



Full wwPDB X-ray Structure Validation Report ⓘ

May 12, 2025 – 02:26 PM JST

PDB ID : 9KSN / pdb_00009ksn
Title : Crystal structure of meso-diaminopimelate dehydrogenase from *Bacillus thermozeamaize* mutant M9 complexed with NADP+
Authors : Wei, Y.; Geng, Q.; Zheng, Y.-C.; Zhang, Z.-J.
Deposited on : 2024-11-30
Resolution : 2.65 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 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 : 4-5-2 with Phenix2.0rc1
Mogul : 1.8.5 (274361), CSD as541be (2020)
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

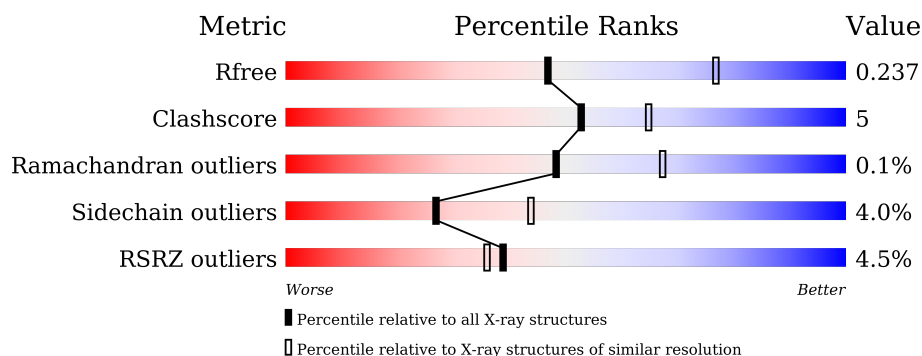
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.65 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	1003 (2.66-2.66)
Clashscore	180529	1063 (2.66-2.66)
Ramachandran outliers	177936	1052 (2.66-2.66)
Sidechain outliers	177891	1052 (2.66-2.66)
RSRZ outliers	164620	1003 (2.66-2.66)

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	347	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> % </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 73% 14% 13% </div> </div>
1	B	347	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> 5% </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 74% 14% • 12% </div> </div>
1	C	347	<div> <div style="width: 100%; height: 10px; background-color: red; position: relative;"> 5% </div> <div style="display: flex; justify-content: space-between; margin-top: 5px;"> 75% 12% • 12% </div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7313 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 Meso-diaminopimelate D-dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	303	Total	C	N	O	S	0	0	0
			2338	1474	413	438	13			
1	B	306	Total	C	N	O	S	0	1	0
			2372	1494	420	445	13			
1	C	305	Total	C	N	O	S	0	0	0
			2352	1483	415	441	13			

There are 156 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-39	MET	-	initiating methionine	UNP A0A1Y3PXT7
A	-38	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-37	SER	-	expression tag	UNP A0A1Y3PXT7
A	-36	SER	-	expression tag	UNP A0A1Y3PXT7
A	-35	HIS	-	expression tag	UNP A0A1Y3PXT7
A	-34	HIS	-	expression tag	UNP A0A1Y3PXT7
A	-33	HIS	-	expression tag	UNP A0A1Y3PXT7
A	-32	HIS	-	expression tag	UNP A0A1Y3PXT7
A	-31	HIS	-	expression tag	UNP A0A1Y3PXT7
A	-30	HIS	-	expression tag	UNP A0A1Y3PXT7
A	-29	SER	-	expression tag	UNP A0A1Y3PXT7
A	-28	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-27	ILE	-	expression tag	UNP A0A1Y3PXT7
A	-26	VAL	-	expression tag	UNP A0A1Y3PXT7
A	-25	PRO	-	expression tag	UNP A0A1Y3PXT7
A	-24	ARG	-	expression tag	UNP A0A1Y3PXT7
A	-23	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-22	SER	-	expression tag	UNP A0A1Y3PXT7
A	-21	HIS	-	expression tag	UNP A0A1Y3PXT7
A	-20	MET	-	expression tag	UNP A0A1Y3PXT7
A	-19	ALA	-	expression tag	UNP A0A1Y3PXT7
A	-18	SER	-	expression tag	UNP A0A1Y3PXT7
A	-17	MET	-	expression tag	UNP A0A1Y3PXT7

