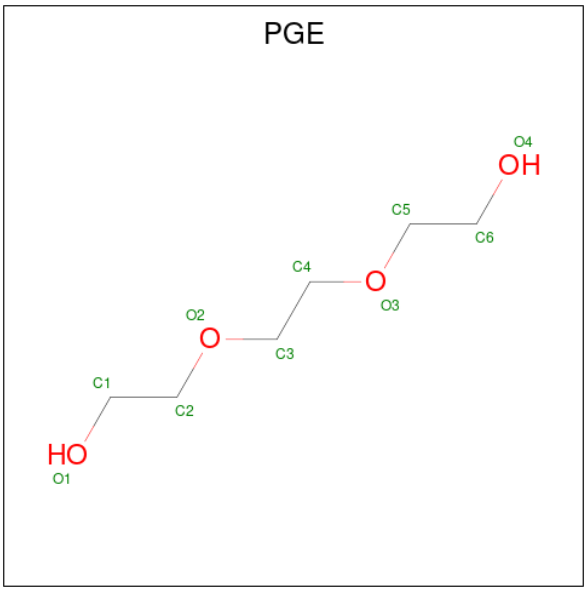
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	H	N	O	P	0	0
			70	21	26	7	14	2		
2	B	1	Total	C	H	N	O	P	0	1
			140	42	52	14	28	4		

- Molecule 3 is DIHYDROFLAVINE-ADENINE DINUCLEOTIDE (CCD ID: FDA) (formula: $C_{27}H_{35}N_9O_{15}P_2$) (labeled as "Ligand of Interest" by depositor).



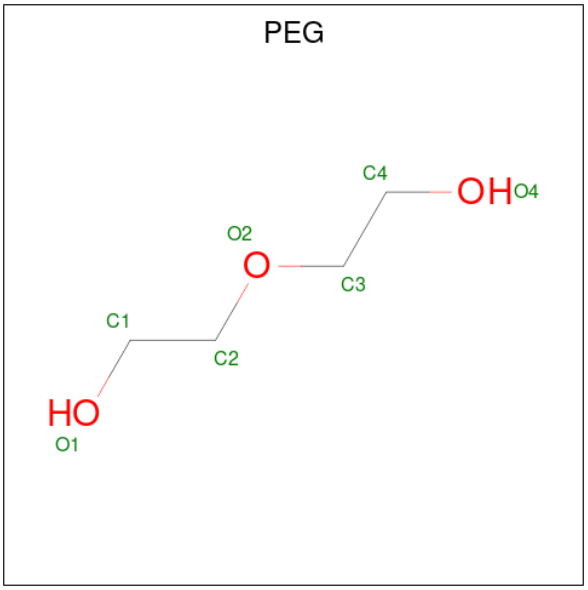
Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	H	N	O	P	0	0
			85	27	32	9	15	2		
3	B	1	Total	C	H	N	O	P	0	0
			85	27	32	9	15	2		

- Molecule 4 is TRIETHYLENE GLYCOL (CCD ID: PGE) (formula: $C_6H_{14}O_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	H	O	0	0
			24	6	14	4		
4	B	1	Total	C	H	O	0	0
			24	6	14	4		

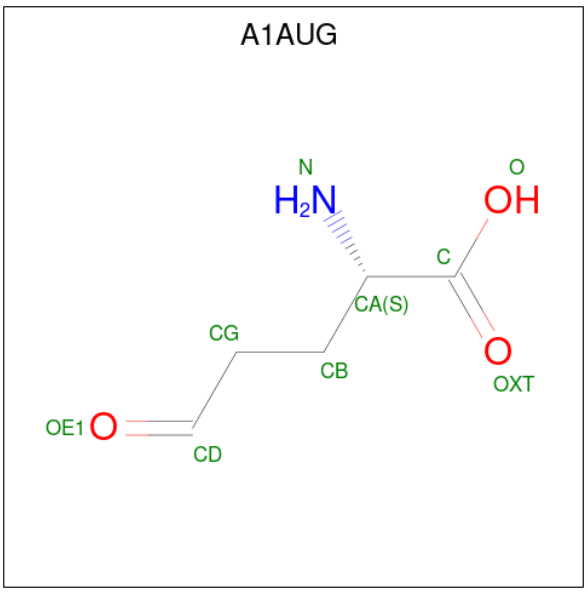
- Molecule 5 is DI(HYDROXYETHYL)ETHER (CCD ID: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	H	O	0	0
			17	4	10	3		

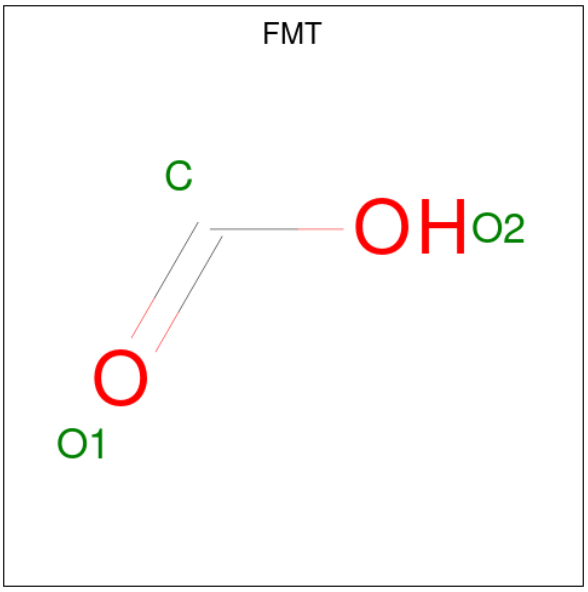
- Molecule 6 is 5-oxo-L-norvaline (CCD ID: A1AUG) (formula: $C_5H_9NO_3$) (labeled as "Ligand

of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
6	A	1	Total	C	H	N	O	0	0
			17	5	8	1	3		
6	B	1	Total	C	H	N	O	0	0
			17	5	8	1	3		

- Molecule 7 is FORMIC ACID (CCD ID: FMT) (formula: CH_2O_2).



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

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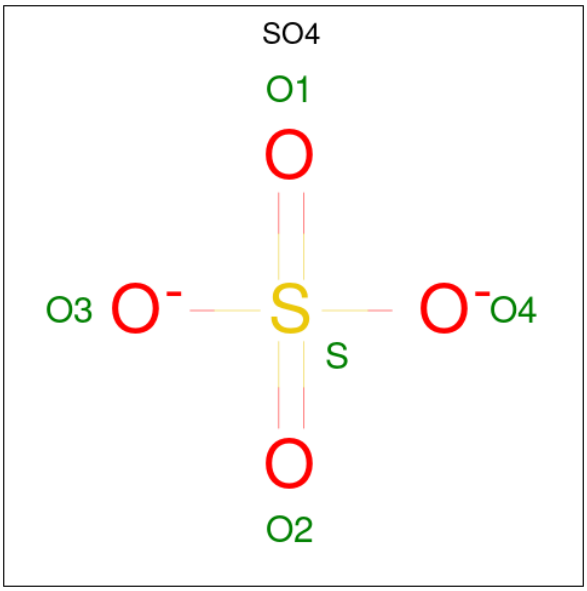
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	B	1	Total C H O 4 1 1 2	0	0

- Molecule 8 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	2	Total Mg 2 2	0	0
8	B	1	Total Mg 2 2	0	1

- Molecule 9 is SULFATE ION (CCD ID: SO4) (formula: O_4S).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total O S 5 4 1	0	0
9	A	1	Total O S 5 4 1	0	0
9	A	1	Total O S 5 4 1	0	0
9	A	1	Total O S 5 4 1	0	0
9	B	1	Total O S 5 4 1	0	0
9	B	1	Total O S 5 4 1	0	0

- Molecule 10 is water.

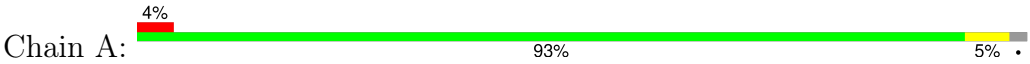
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
10	A	870	Total O 870 870	0	0
10	B	864	Total O 864 864	0	1

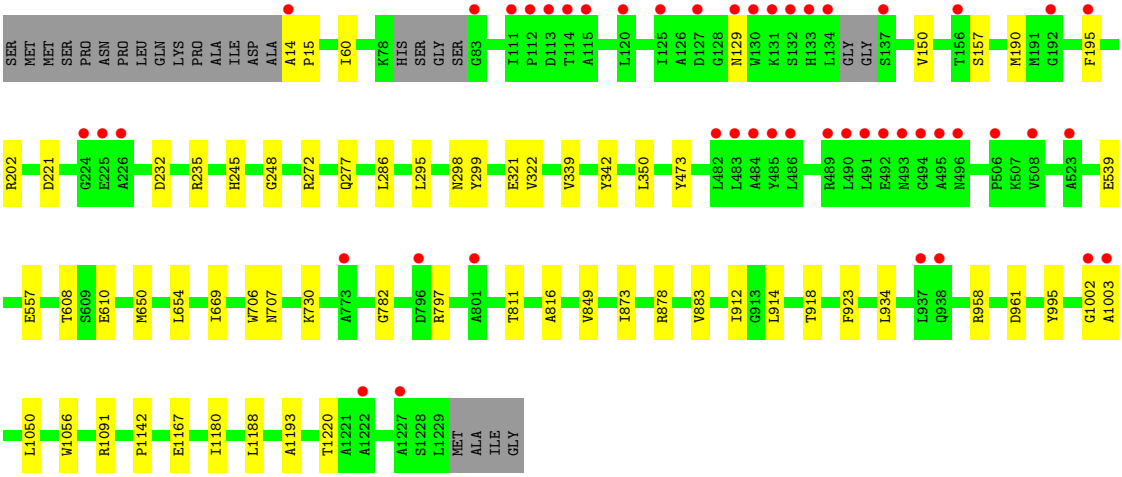
3 Residue-property plots (i)

