



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 24, 2024 – 02:49 PM EDT

PDB ID : 6T3E
Title : Structure of Thermococcus litoralis Delta(1)-pyrroline-2-carboxylate reductase
in complex with NADH and L-proline
Authors : Ferraris, D.M.; Miggiano, R.; Ferrario, E.; Rizzi, M.
Deposited on : 2019-10-10
Resolution : 2.60 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 : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 2.37.1
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) : 2.37.1

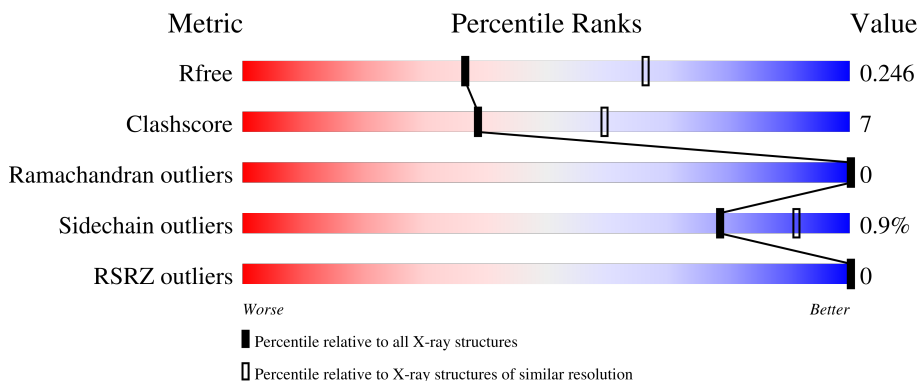
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.60 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	3163 (2.60-2.60)
Clashscore	141614	3518 (2.60-2.60)
Ramachandran outliers	138981	3455 (2.60-2.60)
Sidechain outliers	138945	3455 (2.60-2.60)
RSRZ outliers	127900	3104 (2.60-2.60)

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	349	 77% 15% 7%
1	B	349	 74% 18% 7%

2 Entry composition [i](#)

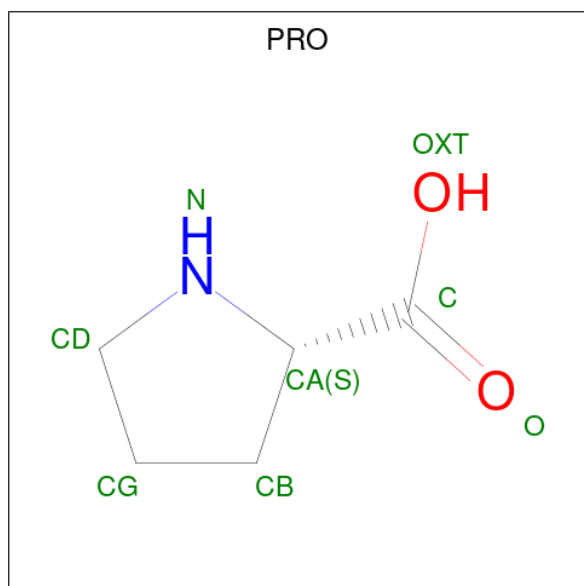
There are 4 unique types of molecules in this entry. The entry contains 5086 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 DELTA1-pyrroline-2-carboxylate reductase.

