



# wwPDB X-ray Structure Validation Summary Report ⓘ

Oct 11, 2021 – 02:27 PM EDT

PDB ID : 2ID2  
Title : GAPN T244S mutant X-ray structure at 2.5 Å  
Authors : Pailot, A.; D'Ambrosio, K.; Corbier, C.; Talfournier, F.; Branlant, G.  
Deposited on : 2006-09-14  
Resolution : 2.50 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](mailto:validation@mail.wwpdb.org)

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467  
Mogul : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.23.2  
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) : 2.23.2

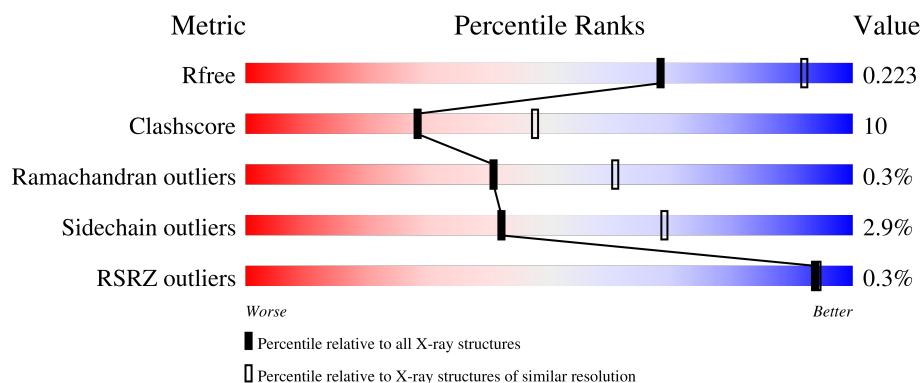
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	4661 (2.50-2.50)
Clashscore	141614	5346 (2.50-2.50)
Ramachandran outliers	138981	5231 (2.50-2.50)
Sidechain outliers	138945	5233 (2.50-2.50)
RSRZ outliers	127900	4559 (2.50-2.50)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions  $\leq 5\%$ . The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	475	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 19%, green 80%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>80%</span> <span>19%</span> </div> </div>
1	B	475	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 19%, green 79%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>79%</span> <span>19%</span> </div> </div>
1	C	475	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 19%, green 80%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>80%</span> <span>19%</span> </div> </div>
1	D	475	<div> <div style="width: 100%; height: 10px; background: linear-gradient(to right, red 1%, orange 1%, yellow 17%, green 81%);"></div> <div style="display: flex; justify-content: space-between; width: 100%;"> <span>81%</span> <span>17%</span> </div> </div>

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
2	SO4	D	2007	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 15702 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 NADP-dependent glyceraldehyde-3-phosphate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	473	Total	C	N	O	S	0	0	0
			3588	2281	599	697	11			
1	B	473	Total	C	N	O	S	0	0	0
			3588	2281	599	697	11			
1	C	474	Total	C	N	O	S	0	0	0
			3595	2285	600	699	11			
1	D	474	Total	C	N	O	S	0	0	0
			3595	2285	600	699	11			

There are 16 discrepancies between the modelled and reference sequences:

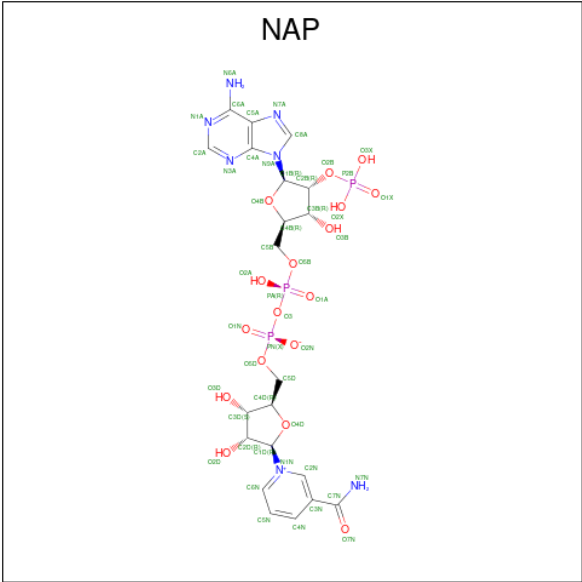
Chain	Residue	Modelled	Actual	Comment	Reference
A	58	ALA	SER	SEE REMARK 999	UNP Q59931
A	85	ILE	VAL	SEE REMARK 999	UNP Q59931
A	229	SER	THR	engineered mutation	UNP Q59931
A	347	THR	ALA	SEE REMARK 999	UNP Q59931
B	58	ALA	SER	SEE REMARK 999	UNP Q59931
B	85	ILE	VAL	SEE REMARK 999	UNP Q59931
B	229	SER	THR	engineered mutation	UNP Q59931
B	347	THR	ALA	SEE REMARK 999	UNP Q59931
C	58	ALA	SER	SEE REMARK 999	UNP Q59931
C	85	ILE	VAL	SEE REMARK 999	UNP Q59931
C	229	SER	THR	engineered mutation	UNP Q59931
C	347	THR	ALA	SEE REMARK 999	UNP Q59931
D	58	ALA	SER	SEE REMARK 999	UNP Q59931
D	85	ILE	VAL	SEE REMARK 999	UNP Q59931
D	229	SER	THR	engineered mutation	UNP Q59931
D	347	THR	ALA	SEE REMARK 999	UNP Q59931