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: Bifunctional protein PutA

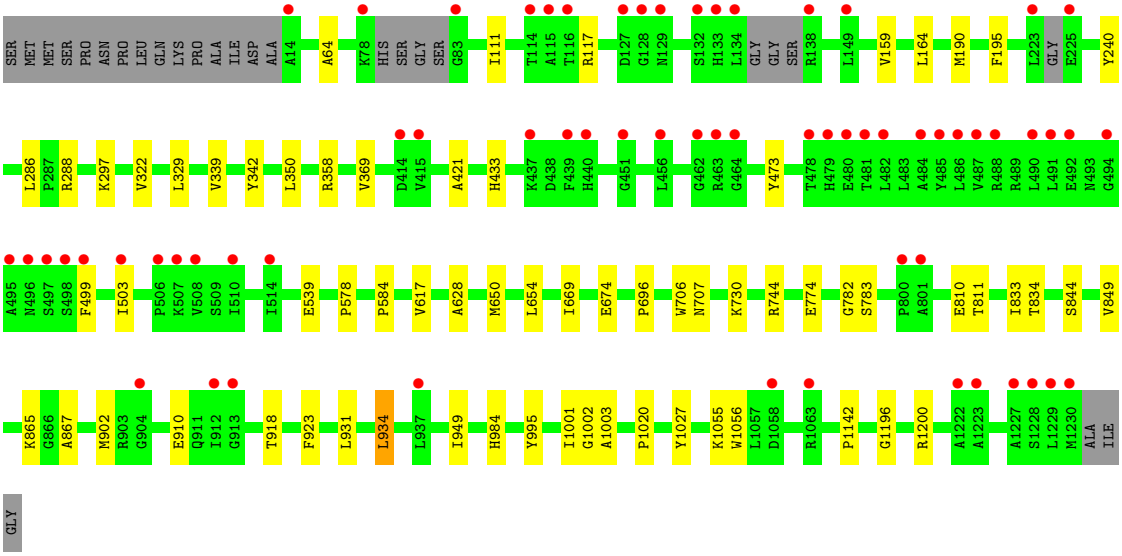
Chain A:





• Molecule 1: Bifunctional protein PutA

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	100.87Å 101.82Å 126.03Å 90.00° 106.53° 90.00°	Depositor
Resolution (Å)	48.35 – 1.47 48.35 – 1.47	Depositor EDS
% Data completeness (in resolution range)	91.9 (48.35-1.47) 97.6 (48.35-1.47)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.37 (at 1.47Å)	Xtriage
Refinement program	PHENIX (1.20.1_4487: ???)	Depositor
R, R_{free}	0.180 , 0.207 0.179 , 0.205	Depositor DCC
R_{free} test set	20554 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å^2)	16.5	Xtriage
Anisotropy	0.142	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.42 , 36.2	EDS
L-test for twinning[2]	$< \|L\| > = 0.46$, $< L^2 > = 0.29$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	37779	wwPDB-VP
Average B, all atoms (Å^2)	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.62% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PEG, FDA, PGE, NAD, SO4, A1AUG, FMT

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	0.42	0/9083	0.56	0/12376
1	B	0.43	0/9069	0.58	0/12358
All	All	0.43	0/18152	0.57	0/24734

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	744	ARG	Sidechain

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	8913	8877	8867	38	0
1	B	8895	8839	8829	44	0
2	A	44	26	26	0	0
2	B	88	52	52	3	0
3	A	53	32	33	3	0
3	B	53	32	32	1	0
4	A	10	14	14	0	0
4	B	10	14	14	0	0
5	A	7	10	10	0	0
6	A	9	8	0	1	0
6	B	9	8	0	2	0
7	A	3	1	1	0	0
7	B	3	1	1	0	0
8	A	2	0	0	0	0
8	B	2	0	0	0	0
9	A	20	0	0	0	0
9	B	10	0	0	0	0
10	A	870	0	0	9	0
10	B	864	0	0	11	0
All	All	19865	17914	17879	85	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 2.

The worst 5 of 85 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:A:539:GLU:OE1	10:A:2201:HOH:O	1.97	0.81
1:B:995:TYR:OH	1:B:1002[B]:GLY:O	2.01	0.79
1:A:995:TYR:OH	1:A:1002[A]:GLY:O	2.06	0.72
1:A:557:GLU:OE2	10:A:2203:HOH:O	2.09	0.70
1:A:232:ASP:OD2	10:A:2202:HOH:O	2.08	0.70

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	1211/1235 (98%)	1185 (98%)	25 (2%)	1 (0%)	48 24
1	B	1210/1235 (98%)	1178 (97%)	32 (3%)	0	100 100
All	All	2421/2470 (98%)	2363 (98%)	57 (2%)	1 (0%)	100 100

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	129	ASN

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	885/951 (93%)	878 (99%)	7 (1%)	79 61
1	B	882/951 (93%)	878 (100%)	4 (0%)	86 74
All	All	1767/1902 (93%)	1756 (99%)	11 (1%)	84 69

5 of 11 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	342	TYR
1	B	730	LYS
1	B	949	ILE
1	B	934	LEU
1	A	730	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	298	ASN
1	B	440	HIS

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Mol	Chain	Res	Type
1	B	504	ASN
1	B	667	ASN
1	B	685	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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 22 ligands modelled in this entry, 4 are monoatomic - leaving 18 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	$\#\|Z\| > 2$
9	SO4	A	2110	-	4,4,4	0.19	0	6,6,6	0.32	0
9	SO4	A	2111	-	4,4,4	0.24	0	6,6,6	0.07	0
9	SO4	A	2112	-	4,4,4	0.20	0	6,6,6	0.21	0
2	NAD	B	2205[B]	8	42,48,48	2.52	13 (30%)	50,73,73	1.55	4 (8%)
2	NAD	A	2101	8	42,48,48	1.99	12 (28%)	50,73,73	1.57	7 (14%)
7	FMT	A	2106	-	2,2,2	0.44	0	1,1,1	0.39	0
6	A1AUG	B	2203	-	6,8,8	0.85	0	6,9,9	1.79	2 (33%)
4	PGE	A	2103	-	9,9,9	0.32	0	8,8,8	0.46	0
6	A1AUG	A	2105	-	6,8,8	1.11	0	6,9,9	1.95	2 (33%)
7	FMT	B	2204	-	2,2,2	0.91	0	1,1,1	0.40	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
9	SO4	A	2109	-	4,4,4	0.34	0	6,6,6	0.47	0
3	FDA	B	2201	-	53,58,58	2.64	18 (33%)	64,89,89	1.77	14 (21%)
2	NAD	B	2205[A]	8	42,48,48	2.33	12 (28%)	50,73,73	1.50	5 (10%)
9	SO4	B	2207	-	4,4,4	0.38	0	6,6,6	0.13	0
4	PGE	B	2202	-	9,9,9	0.30	0	8,8,8	0.57	0
3	FDA	A	2102	-	53,58,58	2.55	18 (33%)	64,89,89	1.55	14 (21%)
5	PEG	A	2104	-	6,6,6	0.21	0	5,5,5	0.13	0
9	SO4	B	2208	-	4,4,4	0.23	0	6,6,6	0.09	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
2	NAD	B	2205[B]	8	-	4/26/62/62	0/5/5/5
2	NAD	A	2101	8	-	1/26/62/62	0/5/5/5
6	A1AUG	B	2203	-	-	1/8/8/8	-
4	PGE	A	2103	-	-	3/7/7/7	-
6	A1AUG	A	2105	-	-	2/8/8/8	-
3	FDA	B	2201	-	-	4/30/50/50	0/6/6/6
2	NAD	B	2205[A]	8	-	2/26/62/62	0/5/5/5
4	PGE	B	2202	-	-	3/7/7/7	-
3	FDA	A	2102	-	-	5/30/50/50	0/6/6/6
5	PEG	A	2104	-	-	1/4/4/4	-

The worst 5 of 73 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	2201	FDA	PA-O3P	-11.25	1.47	1.59
2	B	2205[B]	NAD	PA-O3	-10.39	1.48	1.59
3	A	2102	FDA	PA-O3P	-9.69	1.49	1.59
2	B	2205[A]	NAD	PA-O3	-9.39	1.49	1.59
3	A	2102	FDA	O4-C4	6.77	1.36	1.23

The worst 5 of 48 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	2101	NAD	N3A-C2A-N1A	-6.39	120.00	128.67
2	B	2205[B]	NAD	N3A-C2A-N1A	-6.38	120.01	128.67

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	2205[A]	NAD	N3A-C2A-N1A	-6.22	120.23	128.67
3	A	2102	FDA	N3A-C2A-N1A	-5.87	120.70	128.67
3	B	2201	FDA	N3A-C2A-N1A	-5.17	121.65	128.67

There are no chirality outliers.

5 of 26 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	2105	A1AUG	CA-CB-CG-CD
6	A	2105	A1AUG	OE1-CD-CG-CB
6	B	2203	A1AUG	CA-CB-CG-CD
3	A	2102	FDA	C2'-C3'-C4'-O4'
4	A	2103	PGE	O3-C5-C6-O4

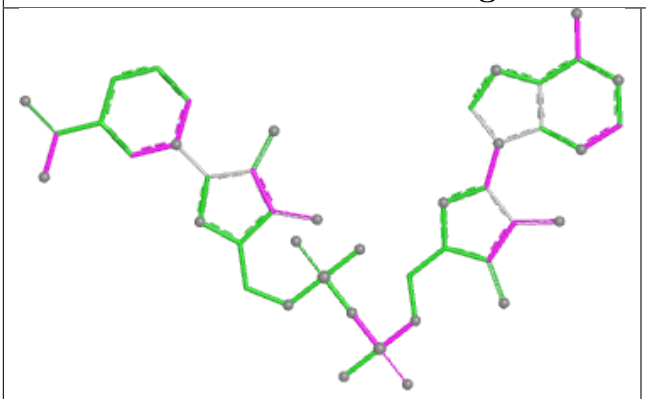
There are no ring outliers.