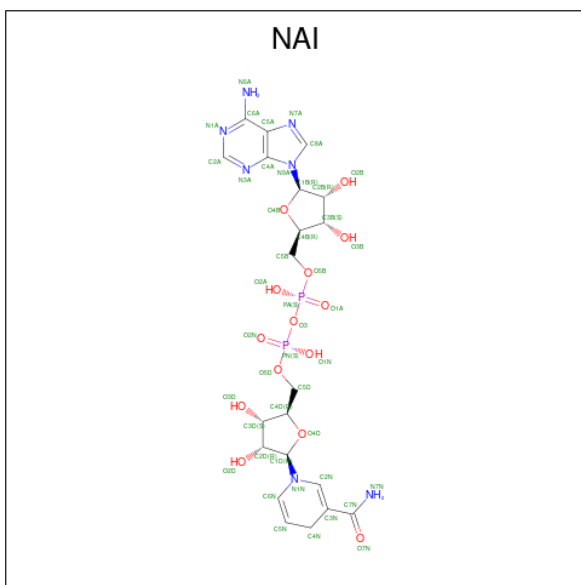
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	323	Total	C	N	O	S	0	0	0
			2473	1567	425	473	8			
1	B	325	Total	C	N	O	S	0	0	0
			2490	1578	427	477	8			

- Molecule 2 is PROLINE (three-letter code: PRO) (formula: C₅H₉NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			8	5	1	2		
2	B	1	Total	C	N	O	0	0
			8	5	1	2		

- Molecule 3 is 1,4-DIHYDRONICOTINAMIDE ADENINE DINUCLEOTIDE (three-letter code: NAI) (formula: C₂₁H₂₉N₇O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



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

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	9	Total O 9 9	0	0
4	B	10	Total O 10 10	0	0

- Molecule 1: DELTA1-pyrroline-2-carboxylate reductase

LEU	T111	GLY	GLY	MET
	R114	SER	SER	
	Y125	HIS	HIS	
	R128	HIS	HIS	
	G140	HIS	HIS	
	A159	SER	SER	
	L160	GLU	GLU	
	D163	ASN	ASN	
	I164	TYR	TYR	
	K170	PHE	PHE	
	K178	GLN	GLN	
	I184	HIS	HIS	
	K185	MET	MET	
	R191	VAL	VAL	
	R207	PHE	PHE	
	W215	GLY	GLY	
	I216			
	G219			
	A232			
	T239			
	S249			
	M264			
	V285			
	R289			
	E294			
	E306			
	I309			
	K312			
	E316			
	K317			
	G324			
	G327			
	V337			

- Molecule 1: DELTA1-pyrroline-2-carboxylate reductase

V285	L68	MET
G288	A69	GLY
R289	P77	SER
R293	P85	HIS
I305	L88	HIS
E306	L93	HIS
K312	L104	HIS
E316	M105	HIS
L329	E106	HIS
	G107	SER
	T108	SER
	R114	GLY
	T115	GLU
	L126	ASN
	V153	LEU
	R154	TYR
	K158	PHE
	A159	GLN
	L160	GLY
	M176	HIS
	K179	MET
	I184	VAL
T204	T205	PHE
A206	A206	GLY
R207	R207	M5
R217	R217	S9
E218	E218	L13
G219	G219	E14
T220	T220	K15
E238	E238	S18
R241	R241	M19
K244	K244	K20
M264	M264	E21
I269	I269	V22
L278	L278	E24
V282	V282	E32
		L33
		Y34
		K37
		R43
		E47
		V48
		E49
		K50
		I55
		L56
		Y57
		Y61
		L62
		E62

4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	82.69Å 51.51Å 92.29Å 90.00° 115.91° 90.00°	Depositor
Resolution (Å)	43.77 – 2.60 43.77 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.3 (43.77-2.60) 92.3 (43.77-2.60)	Depositor EDS
R_{merge}	0.20	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.61Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
R, R_{free}	0.189 , 0.242 0.192 , 0.246	Depositor DCC
R_{free} test set	1012 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	45.1	Xtriage
Anisotropy	0.590	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 38.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.028 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5086	wwPDB-VP
Average B, all atoms (Å ²)	48.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 6.30% 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: NAI

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	0.40	0/2504	0.58	0/3376
1	B	0.38	0/2521	0.56	1/3399 (0.0%)
All	All	0.39	0/5025	0.57	1/6775 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	15	LYS	CA-CB-CG	5.21	124.86	113.40

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	2473	0	2581	34	0
1	B	2490	0	2598	41	0
2	A	8	0	7	0	0
2	B	8	0	7	1	0
3	A	44	0	26	2	0
3	B	44	0	26	5	0
4	A	9	0	0	0	0
4	B	10	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5086	0	5245	77	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 7.