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Chain	Residue	Modelled	Actual	Comment	Reference
A	-16	THR	-	expression tag	UNP A0A1Y3PXT7
A	-15	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-14	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-13	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-12	GLN	-	expression tag	UNP A0A1Y3PXT7
A	-11	MET	-	expression tag	UNP A0A1Y3PXT7
A	-10	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-9	ARG	-	expression tag	UNP A0A1Y3PXT7
A	-8	GLY	-	expression tag	UNP A0A1Y3PXT7
A	-7	SER	-	expression tag	UNP A0A1Y3PXT7
A	-6	GLU	-	expression tag	UNP A0A1Y3PXT7
A	-5	PHE	-	expression tag	UNP A0A1Y3PXT7
A	-4	GLU	-	expression tag	UNP A0A1Y3PXT7
A	-3	LEU	-	expression tag	UNP A0A1Y3PXT7
A	-2	ARG	-	expression tag	UNP A0A1Y3PXT7
A	-1	ARG	-	expression tag	UNP A0A1Y3PXT7
A	0	GLN	-	expression tag	UNP A0A1Y3PXT7
A	79	TYR	ARG	conflict	UNP A0A1Y3PXT7
A	129	LEU	TRP	conflict	UNP A0A1Y3PXT7
A	130	LEU	ASP	conflict	UNP A0A1Y3PXT7
A	134	CYS	ASP	conflict	UNP A0A1Y3PXT7
A	154	VAL	PHE	conflict	UNP A0A1Y3PXT7
A	161	SER	GLY	conflict	UNP A0A1Y3PXT7
A	162	ALA	HIS	conflict	UNP A0A1Y3PXT7
A	177	ALA	SER	conflict	UNP A0A1Y3PXT7
A	179	ILE	THR	conflict	UNP A0A1Y3PXT7
A	213	LEU	TYR	conflict	UNP A0A1Y3PXT7
A	235	ILE	HIS	conflict	UNP A0A1Y3PXT7
A	236	ALA	GLY	conflict	UNP A0A1Y3PXT7
B	-39	MET	-	initiating methionine	UNP A0A1Y3PXT7
B	-38	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-37	SER	-	expression tag	UNP A0A1Y3PXT7
B	-36	SER	-	expression tag	UNP A0A1Y3PXT7
B	-35	HIS	-	expression tag	UNP A0A1Y3PXT7
B	-34	HIS	-	expression tag	UNP A0A1Y3PXT7
B	-33	HIS	-	expression tag	UNP A0A1Y3PXT7
B	-32	HIS	-	expression tag	UNP A0A1Y3PXT7
B	-31	HIS	-	expression tag	UNP A0A1Y3PXT7
B	-30	HIS	-	expression tag	UNP A0A1Y3PXT7
B	-29	SER	-	expression tag	UNP A0A1Y3PXT7
B	-28	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-27	ILE	-	expression tag	UNP A0A1Y3PXT7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-26	VAL	-	expression tag	UNP A0A1Y3PXT7
B	-25	PRO	-	expression tag	UNP A0A1Y3PXT7
B	-24	ARG	-	expression tag	UNP A0A1Y3PXT7
B	-23	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-22	SER	-	expression tag	UNP A0A1Y3PXT7
B	-21	HIS	-	expression tag	UNP A0A1Y3PXT7
B	-20	MET	-	expression tag	UNP A0A1Y3PXT7
B	-19	ALA	-	expression tag	UNP A0A1Y3PXT7
B	-18	SER	-	expression tag	UNP A0A1Y3PXT7
B	-17	MET	-	expression tag	UNP A0A1Y3PXT7
B	-16	THR	-	expression tag	UNP A0A1Y3PXT7
B	-15	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-14	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-13	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-12	GLN	-	expression tag	UNP A0A1Y3PXT7
B	-11	MET	-	expression tag	UNP A0A1Y3PXT7
B	-10	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-9	ARG	-	expression tag	UNP A0A1Y3PXT7
B	-8	GLY	-	expression tag	UNP A0A1Y3PXT7
B	-7	SER	-	expression tag	UNP A0A1Y3PXT7
B	-6	GLU	-	expression tag	UNP A0A1Y3PXT7
B	-5	PHE	-	expression tag	UNP A0A1Y3PXT7
B	-4	GLU	-	expression tag	UNP A0A1Y3PXT7
B	-3	LEU	-	expression tag	UNP A0A1Y3PXT7
B	-2	ARG	-	expression tag	UNP A0A1Y3PXT7
B	-1	ARG	-	expression tag	UNP A0A1Y3PXT7
B	0	GLN	-	expression tag	UNP A0A1Y3PXT7
B	79	TYR	ARG	conflict	UNP A0A1Y3PXT7
B	129	LEU	TRP	conflict	UNP A0A1Y3PXT7
B	130	LEU	ASP	conflict	UNP A0A1Y3PXT7
B	134	CYS	ASP	conflict	UNP A0A1Y3PXT7
B	154	VAL	PHE	conflict	UNP A0A1Y3PXT7
B	161	SER	GLY	conflict	UNP A0A1Y3PXT7
B	162	ALA	HIS	conflict	UNP A0A1Y3PXT7
B	177	ALA	SER	conflict	UNP A0A1Y3PXT7
B	179	ILE	THR	conflict	UNP A0A1Y3PXT7
B	213	LEU	TYR	conflict	UNP A0A1Y3PXT7
B	235	ILE	HIS	conflict	UNP A0A1Y3PXT7
B	236	ALA	GLY	conflict	UNP A0A1Y3PXT7
C	-39	MET	-	initiating methionine	UNP A0A1Y3PXT7
C	-38	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-37	SER	-	expression tag	UNP A0A1Y3PXT7

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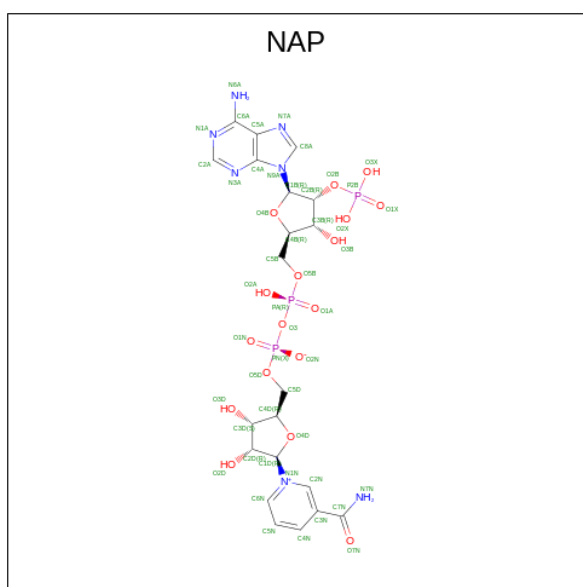
Chain	Residue	Modelled	Actual	Comment	Reference
C	-36	SER	-	expression tag	UNP A0A1Y3PXT7
C	-35	HIS	-	expression tag	UNP A0A1Y3PXT7
C	-34	HIS	-	expression tag	UNP A0A1Y3PXT7
C	-33	HIS	-	expression tag	UNP A0A1Y3PXT7
C	-32	HIS	-	expression tag	UNP A0A1Y3PXT7
C	-31	HIS	-	expression tag	UNP A0A1Y3PXT7
C	-30	HIS	-	expression tag	UNP A0A1Y3PXT7
C	-29	SER	-	expression tag	UNP A0A1Y3PXT7
C	-28	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-27	ILE	-	expression tag	UNP A0A1Y3PXT7
C	-26	VAL	-	expression tag	UNP A0A1Y3PXT7
C	-25	PRO	-	expression tag	UNP A0A1Y3PXT7
C	-24	ARG	-	expression tag	UNP A0A1Y3PXT7
C	-23	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-22	SER	-	expression tag	UNP A0A1Y3PXT7
C	-21	HIS	-	expression tag	UNP A0A1Y3PXT7
C	-20	MET	-	expression tag	UNP A0A1Y3PXT7
C	-19	ALA	-	expression tag	UNP A0A1Y3PXT7
C	-18	SER	-	expression tag	UNP A0A1Y3PXT7
C	-17	MET	-	expression tag	UNP A0A1Y3PXT7
C	-16	THR	-	expression tag	UNP A0A1Y3PXT7
C	-15	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-14	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-13	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-12	GLN	-	expression tag	UNP A0A1Y3PXT7
C	-11	MET	-	expression tag	UNP A0A1Y3PXT7
C	-10	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-9	ARG	-	expression tag	UNP A0A1Y3PXT7
C	-8	GLY	-	expression tag	UNP A0A1Y3PXT7
C	-7	SER	-	expression tag	UNP A0A1Y3PXT7
C	-6	GLU	-	expression tag	UNP A0A1Y3PXT7
C	-5	PHE	-	expression tag	UNP A0A1Y3PXT7
C	-4	GLU	-	expression tag	UNP A0A1Y3PXT7
C	-3	LEU	-	expression tag	UNP A0A1Y3PXT7
C	-2	ARG	-	expression tag	UNP A0A1Y3PXT7
C	-1	ARG	-	expression tag	UNP A0A1Y3PXT7
C	0	GLN	-	expression tag	UNP A0A1Y3PXT7
C	79	TYR	ARG	conflict	UNP A0A1Y3PXT7
C	129	LEU	TRP	conflict	UNP A0A1Y3PXT7
C	130	LEU	ASP	conflict	UNP A0A1Y3PXT7
C	134	CYS	ASP	conflict	UNP A0A1Y3PXT7
C	154	VAL	PHE	conflict	UNP A0A1Y3PXT7