6 monomers are involved in 9 short contacts:

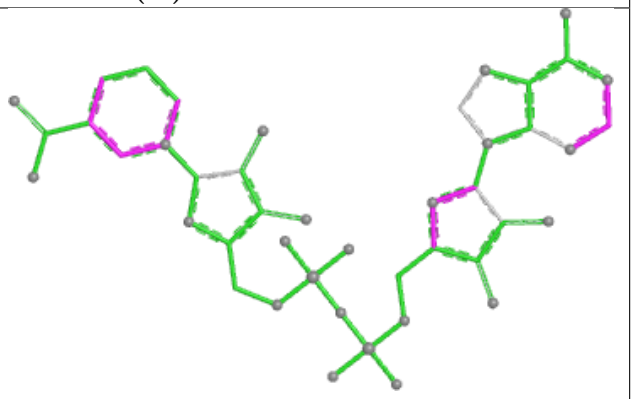
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	2205[B]	NAD	2	0
6	B	2203	A1AUG	2	0
6	A	2105	A1AUG	1	0
3	B	2201	FDA	1	0
2	B	2205[A]	NAD	1	0
3	A	2102	FDA	3	0

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 then 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.

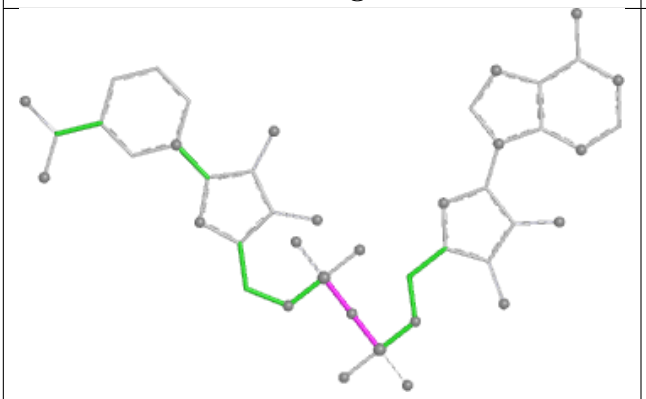
Ligand NAD B 2205 (B)