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O<sub>4</sub>S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NAP) (formula: C<sub>21</sub>H<sub>28</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	B	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	C	1	Total	C	N	O	P	0	0
			48	21	7	17	3		
3	D	1	Total	C	N	O	P	0	0
			48	21	7	17	3		

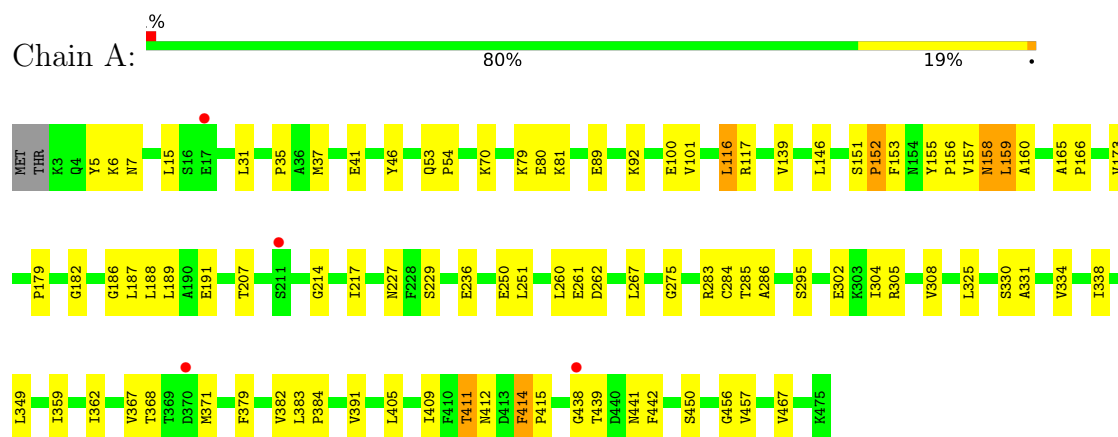
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	250	Total	O	0	0
			250	250		
4	B	243	Total	O	0	0
			243	243		
4	C	309	Total	O	0	0
			309	309		
4	D	307	Total	O	0	0
			307	307		

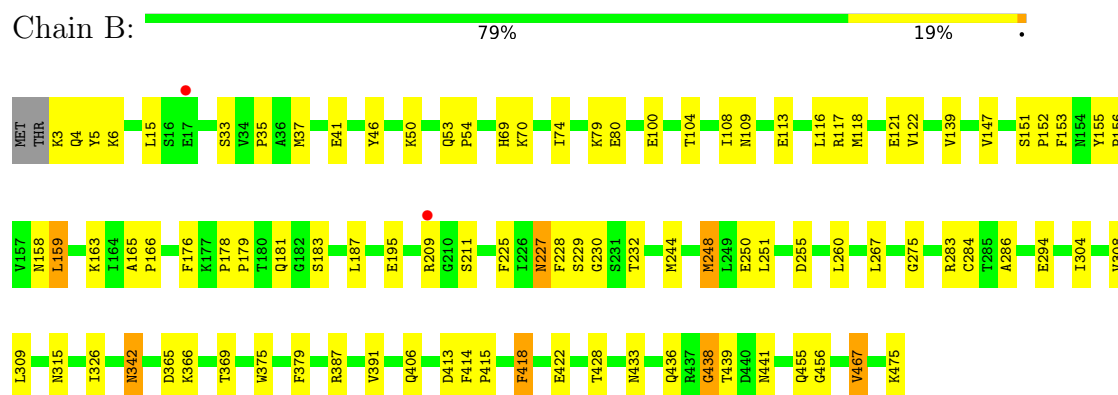
### 3 Residue-property plots [i](#)

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.

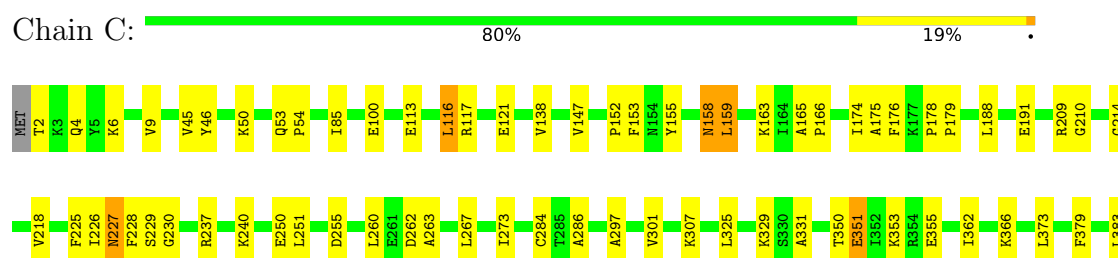
- Molecule 1: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase



- Molecule 1: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase

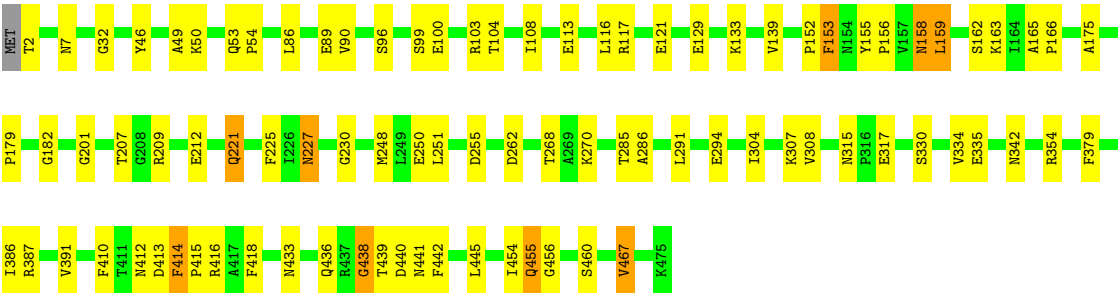
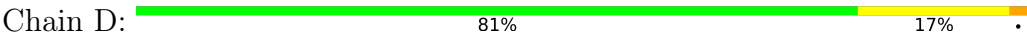