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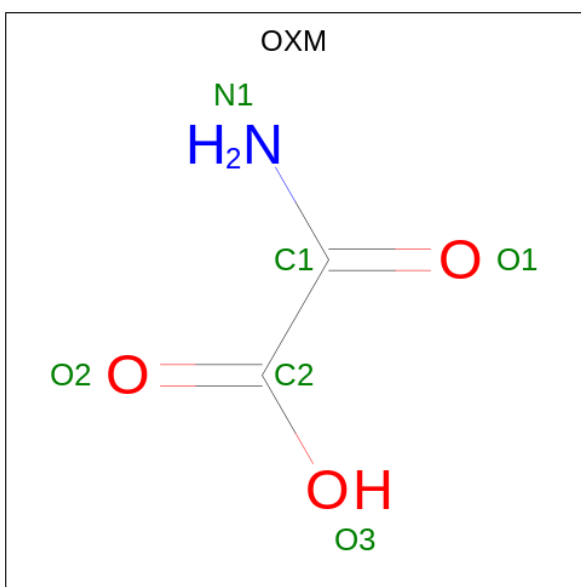
Chain	Residue	Modelled	Actual	Comment	Reference
C	161	SER	GLY	conflict	UNP A0A1Y3PXT7
C	162	ALA	HIS	conflict	UNP A0A1Y3PXT7
C	177	ALA	SER	conflict	UNP A0A1Y3PXT7
C	179	ILE	THR	conflict	UNP A0A1Y3PXT7
C	213	LEU	TYR	conflict	UNP A0A1Y3PXT7
C	235	ILE	HIS	conflict	UNP A0A1Y3PXT7
C	236	ALA	GLY	conflict	UNP A0A1Y3PXT7

- Molecule 2 is NADP NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (CCD ID: NAP) (formula: $C_{21}H_{28}N_7O_{17}P_3$) (labeled as "Ligand of Interest" by depositor).



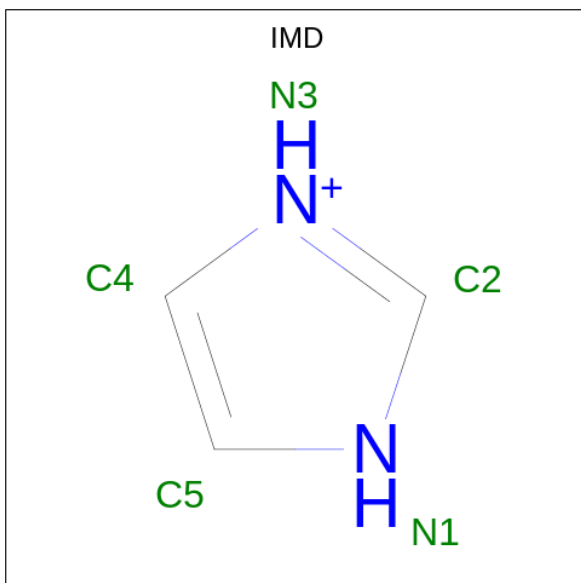
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	B	1	Total 48	C 21	N 7	O 17	P 3	0	0
2	C	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 3 is OXAMIC ACID (CCD ID: OXM) (formula: $\text{C}_2\text{H}_3\text{NO}_3$).



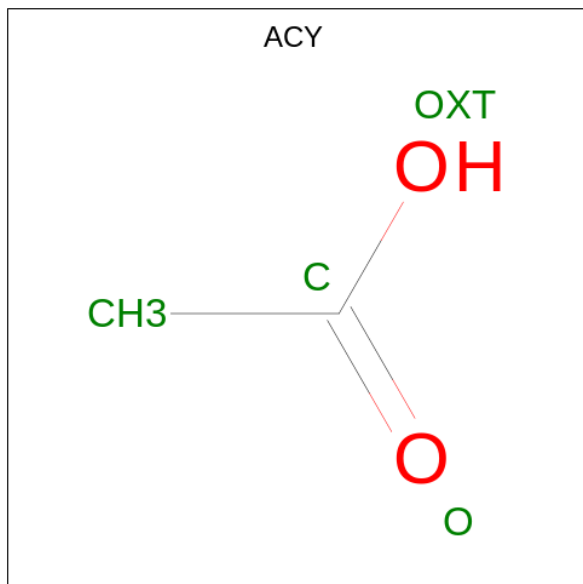
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			6	2	1	3		
3	B	1	Total	C	N	O	0	0
			6	2	1	3		
3	C	1	Total	C	N	O	0	0
			6	2	1	3		
3	C	1	Total	C	N	O	0	0
			6	2	1	3		

- Molecule 4 is IMIDAZOLE (CCD ID: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C N 5 3 2	0	0
4	B	1	Total C N 5 3 2	0	0
4	B	1	Total C N 5 3 2	0	0
4	B	1	Total C N 5 3 2	0	0
4	B	1	Total C N 5 3 2	0	0
4	C	1	Total C N 5 3 2	0	0

- Molecule 5 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



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

- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	18	Total O 18 18	0	0
6	B	15	Total O 15 15	0	0

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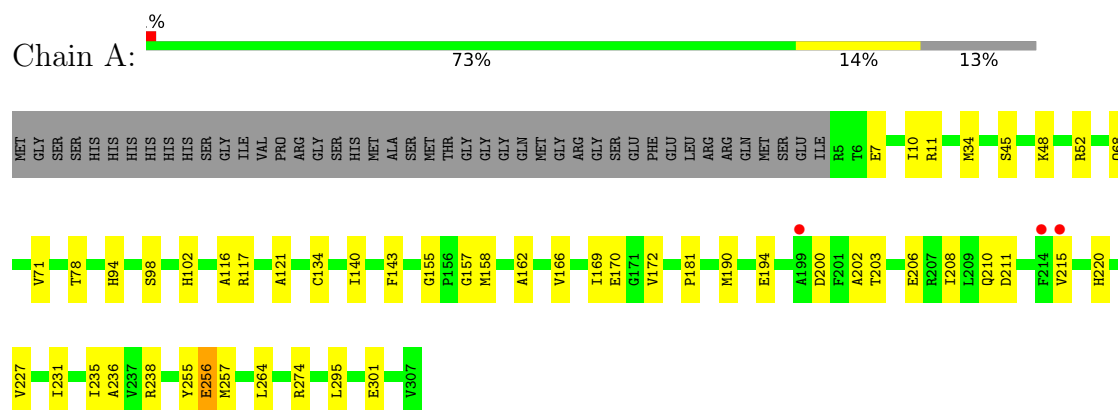
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	12	Total	O	0	0
			12	12		