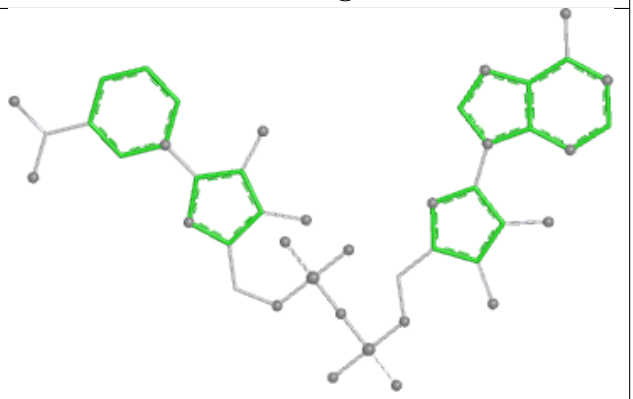
Bond lengths



Bond angles

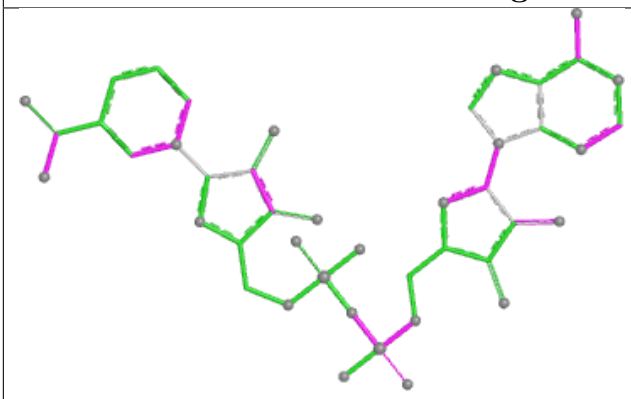


Torsions

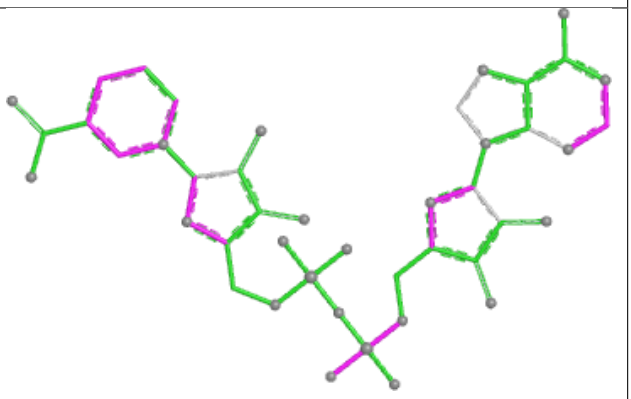


Rings

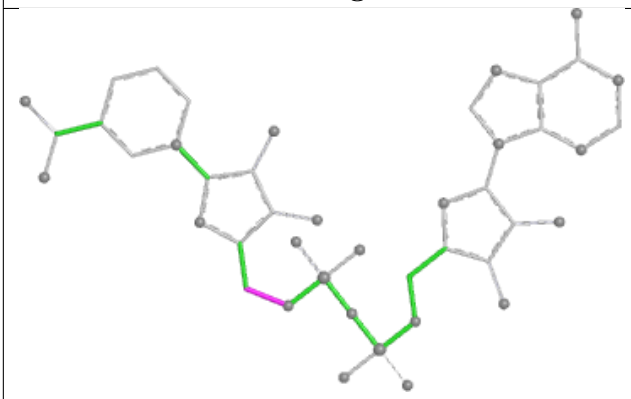
Ligand NAD A 2101



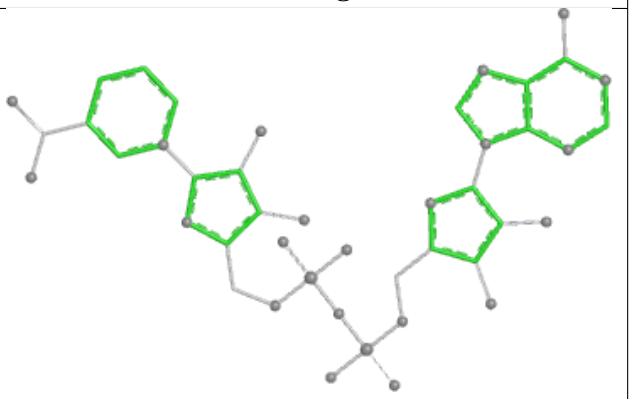
Bond lengths



Bond angles

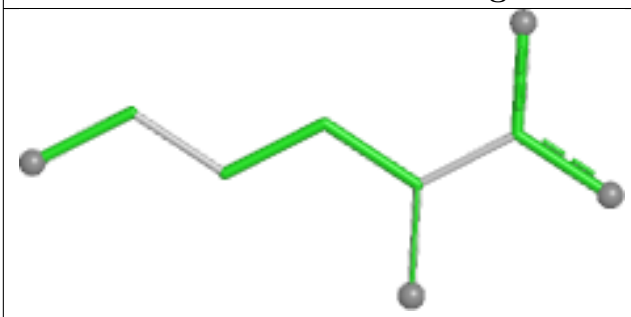


Torsions

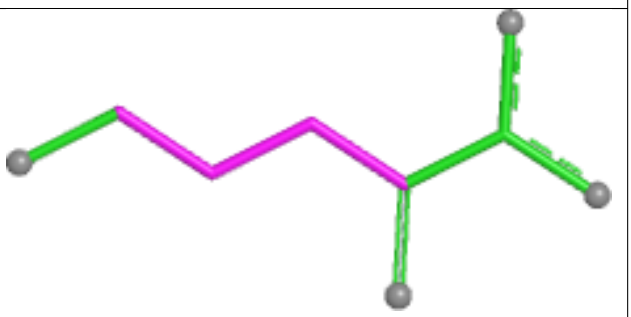


Rings

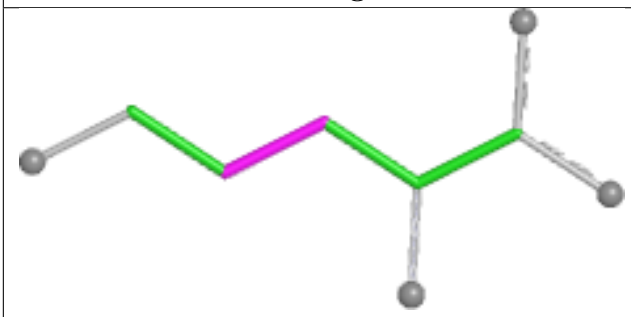
Ligand A1AUG B 2203



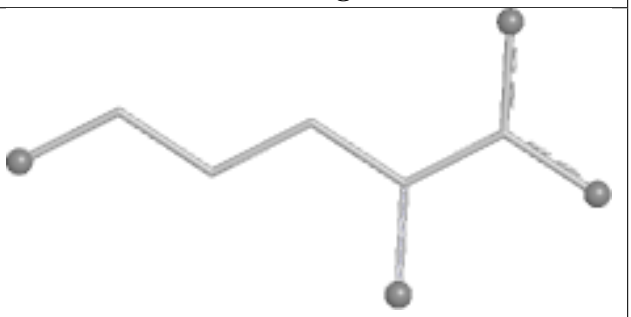
Bond lengths



Bond angles

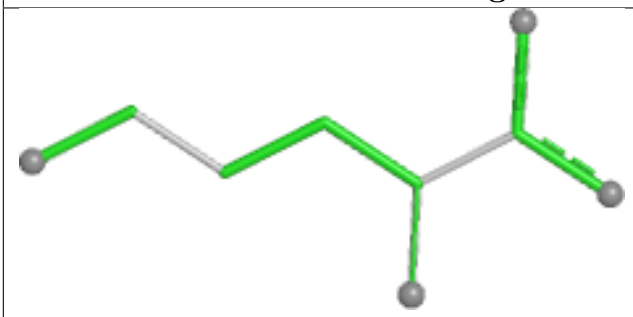


Torsions

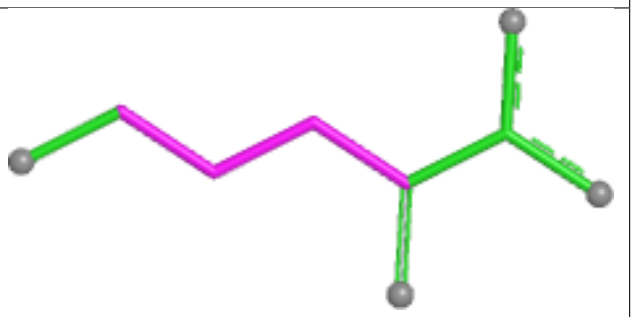


Rings

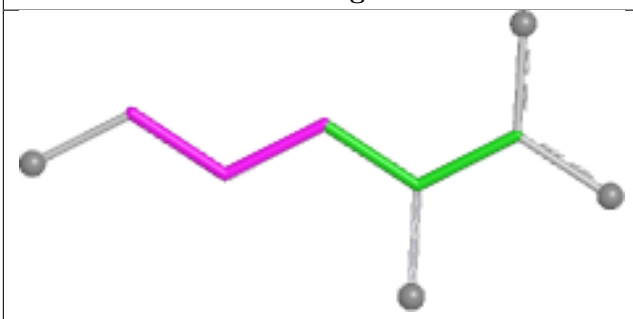
Ligand A1AUG A 2105



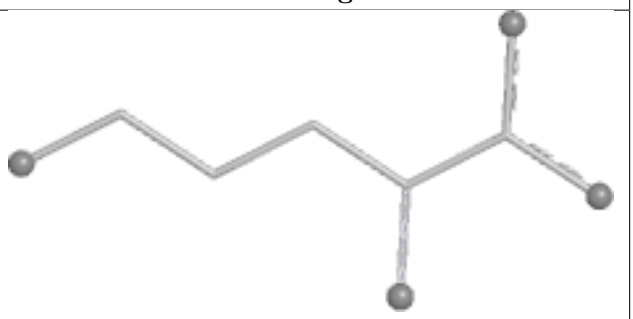
Bond lengths



Bond angles

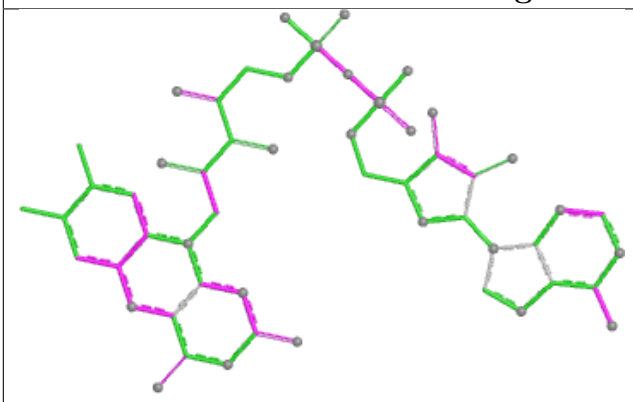


Torsions

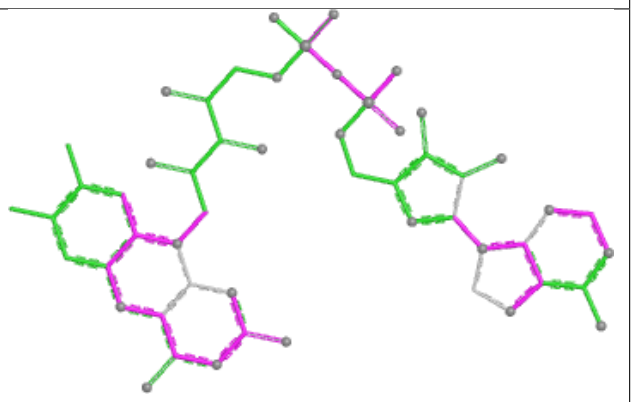


Rings

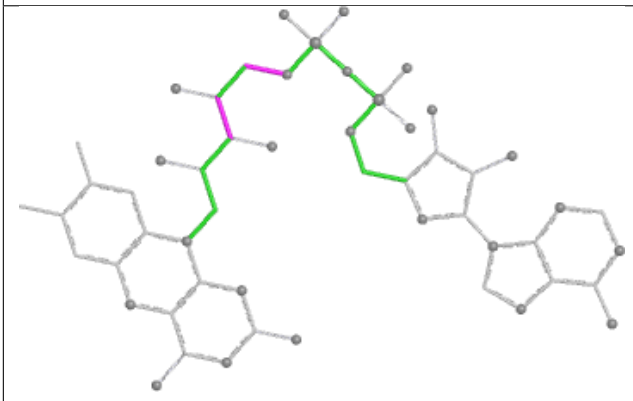
Ligand FDA B 2201



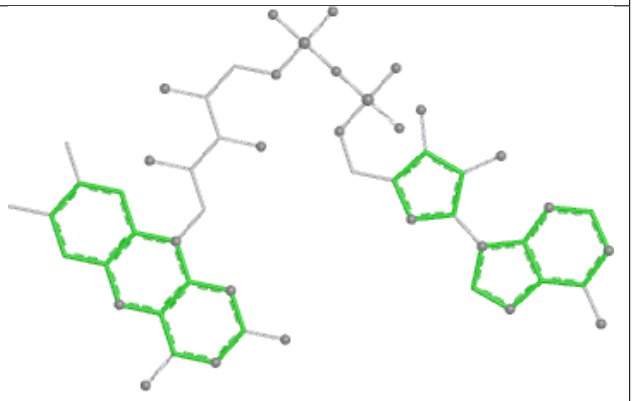
Bond lengths



Bond angles

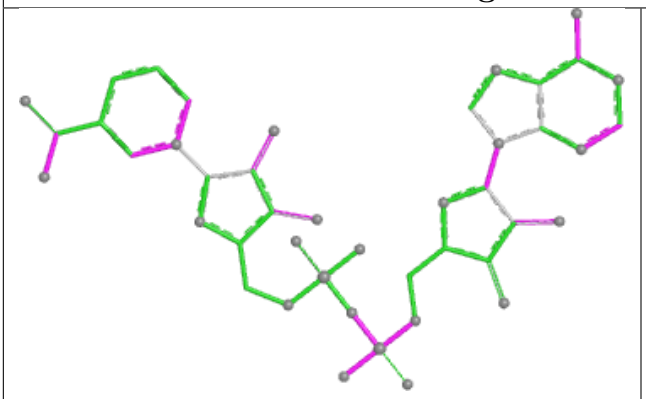


Torsions

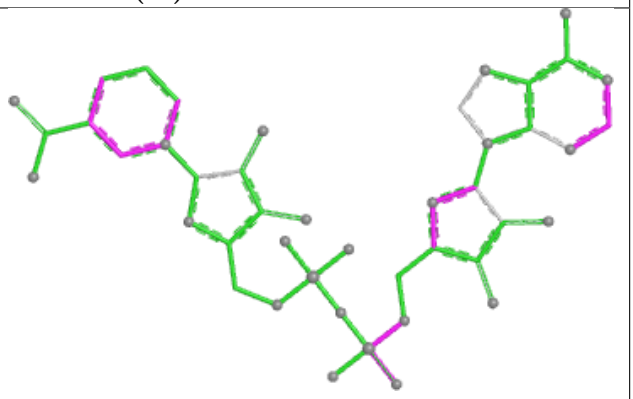


Rings

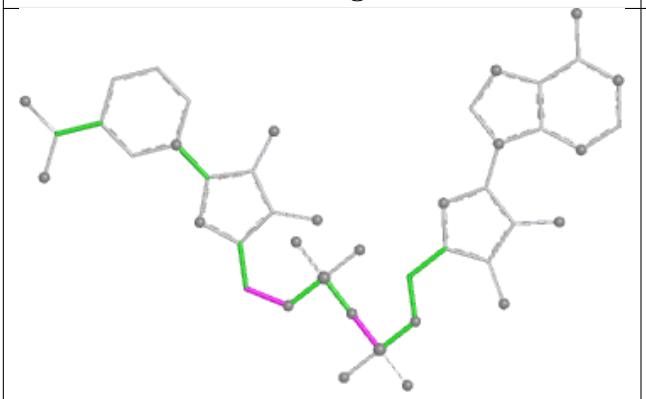
Ligand NAD B 2205 (A)