The worst 5 of 77 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:204:THR:HG22	1:B:206:ALA:H	1.25	0.97
1:A:114:ARG:HD3	1:A:306:GLU:HB2	1.63	0.79
1:A:62:LEU:HD13	1:A:309:ILE:HG23	1.71	0.73
1:B:158:LYS:HE2	1:B:160:LEU:HD21	1.75	0.69
1:B:61:TYR:CE2	1:B:63:GLU:HG2	2.30	0.65

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	321/349 (92%)	315 (98%)	6 (2%)	0	100	100
1	B	323/349 (93%)	317 (98%)	6 (2%)	0	100	100
All	All	644/698 (92%)	632 (98%)	12 (2%)	0	100	100

There are no Ramachandran outliers to report.

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	266/288 (92%)	263 (99%)	3 (1%)	73	88
1	B	268/288 (93%)	266 (99%)	2 (1%)	84	94
All	All	534/576 (93%)	529 (99%)	5 (1%)	78	91

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	50	LYS
1	A	114	ARG
1	A	249	SER
1	B	50	LYS
1	B	114	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	146	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

4 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	$\# Z > 2$
3	NAI	A	402	-	43,48,48	4.33	21 (48%)	50,73,73	2.12	7 (14%)
2	PRO	B	401	-	8,8,8	0.89	1 (12%)	10,10,10	1.41	1 (10%)
3	NAI	B	402	-	43,48,48	4.38	20 (46%)	50,73,73	1.97	5 (10%)
2	PRO	A	401	-	8,8,8	0.81	0	10,10,10	1.54	2 (20%)

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	NAI	A	402	-	-	4/25/72/72	0/5/5/5
2	PRO	B	401	-	-	0/4/11/11	0/1/1/1
3	NAI	B	402	-	-	5/25/72/72	0/5/5/5
2	PRO	A	401	-	-	2/4/11/11	0/1/1/1

The worst 5 of 42 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	402	NAI	O4B-C1B	16.58	1.62	1.40
3	B	402	NAI	O4B-C1B	16.40	1.62	1.40
3	B	402	NAI	O4D-C1D	8.64	1.62	1.42
3	A	402	NAI	O4D-C1D	8.24	1.61	1.42
3	B	402	NAI	C2N-C3N	7.49	1.55	1.35

The worst 5 of 15 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	402	NAI	C5A-C6A-N6A	9.22	134.36	120.31
3	B	402	NAI	C5A-C6A-N6A	7.99	132.48	120.31
3	B	402	NAI	N3A-C2A-N1A	-5.98	120.55	128.67
3	A	402	NAI	N6A-C6A-N1A	-5.92	105.68	118.33
3	A	402	NAI	N3A-C2A-N1A	-5.90	120.66	128.67

There are no chirality outliers.

5 of 11 torsion outliers are listed below:

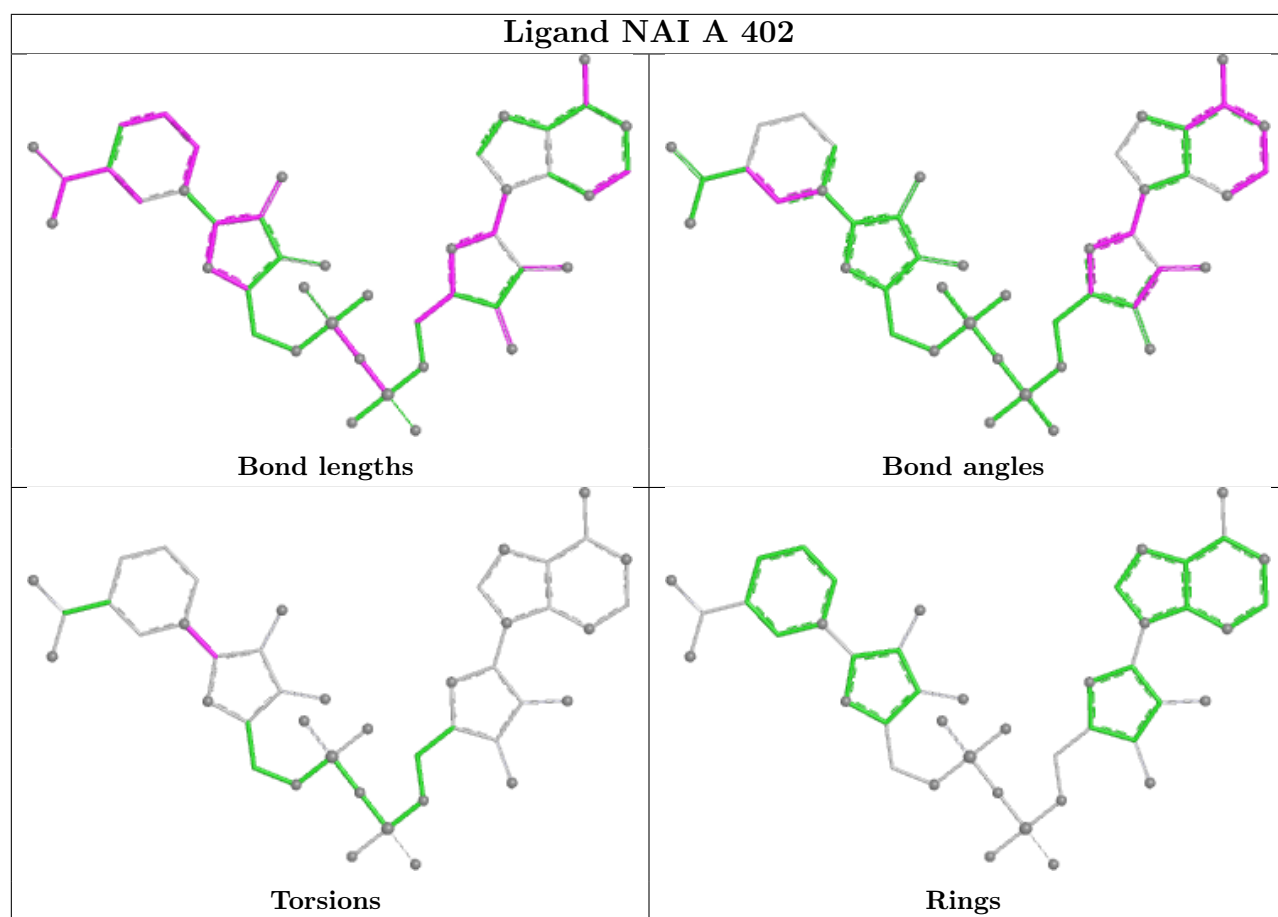
Mol	Chain	Res	Type	Atoms
3	A	402	NAI	C2D-C1D-N1N-C2N
3	A	402	NAI	C2D-C1D-N1N-C6N
3	B	402	NAI	PN-O3-PA-O5B
3	B	402	NAI	C2D-C1D-N1N-C2N
2	A	401	PRO	O-C-CA-CB