- Molecule 1: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase





● Molecule 1: NADP-dependent glyceraldehyde-3-phosphate dehydrogenase





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 <sub>1</sub> 2 <sub>1</sub> 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	143.70Å 154.40Å 115.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.50 19.98 – 2.50	Depositor EDS
% Data completeness (in resolution range)	88.2 (20.00-2.50) 88.2 (19.98-2.50)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.10	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.70 (at 2.50Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.176 , 0.227 0.169 , 0.223	Depositor DCC
$R_{free}$ test set	7903 reflections (10.09%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	24.8	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 52.4	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.95	EDS
Total number of atoms	15702	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	24.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 36.46 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 4.9779e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: NAP, SO4

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	0.31	0/3646	0.59	1/4930 (0.0%)
1	B	0.31	0/3646	0.58	1/4930 (0.0%)
1	C	0.33	0/3653	0.60	1/4940 (0.0%)
1	D	0.33	0/3653	0.60	2/4940 (0.0%)
All	All	0.32	0/14598	0.60	5/19740 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	456	GLY	N-CA-C	-6.49	96.87	113.10
1	A	456	GLY	N-CA-C	-6.35	97.23	113.10
1	C	456	GLY	N-CA-C	-6.06	97.95	113.10
1	B	456	GLY	N-CA-C	-5.83	98.52	113.10
1	D	175	ALA	N-CA-C	-5.10	97.24	111.00

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	3588	0	3640	77	0
1	B	3588	0	3640	75	0

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*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3595	0	3647	76	0
1	D	3595	0	3647	71	0
2	A	5	0	0	0	0
2	B	10	0	0	0	0
2	C	5	0	0	0	0
2	D	15	0	0	2	0
3	A	48	0	25	3	0
3	B	48	0	25	3	0
3	C	48	0	25	4	0
3	D	48	0	25	4	0
4	A	250	0	0	4	0
4	B	243	0	0	4	0
4	C	309	0	0	5	0
4	D	307	0	0	7	0
All	All	15702	0	14674	288	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 10.

The worst 5 of 288 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:368:THR:H	1:A:371:MET:HE3	1.14	1.08
1:D:152:PRO:HG3	3:D:3004:NAP:H5N	1.57	0.86
1:B:152:PRO:HG3	3:B:3002:NAP:H5N	1.59	0.84
1:D:212:GLU:HA	4:D:3190:HOH:O	1.77	0.84
1:C:152:PRO:HG3	3:C:3003:NAP:H5N	1.58	0.84

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	471/475 (99%)	448 (95%)	21 (4%)	2 (0%)	34	54
1	B	471/475 (99%)	447 (95%)	23 (5%)	1 (0%)	47	68
1	C	472/475 (99%)	446 (94%)	24 (5%)	2 (0%)	34	54
1	D	472/475 (99%)	452 (96%)	19 (4%)	1 (0%)	47	68
All	All	1886/1900 (99%)	1793 (95%)	87 (5%)	6 (0%)	41	61

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	438	GLY
1	B	438	GLY
1	C	438	GLY
1	D	438	GLY
1	A	457	VAL

### 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	377/379 (100%)	367 (97%)	10 (3%)	44	71
1	B	377/379 (100%)	366 (97%)	11 (3%)	42	69
1	C	378/379 (100%)	367 (97%)	11 (3%)	42	69
1	D	378/379 (100%)	366 (97%)	12 (3%)	39	65
All	All	1510/1516 (100%)	1466 (97%)	44 (3%)	42	69

5 of 44 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	379	PHE
1	D	159	LEU
1	C	414	PHE
1	D	121	GLU
1	D	227	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 30 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	436	GLN
1	D	423	GLN
1	C	158	ASN
1	D	455	GLN
1	D	227	ASN

### 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](#)

11 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with  $|Z| > 2$  is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z  > 2$	Counts	RMSZ	$\# Z  > 2$
2	SO4	D	2006	-	4,4,4	1.93	2 (50%)	6,6,6	0.95	0
2	SO4	A	2001	-	4,4,4	1.94	2 (50%)	6,6,6	0.98	0
2	SO4	B	2003	-	4,4,4	1.93	2 (50%)	6,6,6	0.99	0
3	NAP	B	3002	-	45,52,52	2.07	11 (24%)	56,80,80	1.50	10 (17%)
2	SO4	D	2007	-	4,4,4	1.91	2 (50%)	6,6,6	0.97	0
2	SO4	C	2004	-	4,4,4	1.94	2 (50%)	6,6,6	0.94	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	SO4	B	2002	-	4,4,4	1.92	2 (50%)	6,6,6	0.98	0
3	NAP	C	3003	-	45,52,52	2.07	12 (26%)	56,80,80	1.52	10 (17%)
2	SO4	D	2005	-	4,4,4	1.92	2 (50%)	6,6,6	0.98	0
3	NAP	A	3001	-	45,52,52	2.08	13 (28%)	56,80,80	1.47	10 (17%)
3	NAP	D	3004	-	45,52,52	2.11	12 (26%)	56,80,80	1.52	9 (16%)