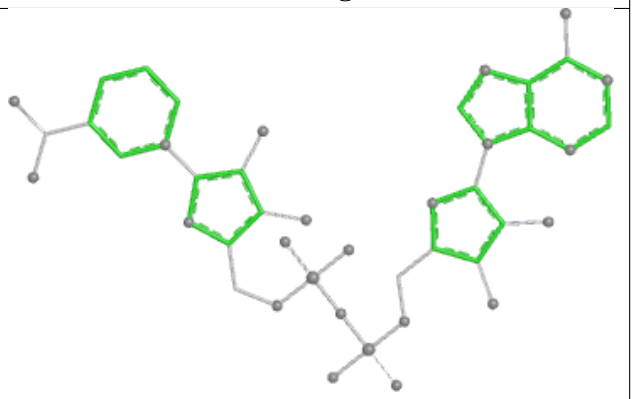
Bond lengths



Bond angles

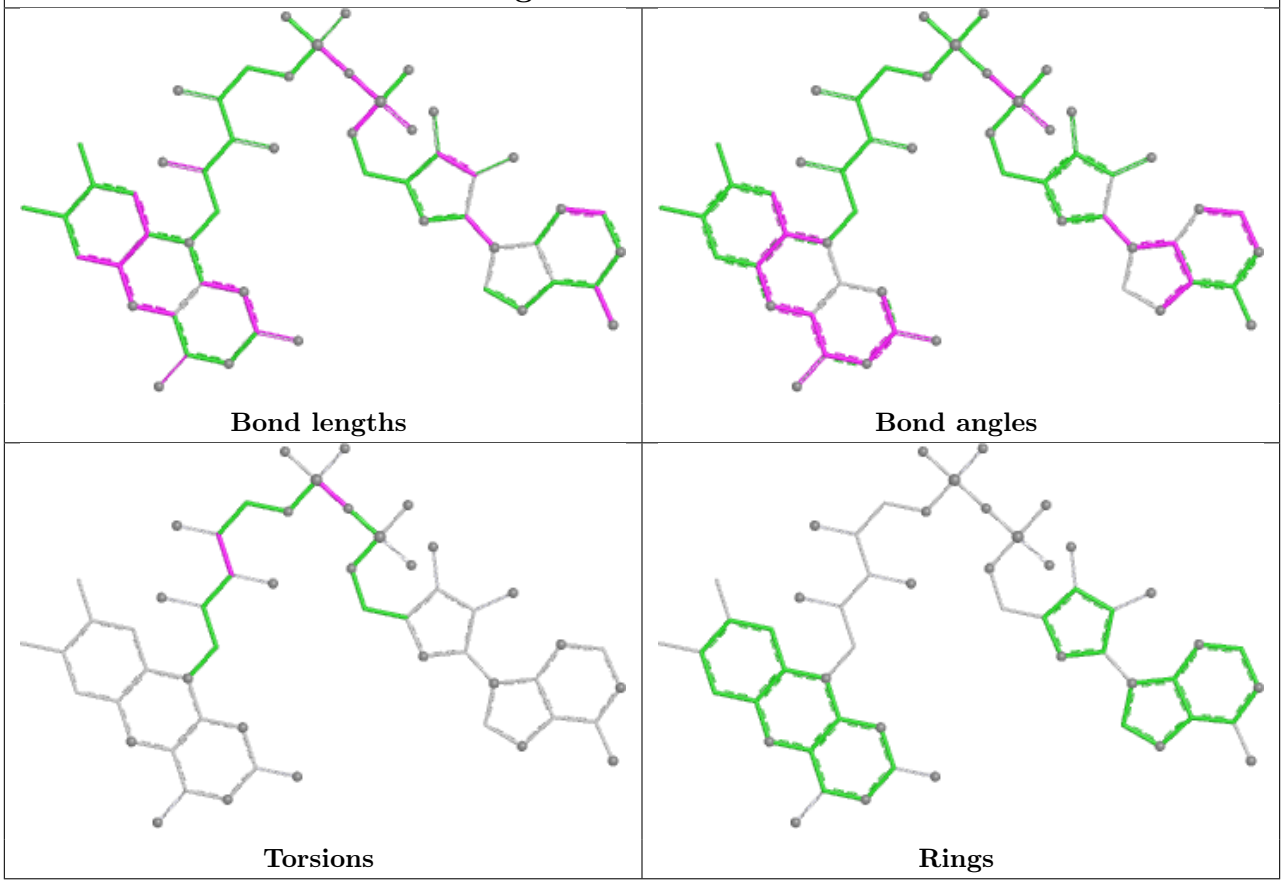


Torsions



Rings

Ligand FDA A 2102



5.7 Other polymers

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

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^{th} 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	1210/1235 (97%)	-0.05	48 (3%)	43	46	8, 22, 43, 69	6 (0%)
1	B	1209/1235 (97%)	0.03	65 (5%)	32	34	7, 21, 43, 65	8 (0%)
All	All	2419/2470 (97%)	-0.01	113 (4%)	37	39	7, 21, 43, 69	14 (0%)

The worst 5 of 113 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	485	TYR	6.3
1	A	493	ASN	5.6
1	A	485	TYR	5.6
1	B	1227	ALA	5.1
1	A	224	GLY	5.1

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

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

6.3 Carbohydrates

There are no monosaccharides in this entry.

6.4 Ligands

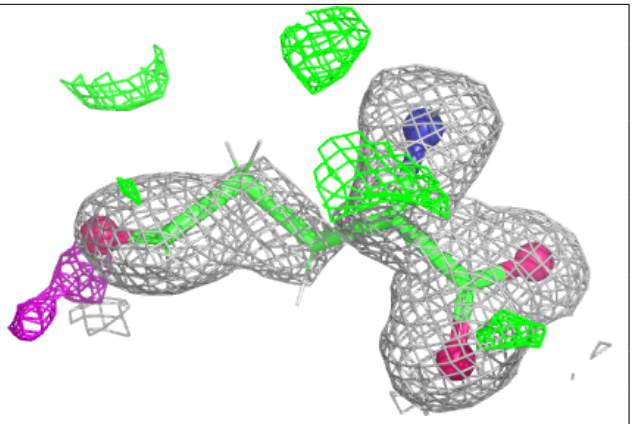
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

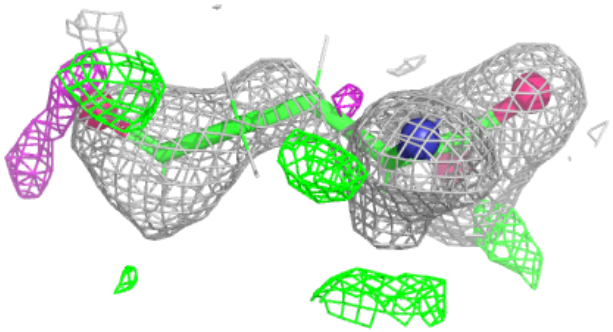
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
9	SO4	B	2208	5/5	0.81	0.13	43,48,53,53	5
9	SO4	A	2111	5/5	0.89	0.09	50,53,56,57	0
4	PGE	A	2103	10/10	0.90	0.10	23,32,46,55	0
6	A1AUG	B	2203	9/9	0.90	0.14	8,23,28,28	17
6	A1AUG	A	2105	9/9	0.91	0.14	6,25,34,34	17
9	SO4	A	2110	5/5	0.91	0.11	33,34,43,45	5
5	PEG	A	2104	7/7	0.92	0.08	26,32,40,42	0
4	PGE	B	2202	10/10	0.93	0.09	23,34,45,48	0
9	SO4	A	2112	5/5	0.94	0.10	24,26,35,44	5
7	FMT	A	2106	3/3	0.95	0.10	15,18,29,30	0
2	NAD	B	2205[B]	44/44	0.96	0.07	12,16,21,22	70
7	FMT	B	2204	3/3	0.96	0.10	11,13,28,32	0
2	NAD	B	2205[A]	44/44	0.96	0.07	7,15,19,22	70
3	FDA	B	2201	53/53	0.97	0.06	13,19,27,32	0
2	NAD	A	2101	44/44	0.97	0.06	14,18,23,28	0
3	FDA	A	2102	53/53	0.97	0.06	12,19,27,30	0
9	SO4	A	2109	5/5	0.99	0.03	15,16,17,18	0
8	MG	A	2107	1/1	0.99	0.05	22,22,22,22	0
8	MG	A	2108	1/1	0.99	0.12	23,23,23,23	0
8	MG	B	2206[A]	1/1	0.99	0.02	13,13,13,13	1
9	SO4	B	2207	5/5	0.99	0.04	13,15,18,19	0
8	MG	B	2206[B]	1/1	0.99	0.02	20,20,20,20	1

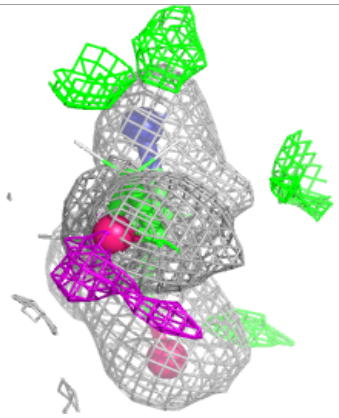
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1AUG B 2203:

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

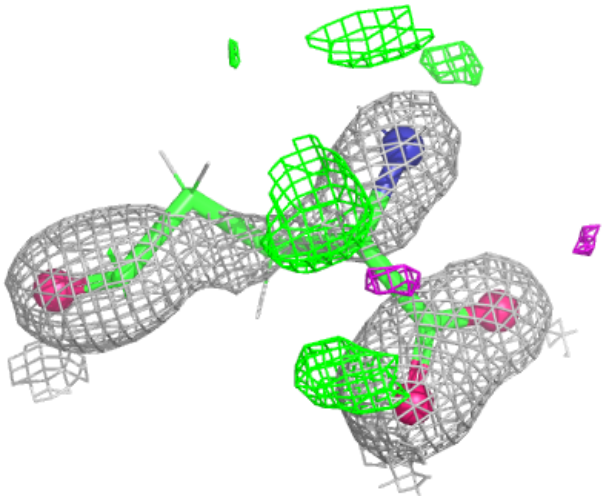


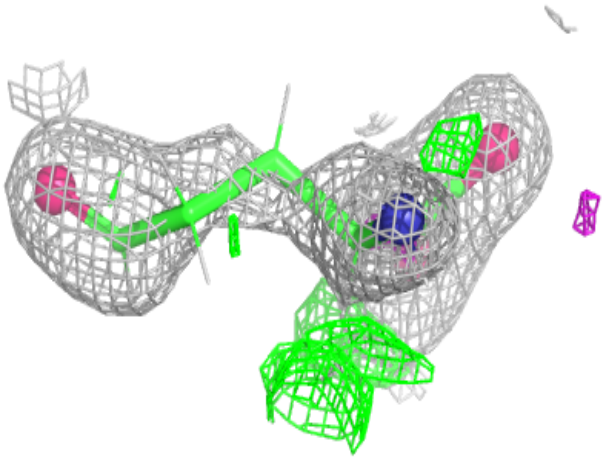


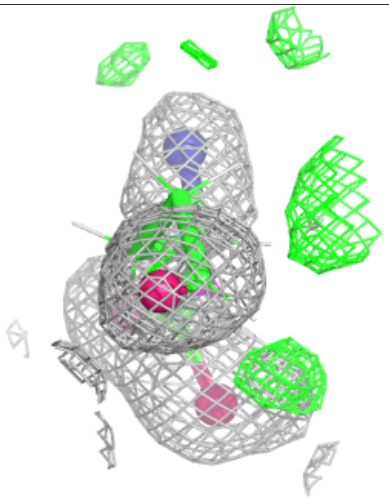


Electron density around A1AUG A 2105:

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

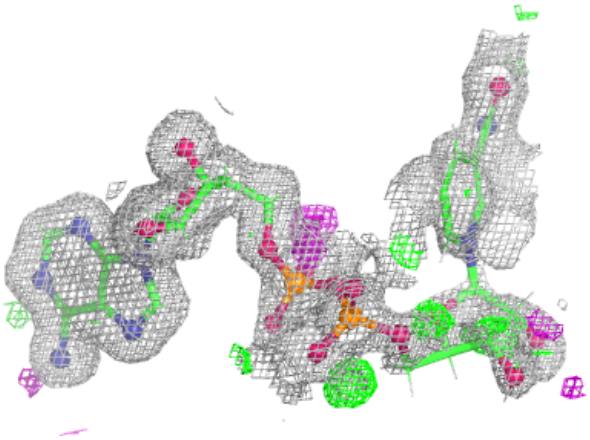


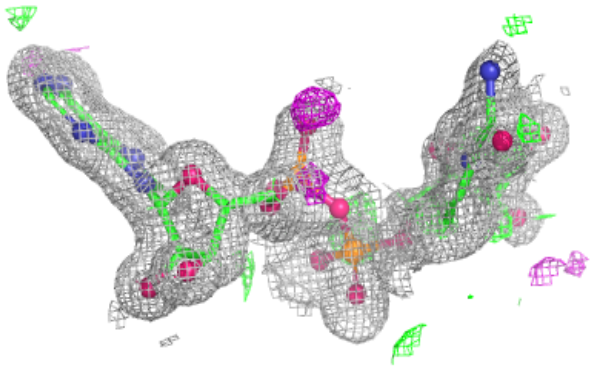


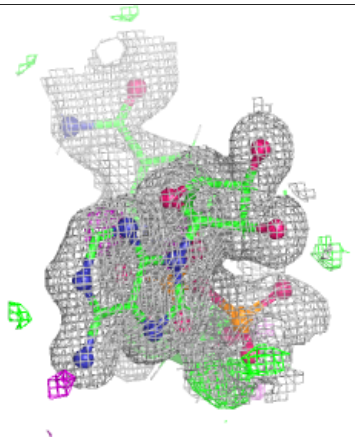


Electron density around NAD B 2205 (B):

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

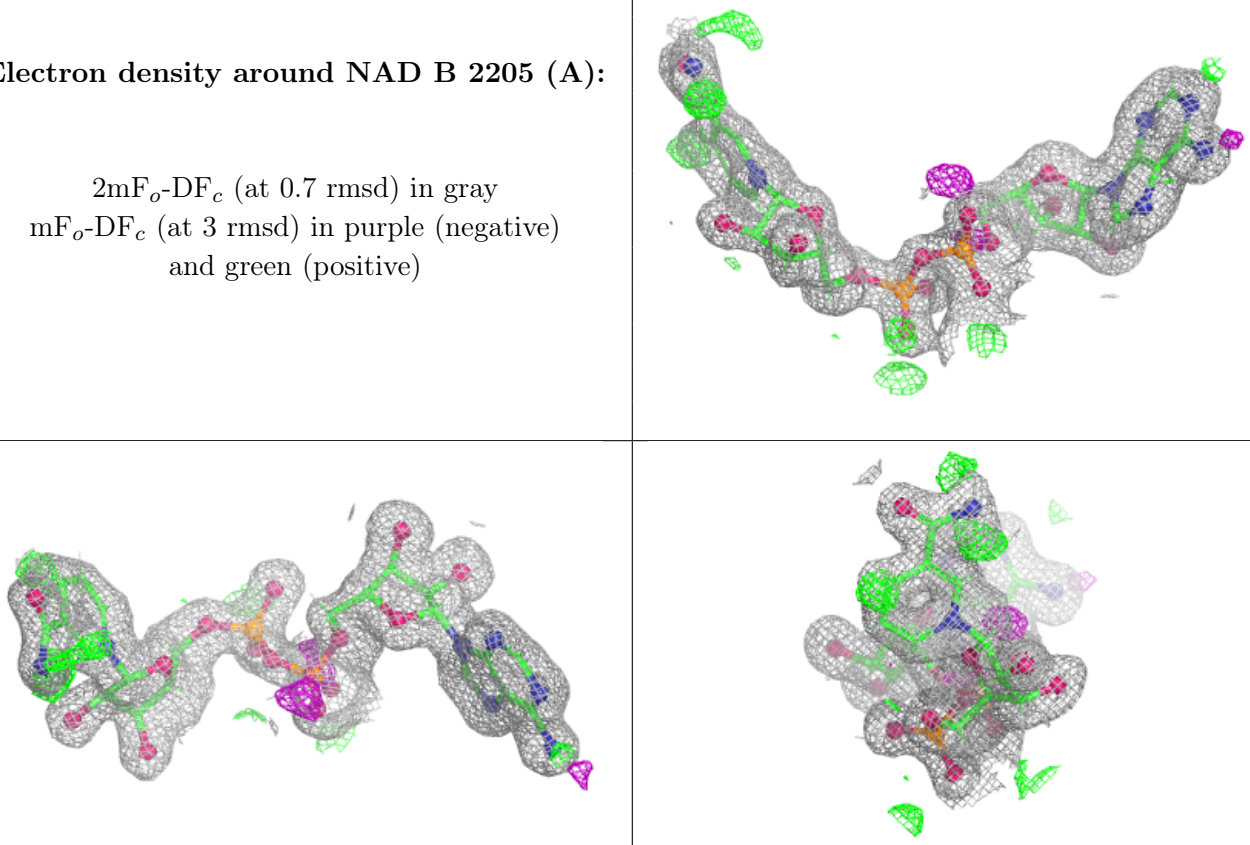






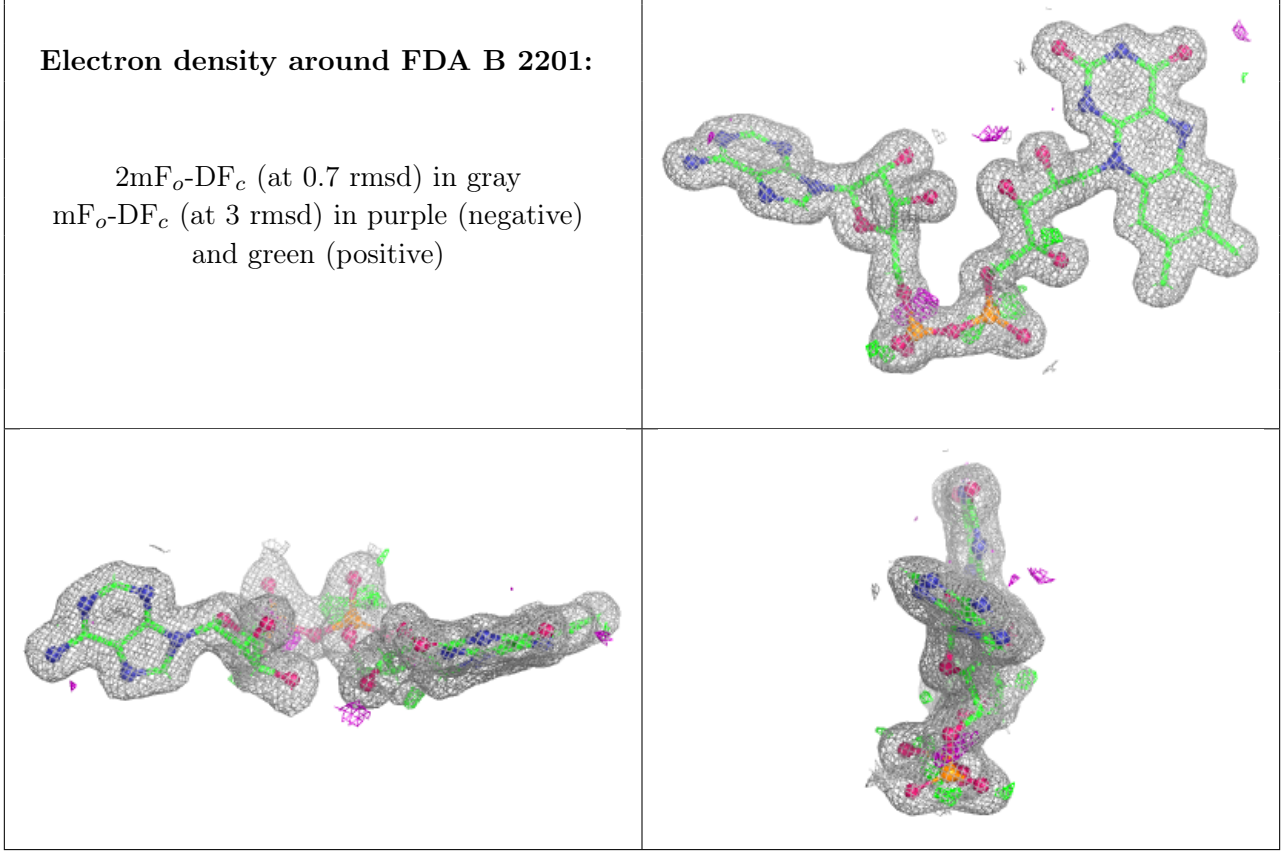
Electron density around NAD B 2205 (A):