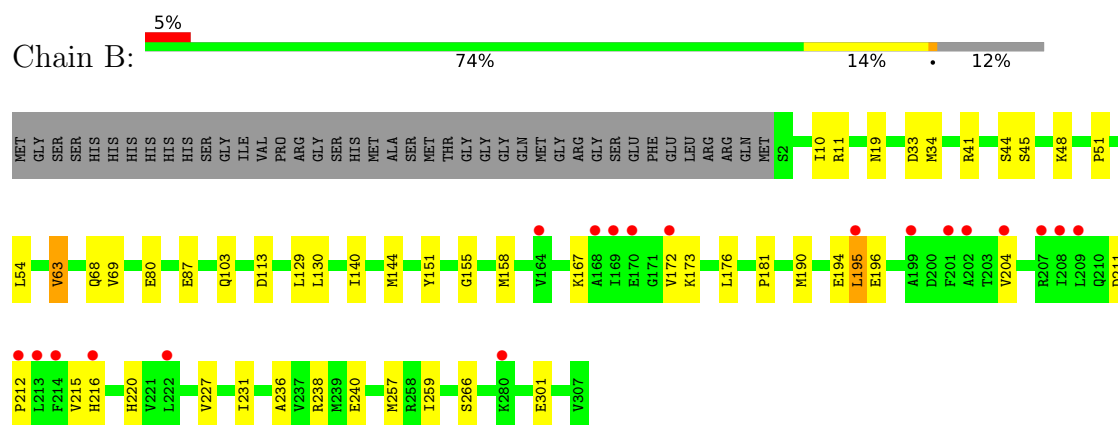
3 Residue-property plots [i](#)

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.

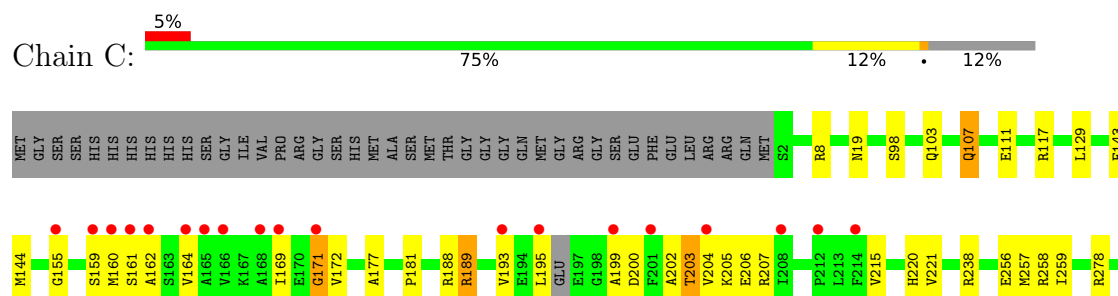
• Molecule 1: Meso-diaminopimelate D-dehydrogenase



• Molecule 1: Meso-diaminopimelate D-dehydrogenase



• Molecule 1: Meso-diaminopimelate D-dehydrogenase





4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	156.07Å 156.07Å 112.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.05 – 2.65 50.05 – 2.65	Depositor EDS
% Data completeness (in resolution range)	99.9 (50.05-2.65) 91.9 (50.05-2.65)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.78 (at 2.65Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487, PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.201 , 0.237 0.204 , 0.237	Depositor DCC
R_{free} test set	1976 reflections (4.84%)	wwPDB-VP
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.683	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	7313	wwPDB-VP
Average B, all atoms (Å ²)	66.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.48% 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: IMD, NAP, ACY, OXM

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	0.13	0/2374	0.36	0/3218
1	B	0.13	0/2408	0.36	0/3263
1	C	0.14	0/2387	0.40	0/3234
All	All	0.13	0/7169	0.37	0/9715

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	C	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	C	171	GLY	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	2338	0	2390	31	0
1	B	2372	0	2424	24	0
1	C	2352	0	2405	21	0
2	A	48	0	25	2	0
2	B	48	0	25	2	0
2	C	48	0	25	1	0
3	A	6	0	2	0	0
3	B	6	0	2	0	0
3	C	12	0	4	0	0
4	A	5	0	5	2	0
4	B	20	0	20	1	0
4	C	5	0	5	0	0
5	A	4	0	3	0	0
5	B	4	0	3	0	0
6	A	18	0	0	1	0
6	B	15	0	0	1	1
6	C	12	0	0	0	1
All	All	7313	0	7338	71	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 5.