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
3	NAP	B	3002	-	-	5/31/67/67	0/5/5/5
3	NAP	C	3003	-	-	6/31/67/67	0/5/5/5
3	NAP	A	3001	-	-	7/31/67/67	0/5/5/5
3	NAP	D	3004	-	-	3/31/67/67	0/5/5/5

The worst 5 of 62 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	3004	NAP	C2N-N1N	6.49	1.42	1.35
3	C	3003	NAP	C2N-N1N	6.30	1.42	1.35
3	A	3001	NAP	C2N-N1N	6.01	1.42	1.35
3	B	3002	NAP	C2N-N1N	5.90	1.42	1.35
3	C	3003	NAP	C4N-C3N	4.63	1.47	1.39

The worst 5 of 39 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3004	NAP	C5A-C6A-N6A	4.60	127.34	120.35
3	C	3003	NAP	C5A-C6A-N6A	4.54	127.25	120.35
3	A	3001	NAP	C5A-C6A-N6A	4.44	127.10	120.35
3	B	3002	NAP	C5A-C6A-N6A	4.43	127.08	120.35
3	B	3002	NAP	N3A-C2A-N1A	-3.63	123.01	128.68

There are no chirality outliers.

5 of 21 torsion outliers are listed below:

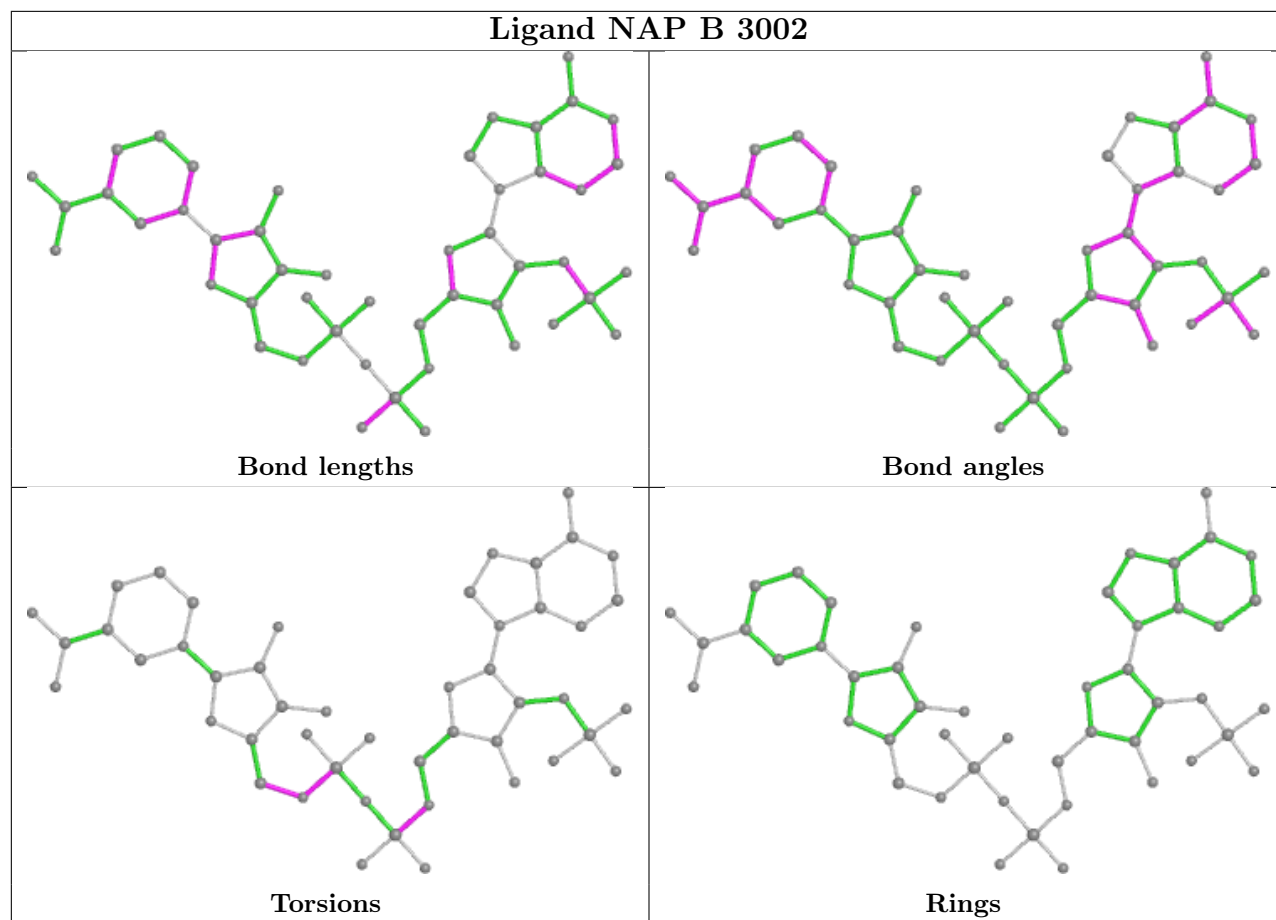
Mol	Chain	Res	Type	Atoms
3	A	3001	NAP	C5B-O5B-PA-O3
3	A	3001	NAP	C5D-O5D-PN-O1N
3	B	3002	NAP	C5B-O5B-PA-O3
3	C	3003	NAP	C5B-O5B-PA-O3
3	C	3003	NAP	C5D-O5D-PN-O1N

There are no ring outliers.