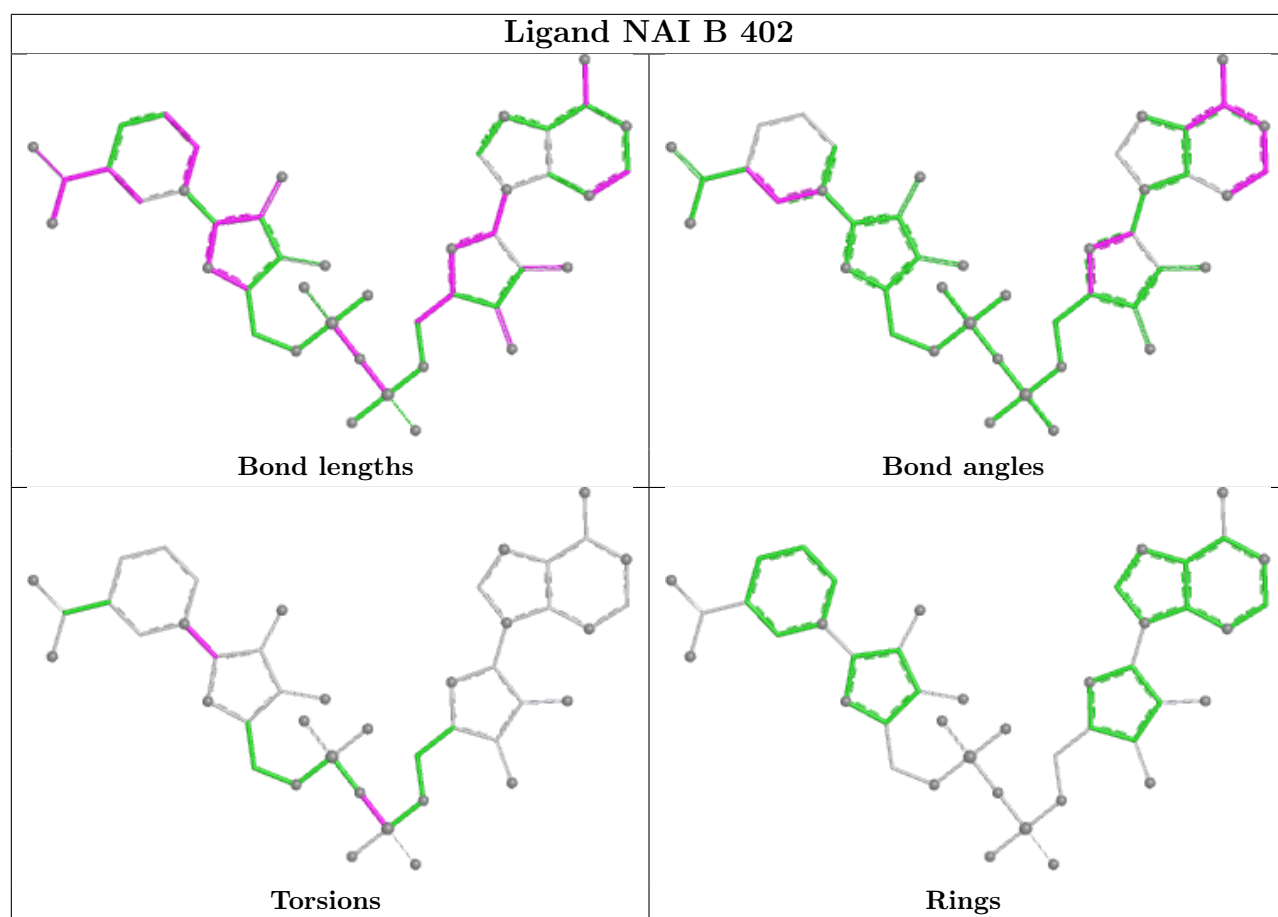
There are no ring outliers.

3 monomers are involved in 7 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	NAI	2	0
2	B	401	PRO	1	0
3	B	402	NAI	5	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, 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	323/349 (92%)	-0.29	0 100 100	27, 44, 62, 72	0
1	B	325/349 (93%)	-0.26	0 100 100	29, 50, 73, 99	0
All	All	648/698 (92%)	-0.28	0 100 100	27, 47, 70, 99	0

There are no RSRZ outliers to report.

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.