All (71) 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:C:238:ARG:NH1	1:C:256:GLU:OE1	2.18	0.76
1:B:195:LEU:HD11	1:B:204:VAL:HG21	1.69	0.73
1:B:151:TYR:HA	4:B:407:IMD:H5	1.71	0.72
1:C:155:GLY:HA2	1:C:181:PRO:HG3	1.74	0.69
1:A:155:GLY:HA2	1:A:181:PRO:HG3	1.75	0.69
1:C:204:VAL:HA	1:C:207:ARG:HD2	1.74	0.69
1:C:257:MET:HE2	1:C:259:ILE:HG12	1.73	0.68
1:B:130:LEU:H	2:B:401:NAP:H72N	1.42	0.67
1:A:190:MET:HG2	1:A:220:HIS:HB2	1.75	0.67
1:C:107:GLN:NE2	1:C:111:GLU:OE2	2.26	0.66
1:B:238:ARG:NH1	1:B:240:GLU:OE2	2.29	0.66
1:B:266:SER:OG	6:B:501:HOH:O	2.14	0.65
1:A:274:ARG:O	6:A:502:HOH:O	2.16	0.62
1:B:45:SER:HA	1:B:48:LYS:HE2	1.83	0.61
1:B:158:MET:HG2	1:B:176:LEU:HD11	1.82	0.59
1:A:158:MET:HE1	1:A:231:ILE:HG23	1.85	0.59
1:A:78:THR:HG1	2:A:401:NAP:HO2N	1.46	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:172:VAL:HG13	1:C:193:VAL:HG23	1.83	0.59
1:C:256:GLU:OE2	1:C:258:ARG:NH2	2.35	0.59
1:A:169:ILE:HD12	1:A:208:ILE:HG12	1.86	0.58
1:B:51:PRO:HG2	1:B:54:LEU:HD12	1.86	0.57
1:A:264:LEU:HD11	1:C:144:MET:HE2	1.85	0.57
1:B:257:MET:HE2	1:B:259:ILE:HG12	1.88	0.56
1:C:202:ALA:O	1:C:206:GLU:HG2	2.08	0.54
1:A:45:SER:HA	1:A:48:LYS:HE2	1.90	0.53
1:C:161:SER:O	1:C:164:VAL:HG22	2.09	0.52
1:B:87:GLU:CD	1:C:8:ARG:HE	2.18	0.51
1:A:117:ARG:NH2	1:B:113:ASP:OD2	2.43	0.51
1:A:211:ASP:O	1:A:215:VAL:HG23	2.11	0.51
1:B:155:GLY:HA2	1:B:181:PRO:HG3	1.92	0.50
1:B:11:ARG:NH1	1:B:68:GLN:O	2.40	0.50
1:A:102:HIS:CE1	4:A:403:IMD:H5	2.46	0.50
1:A:200:ASP:OD1	1:A:203:THR:OG1	2.29	0.49
1:B:140:ILE:HG22	1:B:144:MET:HE2	1.94	0.49
1:C:195:LEU:HD11	1:C:199:ALA:HB3	1.94	0.49
1:A:140:ILE:HA	1:A:143:PHE:CE2	2.48	0.49
1:A:162:ALA:O	1:A:166:VAL:HG23	2.12	0.49
1:C:205:LYS:HG2	1:C:221:VAL:HB	1.95	0.48
1:B:190:MET:HG3	1:B:220:HIS:HB2	1.95	0.48
1:C:98:SER:O	2:C:401:NAP:H2N	2.14	0.48
1:A:238:ARG:HH11	1:A:256:GLU:HG3	1.78	0.47
1:A:194:GLU:HB2	1:A:227:VAL:HG13	1.96	0.47
1:C:200:ASP:HB3	1:C:203:THR:OG1	2.15	0.47
1:A:102:HIS:NE2	4:A:403:IMD:H5	2.31	0.46
1:C:278:ARG:NH1	1:C:293:ASP:O	2.47	0.46
1:B:194:GLU:HB2	1:B:227:VAL:HG13	1.96	0.46
1:B:63:VAL:HG22	1:B:69:VAL:HG21	1.98	0.46
1:A:255:TYR:OH	1:A:257:MET:HE2	2.17	0.45
1:B:33:ASP:OD1	1:B:33:ASP:N	2.47	0.45
1:A:134:CYS:SG	1:A:257:MET:HE3	2.57	0.45
1:C:169:ILE:C	1:C:171:GLY:H	2.25	0.45
1:B:173:LYS:N	1:B:194:GLU:O	2.50	0.44
1:C:188:ARG:HG2	1:C:189:ARG:N	2.31	0.44
1:B:10:ILE:HB	1:B:34:MET:HG2	1.99	0.44
1:A:11:ARG:NH1	1:A:68:GLN:O	2.42	0.44
1:A:202:ALA:O	1:A:206:GLU:HG2	2.18	0.44
1:A:71:VAL:HG22	1:A:94:HIS:HB2	2.00	0.43
1:B:176:LEU:HD22	1:B:231:ILE:HD13	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:295:LEU:HD23	1:C:143:PHE:HB3	2.01	0.43
1:A:116:ALA:HB1	1:A:121:ALA:O	2.19	0.42
1:A:157:GLY:HA3	1:A:235:ILE:HG13	2.00	0.42
1:A:210:GLN:HA	1:A:215:VAL:HG22	2.00	0.42
1:A:143:PHE:HB3	1:C:295:LEU:HD23	2.01	0.42
1:B:211:ASP:CG	1:B:212:PRO:HD2	2.45	0.42
1:A:155:GLY:N	1:A:236:ALA:O	2.49	0.41
1:B:41:ARG:NE	2:B:401:NAP:O1X	2.35	0.41
1:A:10:ILE:HB	1:A:34:MET:HG2	2.01	0.41
1:A:238:ARG:NH1	1:A:256:GLU:HG3	2.36	0.41
1:A:98:SER:O	2:A:401:NAP:H2N	2.21	0.41
1:B:155:GLY:N	1:B:236:ALA:O	2.52	0.41
1:C:162:ALA:HB2	1:C:177:ALA:H	1.85	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)
6:B:509:HOH:O	6:C:512:HOH:O[6_545]	1.87	0.33

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	301/347 (87%)	294 (98%)	6 (2%)	1 (0%)	37	53
1	B	305/347 (88%)	299 (98%)	6 (2%)	0	100	100
1	C	301/347 (87%)	289 (96%)	12 (4%)	0	100	100
All	All	907/1041 (87%)	882 (97%)	24 (3%)	1 (0%)	48	67

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	7	GLU

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	251/286 (88%)	246 (98%)	5 (2%)	50	71
1	B	255/286 (89%)	242 (95%)	13 (5%)	20	34
1	C	253/286 (88%)	241 (95%)	12 (5%)	22	37
All	All	759/858 (88%)	729 (96%)	30 (4%)	27	44

All (30) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	52	ARG
1	A	170	GLU
1	A	172	VAL
1	A	256	GLU
1	A	301	GLU
1	B	19	ASN
1	B	44	SER
1	B	63	VAL
1	B	80	GLU
1	B	103	GLN
1	B	129	LEU
1	B	167	LYS
1	B	172	VAL
1	B	195	LEU
1	B	196	GLU
1	B	215	VAL
1	B	216	HIS
1	B	301	GLU
1	C	19	ASN
1	C	103	GLN
1	C	107	GLN
1	C	117	ARG

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Mol	Chain	Res	Type
1	C	129	LEU
1	C	159	SER
1	C	160	MET
1	C	189	ARG
1	C	203	THR
1	C	215	VAL
1	C	220	HIS
1	C	301	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	110	HIS
1	B	120	GLN
1	B	220	HIS

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](#)

15 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	OXM	C	403	-	5,5,5	2.68	1 (20%)	4,6,6	1.30	1 (25%)
5	ACY	A	404	-	3,3,3	1.33	0	3,3,3	1.35	0
4	IMD	A	403	-	3,5,5	0.42	0	4,5,5	0.56	0
2	NAP	B	401	-	45,52,52	1.71	3 (6%)	56,80,80	1.08	2 (3%)
3	OXM	A	402	-	5,5,5	2.62	1 (20%)	4,6,6	1.35	1 (25%)
4	IMD	C	404	-	3,5,5	0.42	0	4,5,5	0.59	0
4	IMD	B	405	-	3,5,5	0.42	0	4,5,5	0.55	0
2	NAP	A	401	-	45,52,52	1.70	3 (6%)	56,80,80	1.04	2 (3%)
2	NAP	C	401	-	45,52,52	1.70	3 (6%)	56,80,80	1.11	2 (3%)
3	OXM	C	402	-	5,5,5	2.62	1 (20%)	4,6,6	1.27	1 (25%)
4	IMD	B	403	-	3,5,5	0.47	0	4,5,5	0.44	0
5	ACY	B	406	-	3,3,3	1.38	1 (33%)	3,3,3	1.44	0
3	OXM	B	402	-	5,5,5	2.64	1 (20%)	4,6,6	1.50	1 (25%)
4	IMD	B	407	-	3,5,5	0.40	0	4,5,5	0.61	0
4	IMD	B	404	-	3,5,5	0.41	0	4,5,5	0.60	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
3	OXM	C	403	-	-	0/3/4/4	-
4	IMD	A	403	-	-	-	0/1/1/1
2	NAP	B	401	-	-	8/31/67/67	0/5/5/5
3	OXM	A	402	-	-	0/3/4/4	-
4	IMD	C	404	-	-	-	0/1/1/1
4	IMD	B	405	-	-	-	0/1/1/1
2	NAP	A	401	-	-	2/31/67/67	0/5/5/5
2	NAP	C	401	-	-	8/31/67/67	0/5/5/5
3	OXM	C	402	-	-	0/3/4/4	-
4	IMD	B	403	-	-	-	0/1/1/1
3	OXM	B	402	-	-	0/3/4/4	-
4	IMD	B	407	-	-	-	0/1/1/1
4	IMD	B	404	-	-	-	0/1/1/1