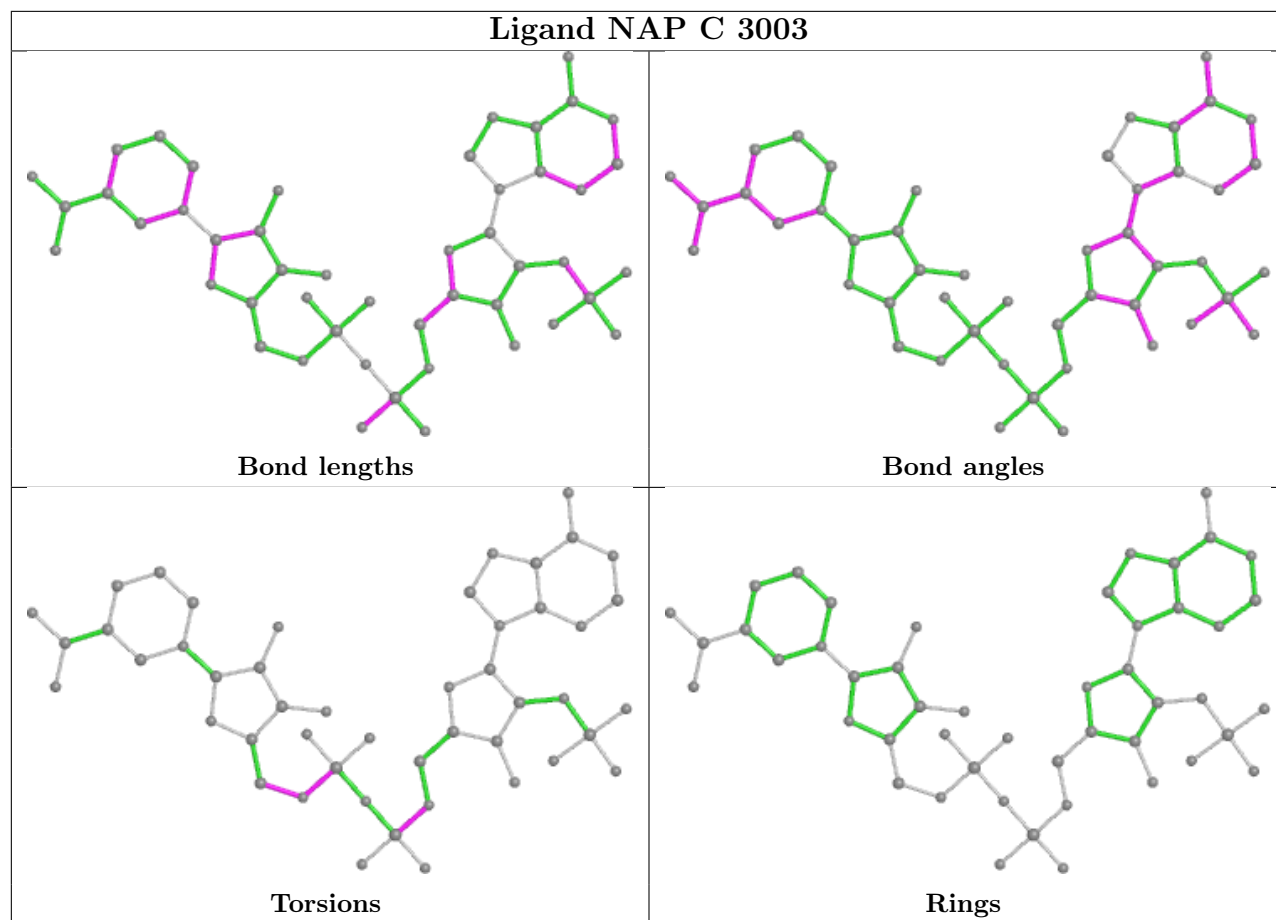
5 monomers are involved in 16 short contacts:

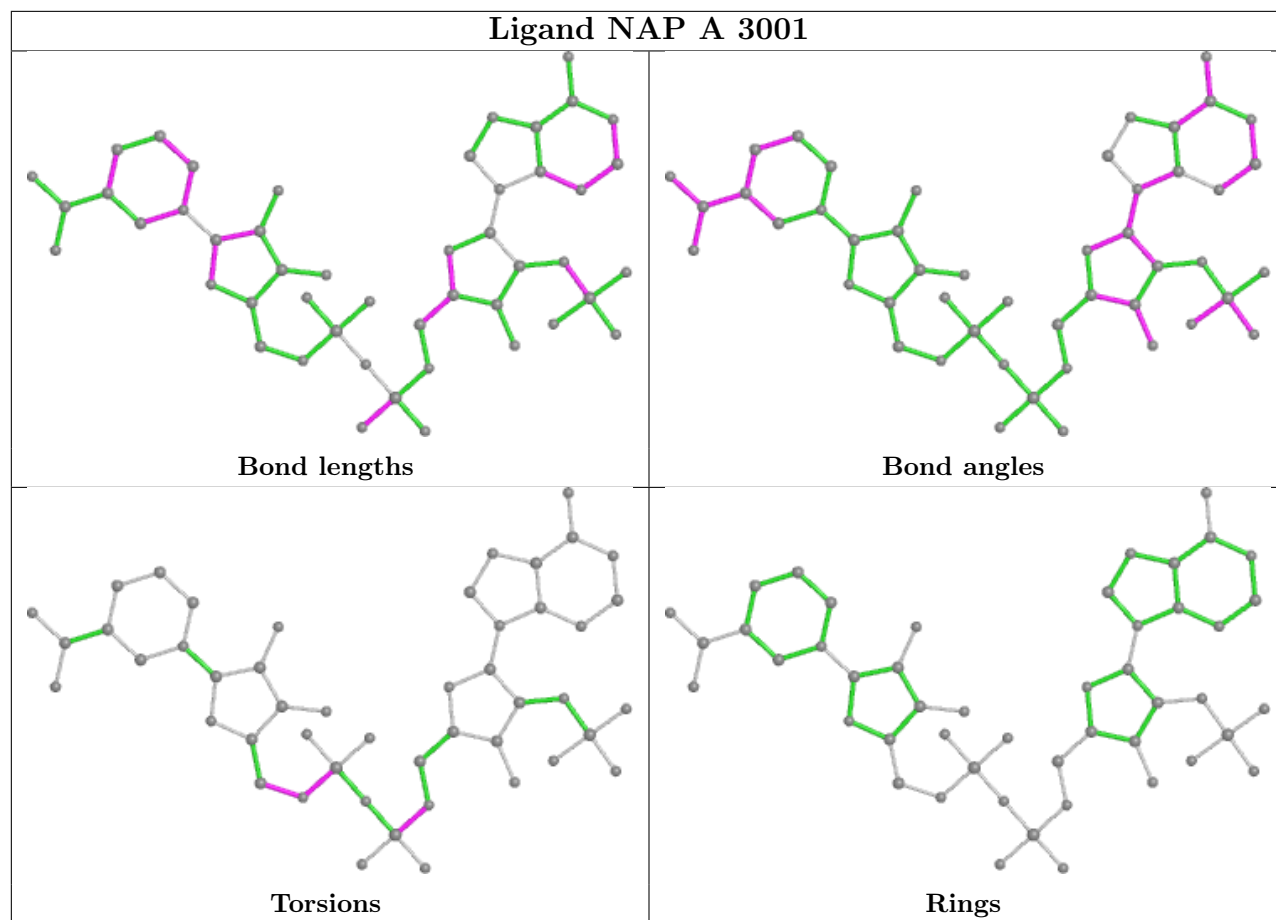
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	3002	NAP	3	0
2	D	2007	SO4	2	0
3	C	3003	NAP	4	0
3	A	3001	NAP	3	0
3	D	3004	NAP	4	0

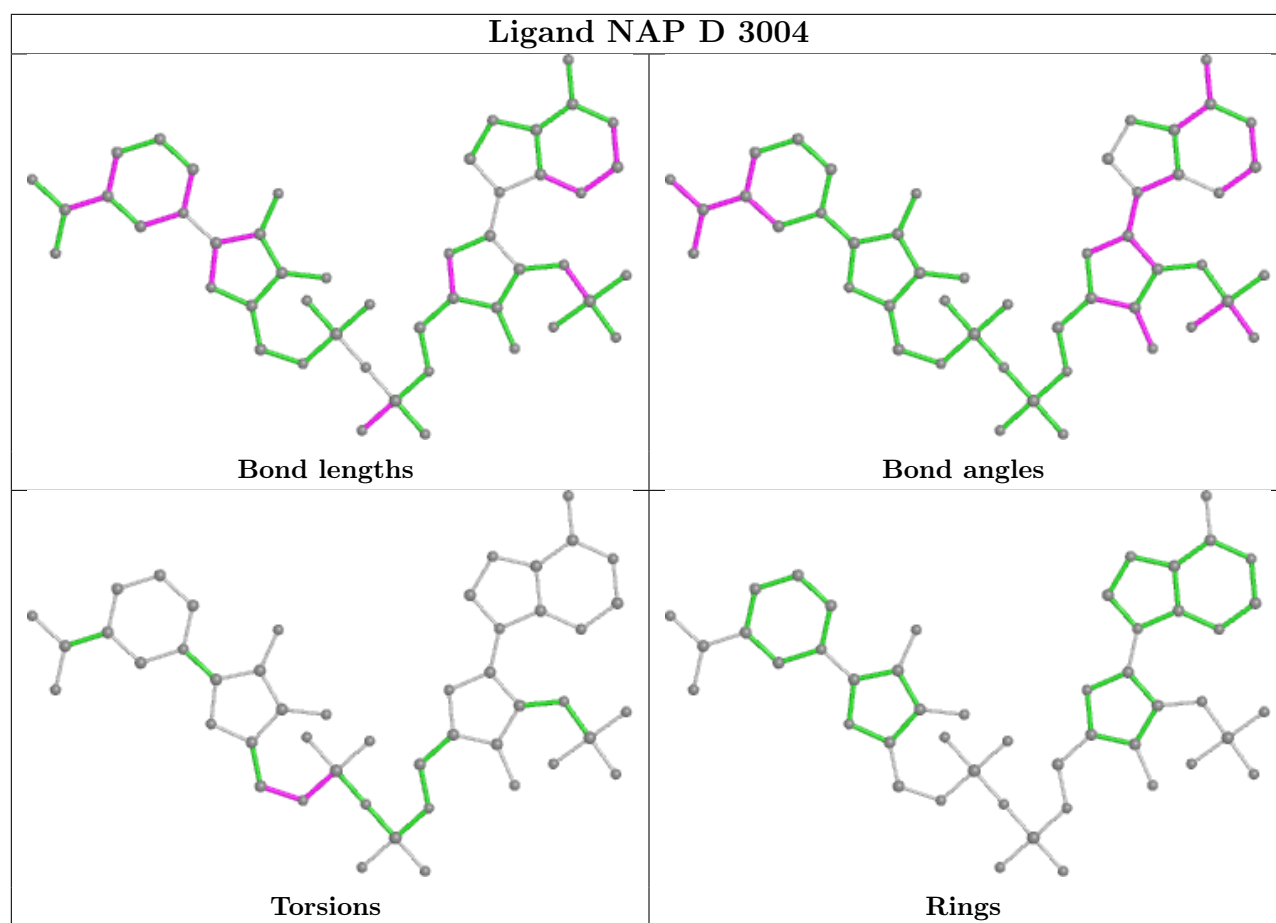
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included.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