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



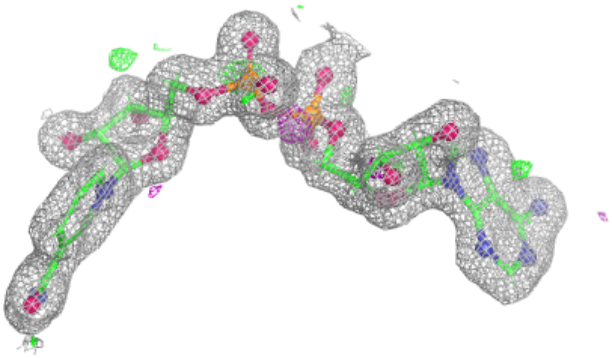
Electron density around FDA B 2201:

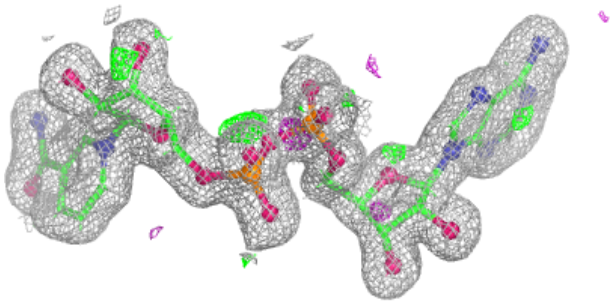
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

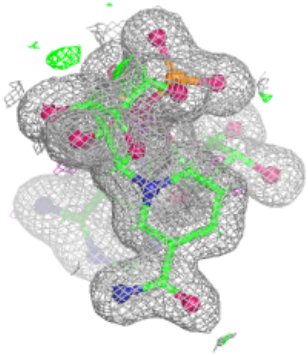


Electron density around NAD A 2101:

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

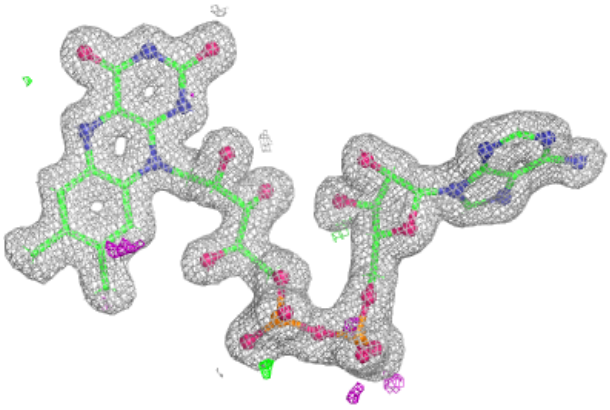


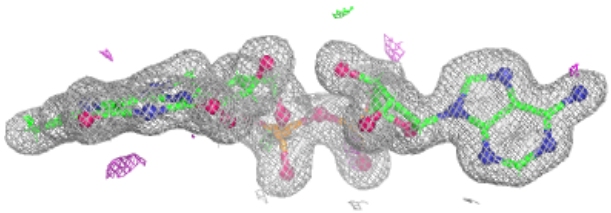


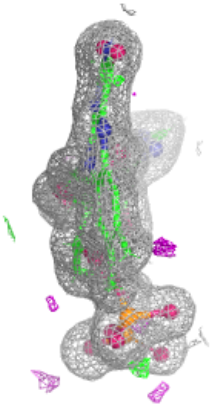


Electron density around FDA A 2102:

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

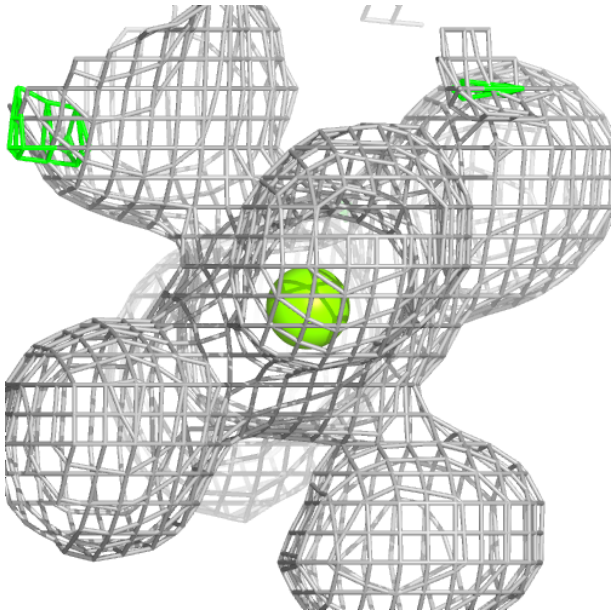


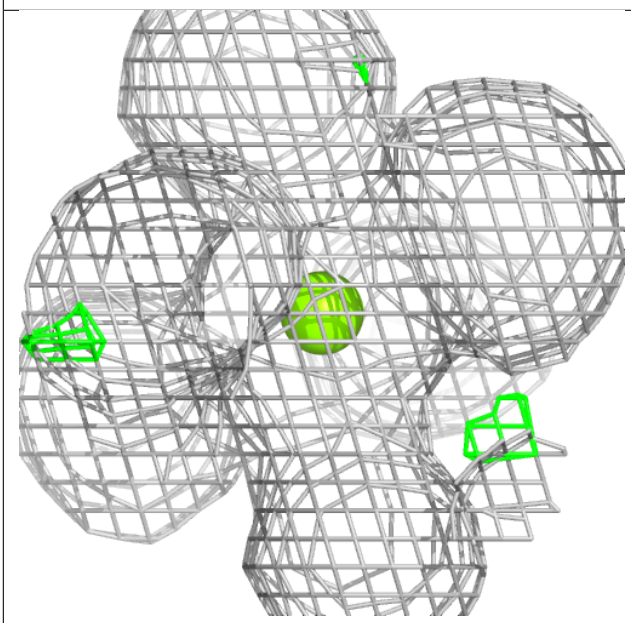


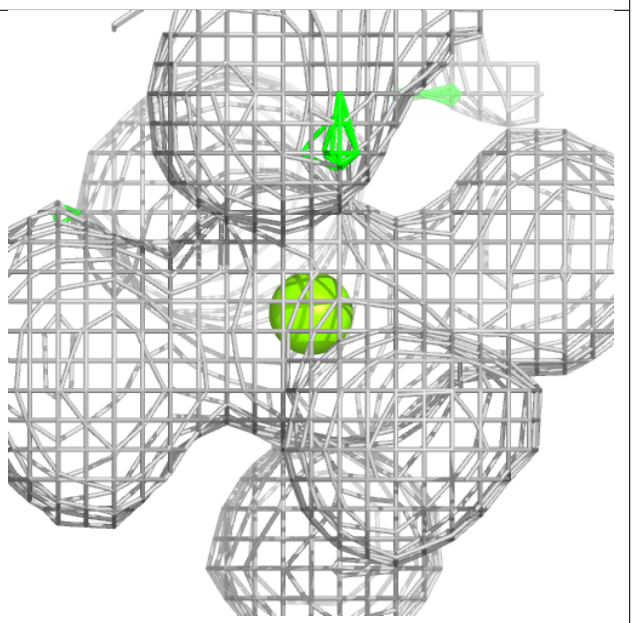


Electron density around MG A 2107:

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

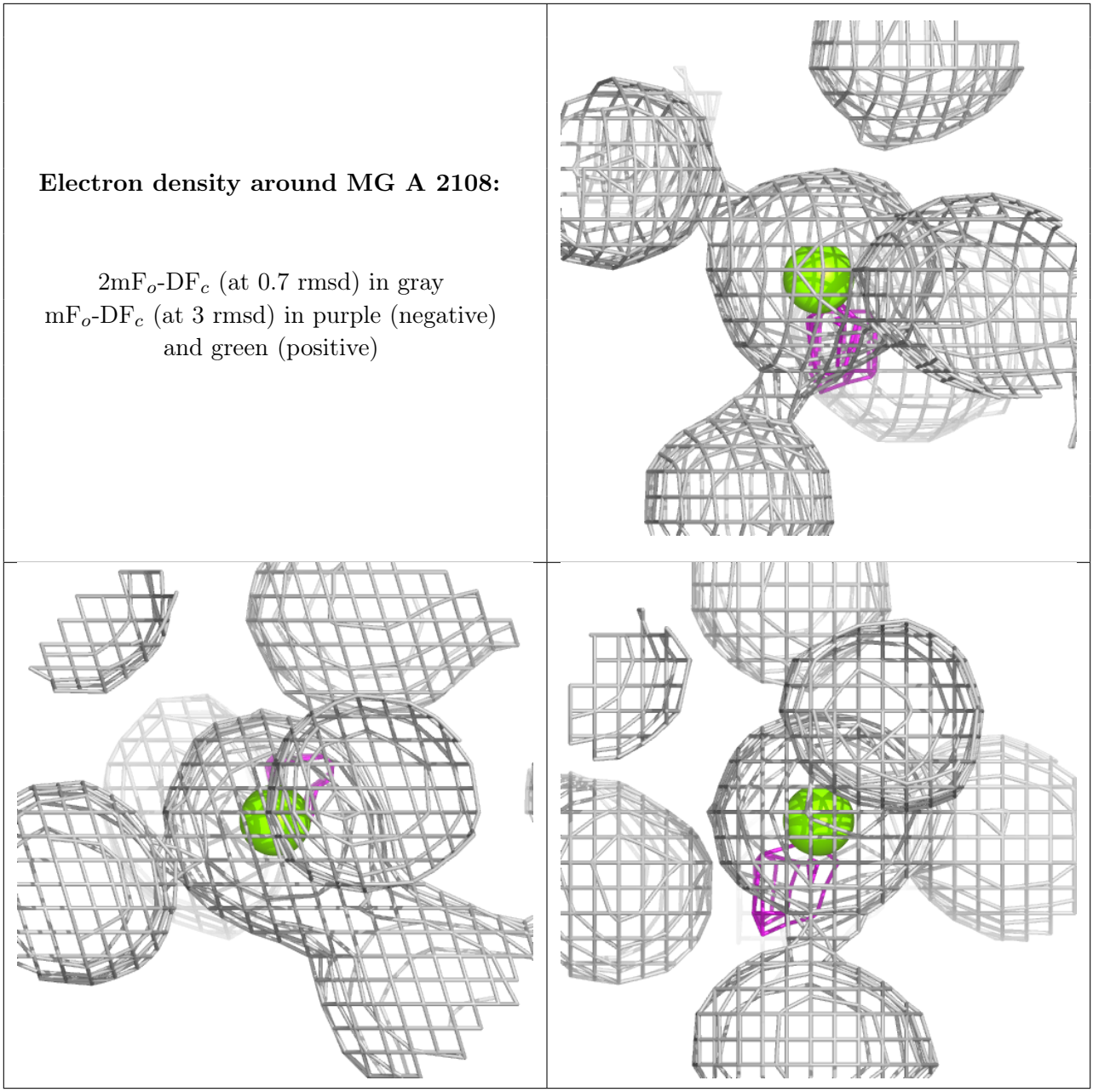






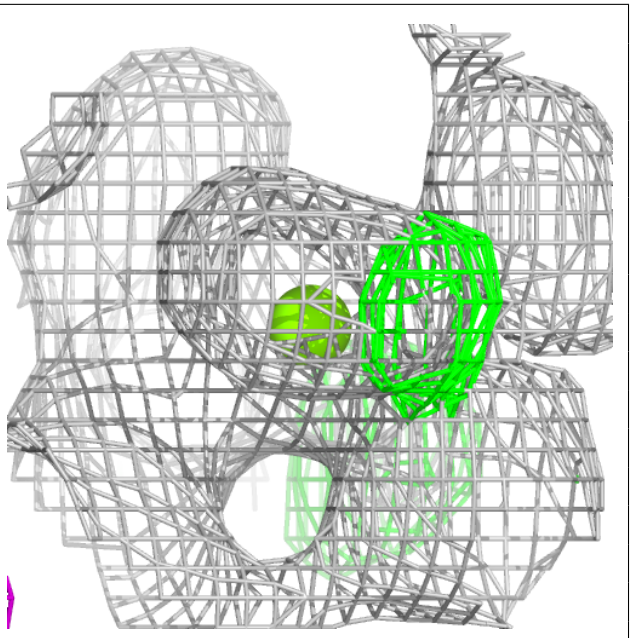
Electron density around MG A 2108:

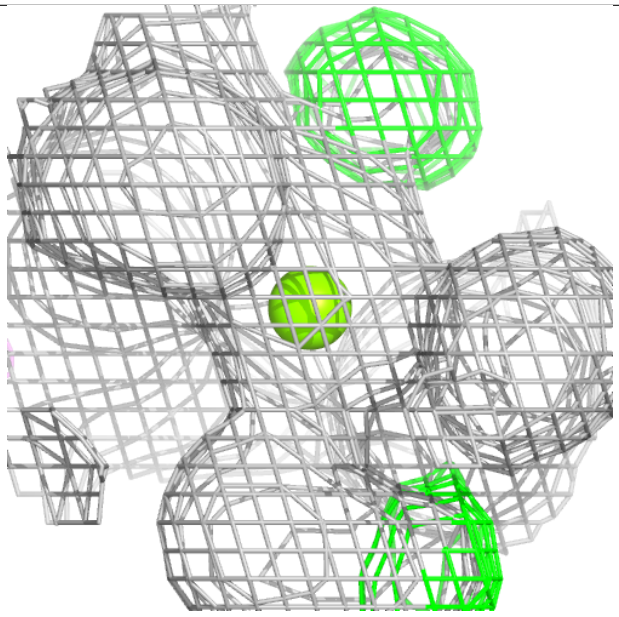
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

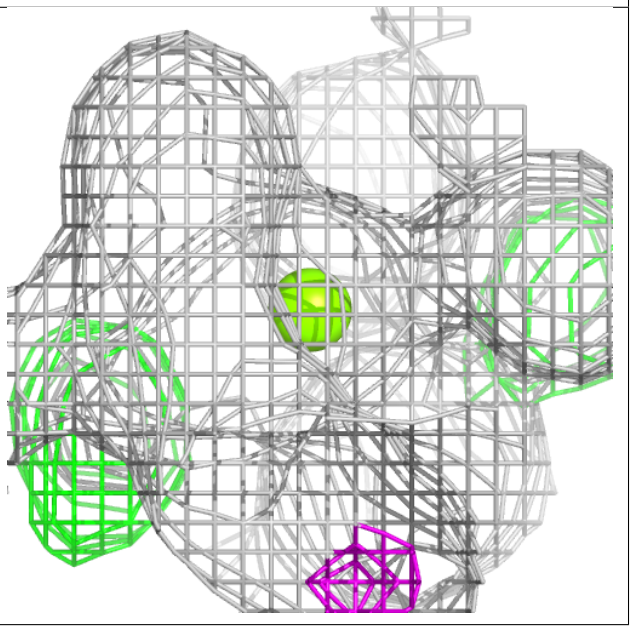


Electron density around MG B 2206 (A):

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

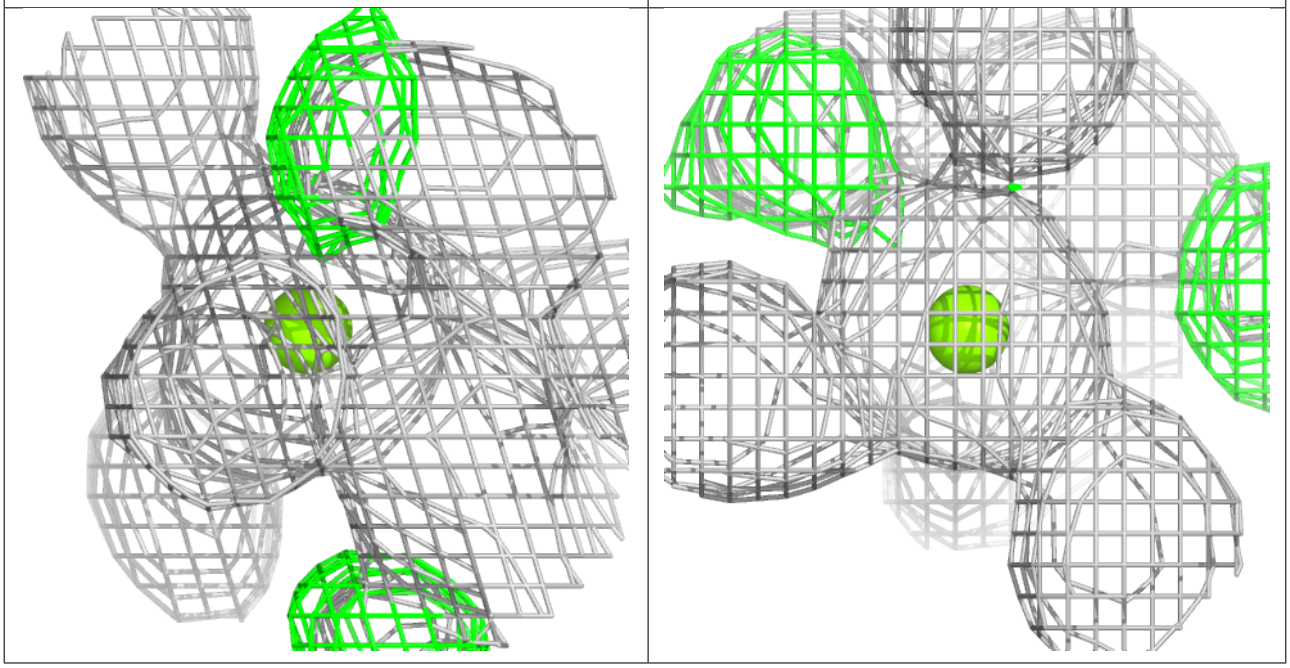






Electron density around MG B 2206 (B):

$2mF_o$-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.