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	401	NAP	O7N-C7N	9.08	1.41	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	401	NAP	O7N-C7N	9.05	1.41	1.24
2	A	401	NAP	O7N-C7N	9.00	1.41	1.24
3	C	403	OXM	C1-C2	-5.60	1.48	1.55
3	B	402	OXM	C1-C2	-5.54	1.48	1.55
3	A	402	OXM	C1-C2	-5.47	1.48	1.55
3	C	402	OXM	C1-C2	-5.46	1.48	1.55
2	A	401	NAP	C2A-N3A	4.07	1.38	1.32
2	B	401	NAP	C2A-N3A	4.05	1.38	1.32
2	C	401	NAP	C2A-N3A	4.00	1.38	1.32
2	B	401	NAP	C2A-N1A	2.56	1.38	1.33
2	A	401	NAP	C2A-N1A	2.56	1.38	1.33
2	C	401	NAP	C2A-N1A	2.47	1.38	1.33
5	B	406	ACY	CH3-C	2.02	1.57	1.49

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	401	NAP	N3A-C2A-N1A	-5.49	120.10	128.68
2	A	401	NAP	N3A-C2A-N1A	-5.36	120.29	128.68
2	C	401	NAP	N3A-C2A-N1A	-5.34	120.33	128.68
2	C	401	NAP	C3D-C2D-C1D	2.86	105.28	100.98
2	B	401	NAP	C3D-C2D-C1D	2.75	105.12	100.98
2	A	401	NAP	C3D-C2D-C1D	2.74	105.10	100.98
3	B	402	OXM	O3-C2-C1	2.45	119.50	113.84
3	A	402	OXM	O3-C2-C1	2.23	118.99	113.84
3	C	403	OXM	O3-C2-C1	2.14	118.79	113.84
3	C	402	OXM	O3-C2-C1	2.11	118.71	113.84

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	401	NAP	C5D-O5D-PN-O3
2	B	401	NAP	O4D-C4D-C5D-O5D
2	C	401	NAP	C5D-O5D-PN-O3
2	C	401	NAP	C5D-O5D-PN-O1N
2	C	401	NAP	C5D-O5D-PN-O2N
2	C	401	NAP	O4D-C4D-C5D-O5D
2	C	401	NAP	C3D-C4D-C5D-O5D
2	A	401	NAP	O4B-C4B-C5B-O5B
2	B	401	NAP	O4B-C4B-C5B-O5B
2	B	401	NAP	C3D-C4D-C5D-O5D

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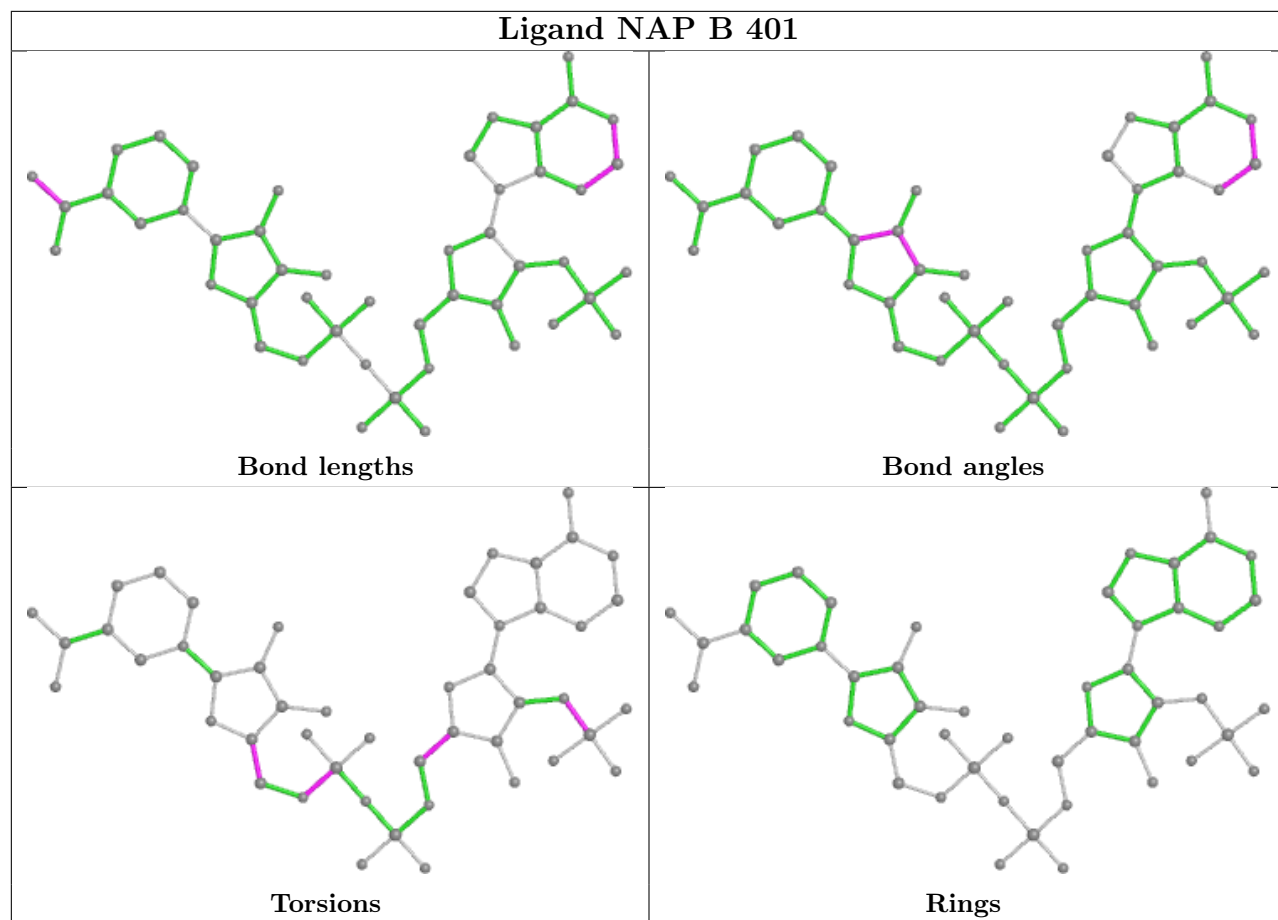
Mol	Chain	Res	Type	Atoms
2	C	401	NAP	O4B-C4B-C5B-O5B
2	C	401	NAP	C3B-C4B-C5B-O5B
2	A	401	NAP	C3B-C4B-C5B-O5B
2	B	401	NAP	C3B-C4B-C5B-O5B
2	B	401	NAP	C2B-O2B-P2B-O2X
2	B	401	NAP	C5D-O5D-PN-O1N
2	B	401	NAP	C5D-O5D-PN-O2N
2	C	401	NAP	C2B-O2B-P2B-O1X