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, 95<sup>th</sup> percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å <sup>2</sup> )	Q<0.9
1	A	473/475 (99%)	-0.47	4 (0%) 86 87	12, 24, 40, 59	0
1	B	473/475 (99%)	-0.50	2 (0%) 92 93	15, 28, 41, 58	0
1	C	474/475 (99%)	-0.64	0 100 100	10, 19, 31, 44	0
1	D	474/475 (99%)	-0.65	0 100 100	11, 20, 32, 54	0
All	All	1894/1900 (99%)	-0.57	6 (0%) 94 94	10, 23, 37, 59	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	438	GLY	3.6
1	A	17	GLU	3.1
1	B	17	GLU	2.9
1	A	211	SER	2.4
1	B	209	ARG	2.3

### 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](#)

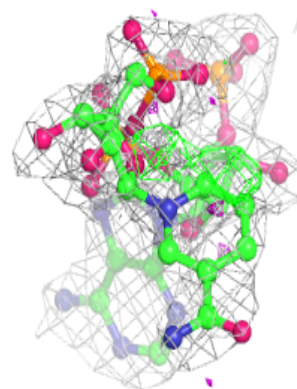
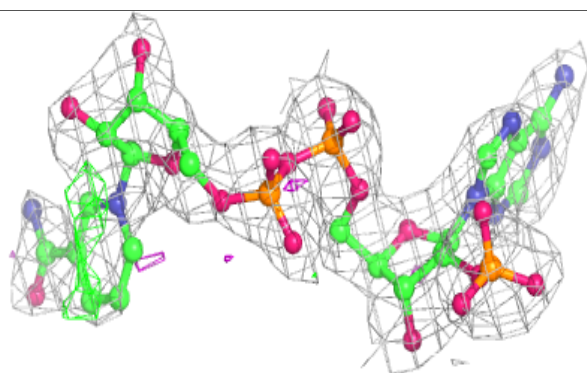
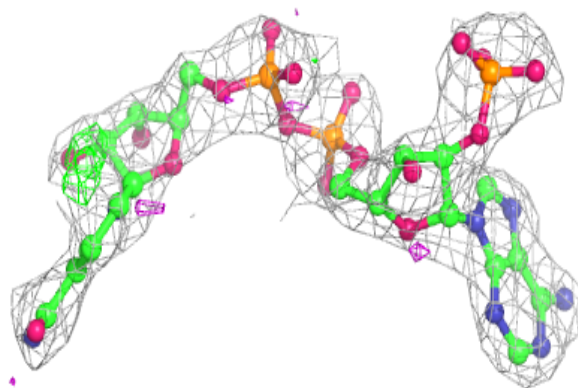
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95<sup>th</sup> percentile and maximum values of B factors of atoms in the group. The column labelled ‘Q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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NAP	B	3002	48/48	0.93	0.17	32,35,41,41	48
3	NAP	A	3001	48/48	0.94	0.15	30,34,39,40	48
3	NAP	D	3004	48/48	0.95	0.14	21,27,35,37	48
3	NAP	C	3003	48/48	0.96	0.13	13,24,32,32	48
2	SO4	B	2002	5/5	0.96	0.15	48,48,51,51	0
2	SO4	C	2004	5/5	0.97	0.11	28,31,33,35	0
2	SO4	D	2005	5/5	0.97	0.17	43,43,45,45	0
2	SO4	A	2001	5/5	0.97	0.16	40,43,43,44	0
2	SO4	B	2003	5/5	0.98	0.12	20,20,20,21	5
2	SO4	D	2006	5/5	0.98	0.18	31,32,33,34	5
2	SO4	D	2007	5/5	0.99	0.11	39,39,40,41	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.