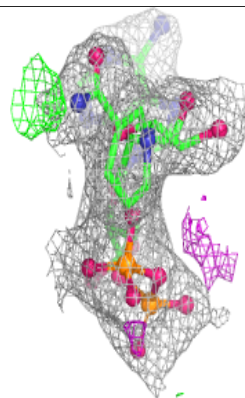
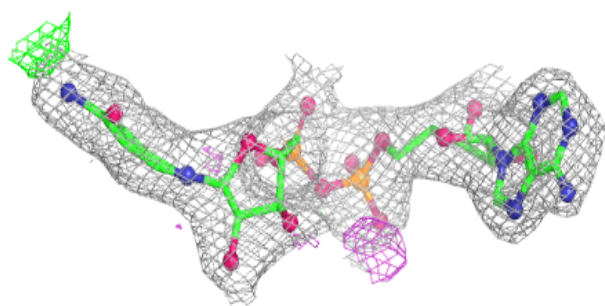
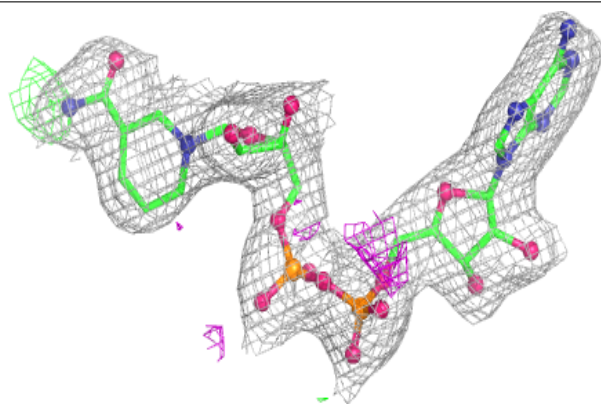
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	PRO	A	401	8/8	0.97	0.16	38,42,44,46	0
3	NAI	B	402	44/44	0.97	0.14	25,38,44,48	0
3	NAI	A	402	44/44	0.98	0.14	26,38,41,44	0
2	PRO	B	401	8/8	0.98	0.14	43,45,51,53	0

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.

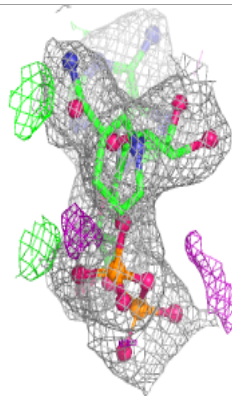
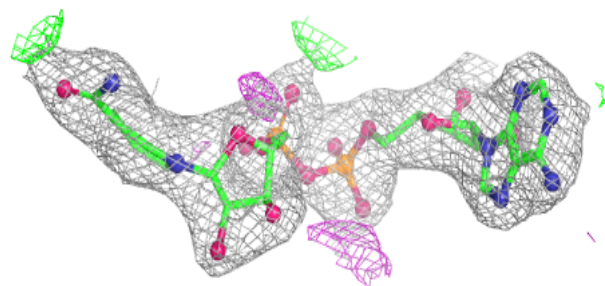
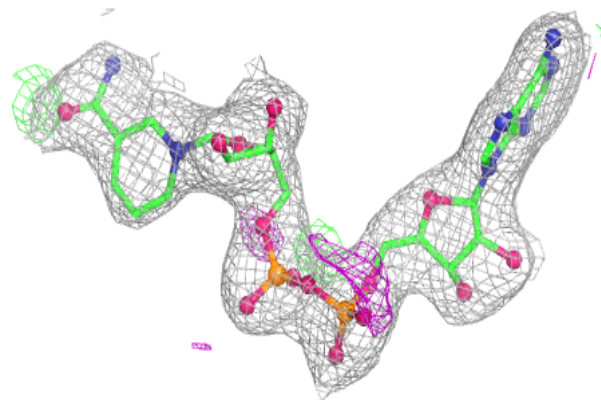
Electron density around NAI B 402:

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



Electron density around NAI A 402:

$2mF_o-DF_c$ (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.