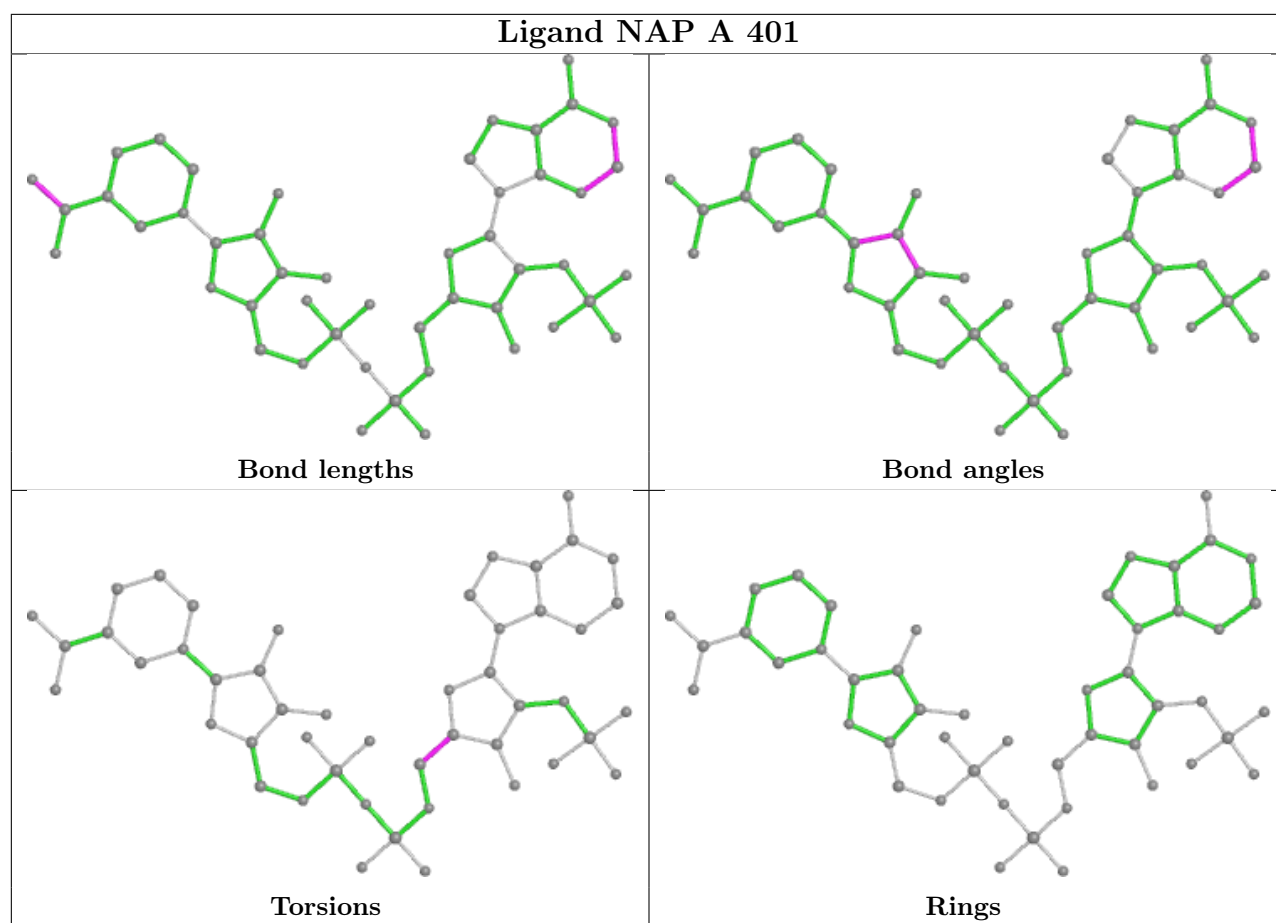
There are no ring outliers.