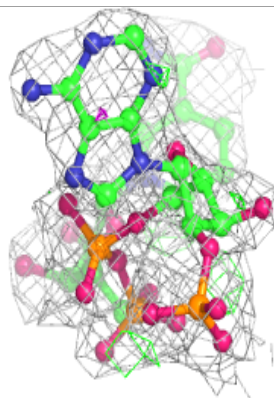
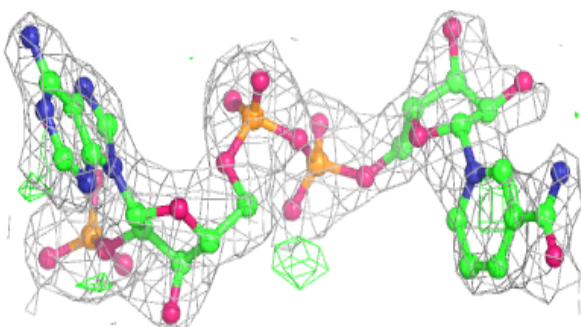
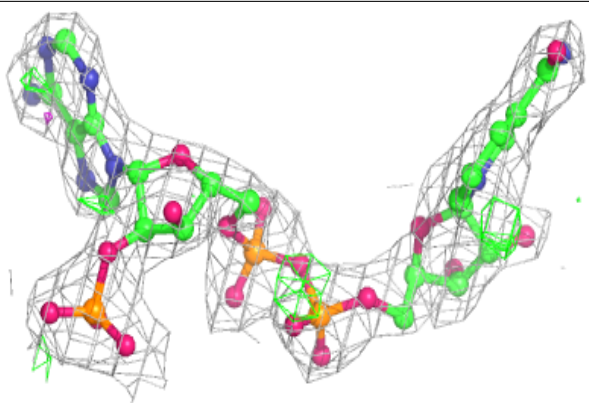
**Electron density around NAP B 3002:**

2mF<sub>o</sub>-DF<sub>c</sub> (at 0.7 rmsd) in gray  
mF<sub>o</sub>-DF<sub>c</sub> (at 3 rmsd) in purple (negative)  
and green (positive)

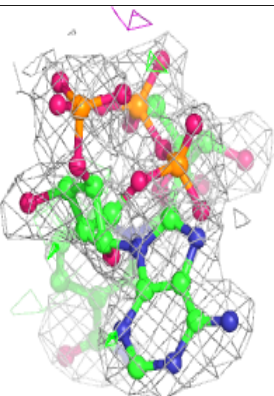
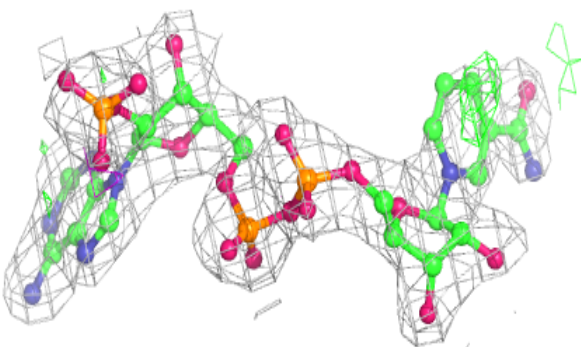
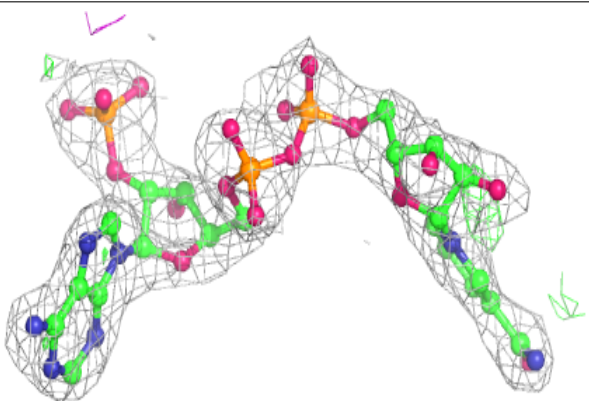


**Electron density around NAP A 3001:**

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

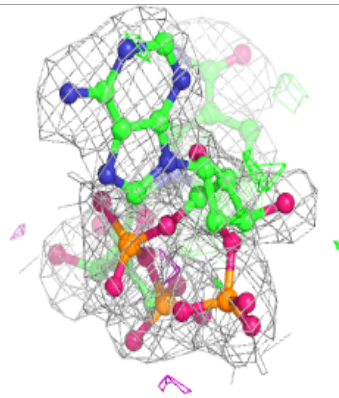
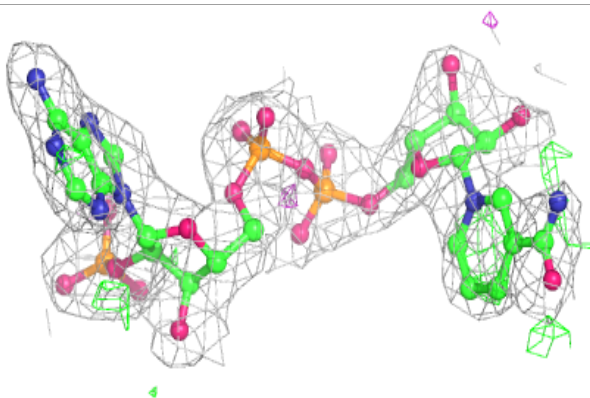
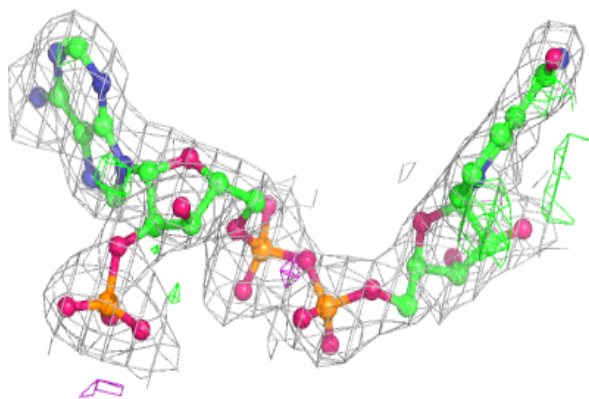
**Electron density around NAP D 3004:**

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



**Electron density around NAP C 3003:**

$2mF_o-DF_c$  (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.