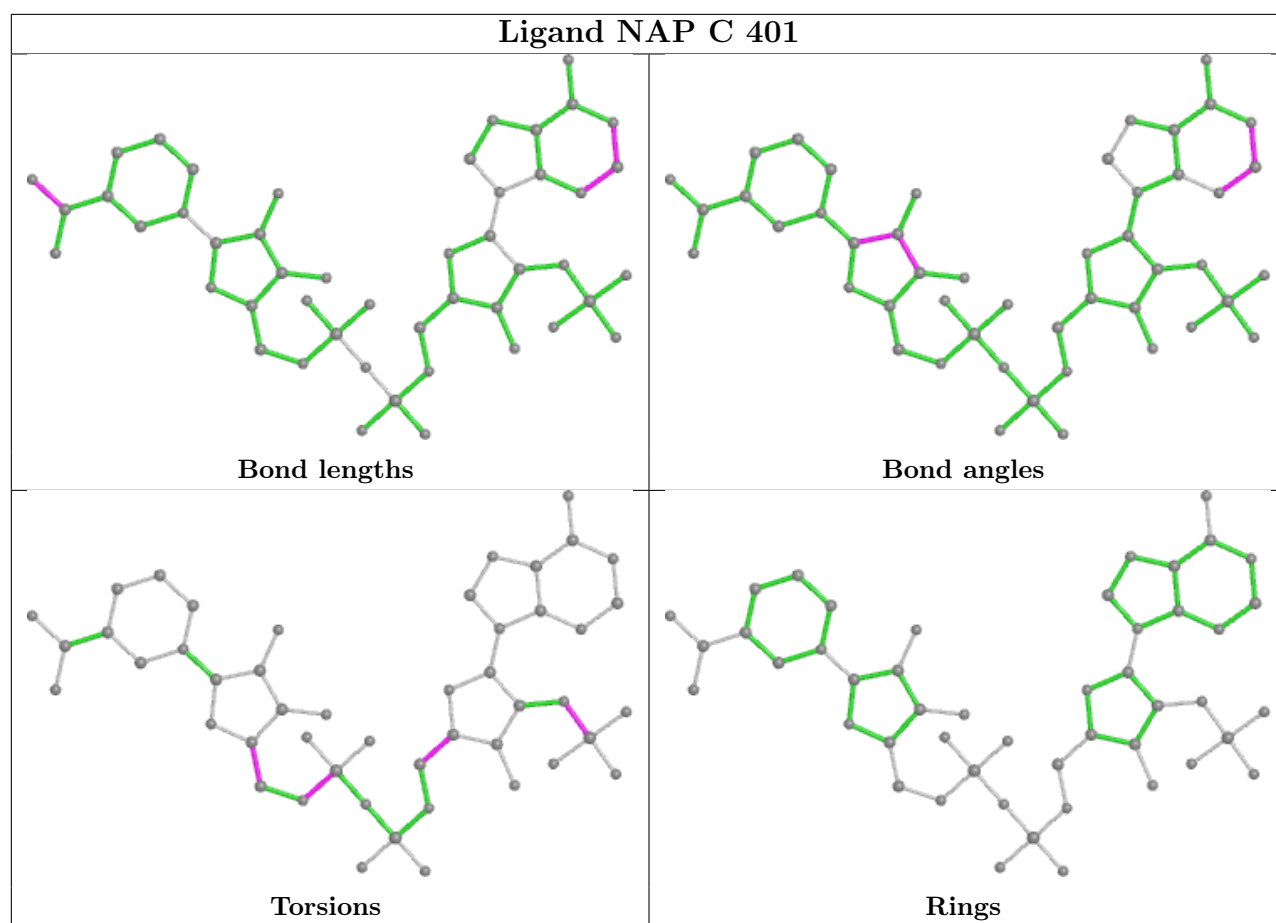
5 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	403	IMD	2	0
2	B	401	NAP	2	0
2	A	401	NAP	2	0
2	C	401	NAP	1	0
4	B	407	IMD	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	303/347 (87%)	0.06	3 (0%) 79 77	44, 56, 102, 122	0
1	B	306/347 (88%)	0.18	19 (6%) 28 25	27, 58, 112, 130	1 (0%)
1	C	305/347 (87%)	0.27	19 (6%) 28 25	41, 62, 115, 140	0
All	All	914/1041 (87%)	0.17	41 (4%) 39 36	27, 59, 111, 140	1 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	169	ILE	6.6
1	C	168	ALA	5.3
1	C	208	ILE	4.2
1	A	199	ALA	3.3
1	C	164	VAL	3.3
1	B	201	PHE	3.3
1	C	171	GLY	3.3
1	C	204	VAL	3.0
1	B	170	GLU	3.0
1	C	214	PHE	2.9
1	B	169	ILE	2.8
1	C	212	PRO	2.8
1	C	195	LEU	2.8
1	B	164	VAL	2.8
1	C	162	ALA	2.8
1	A	214	PHE	2.8
1	B	202	ALA	2.7
1	C	165	ALA	2.7
1	B	212	PRO	2.7
1	C	201	PHE	2.7
1	B	172	VAL	2.6
1	B	199	ALA	2.6
1	B	222	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	B	208	ILE	2.6
1	B	280	LYS	2.5
1	C	166	VAL	2.5
1	C	161	SER	2.4
1	B	214	PHE	2.4
1	C	155	GLY	2.4
1	C	160	MET	2.3
1	A	215	VAL	2.3
1	B	209	LEU	2.3
1	C	193	VAL	2.2
1	B	168	ALA	2.2
1	B	213	LEU	2.2
1	B	204	VAL	2.2
1	B	195	LEU	2.2
1	C	159	SER	2.1
1	C	199	ALA	2.1
1	B	216	HIS	2.0
1	B	207	ARG	2.0

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.

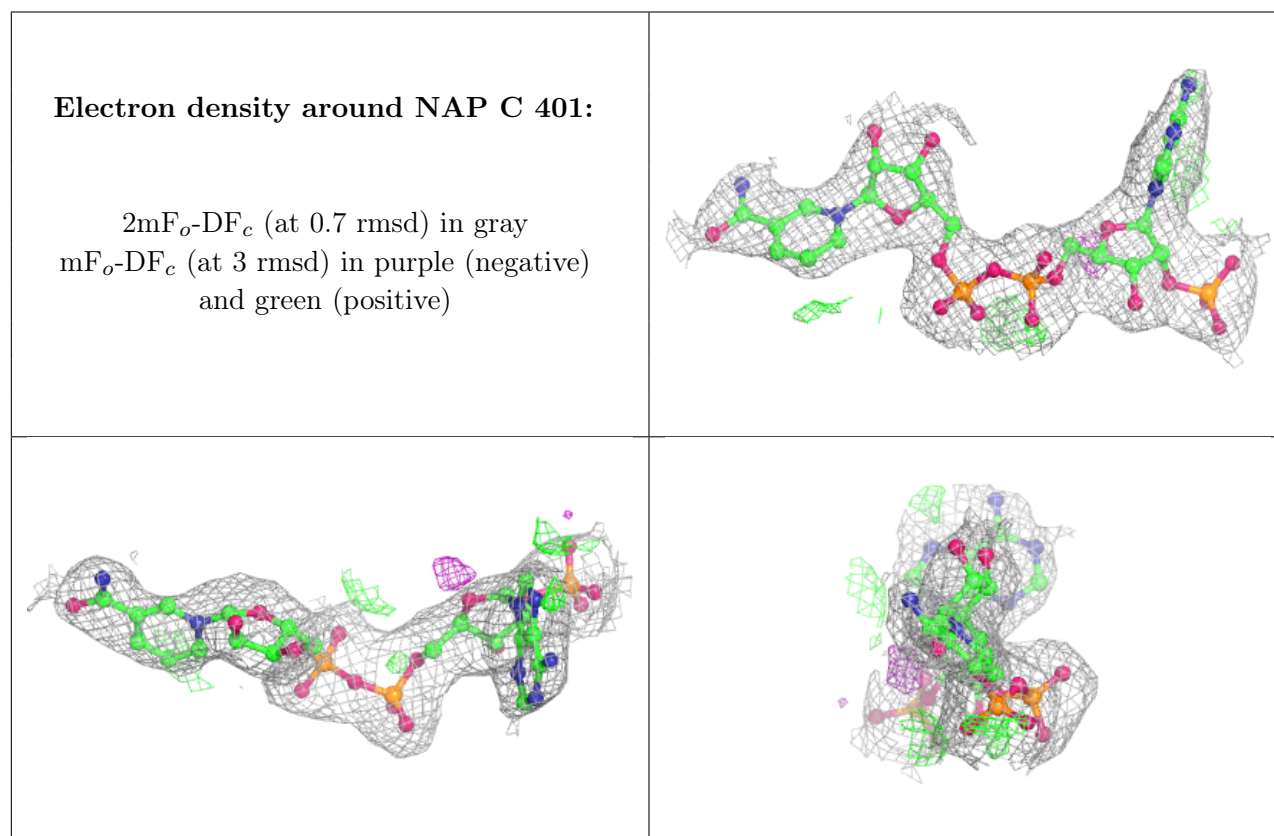
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	IMD	B	407	5/5	0.64	0.26	58,74,86,99	0
3	OXM	A	402	6/6	0.66	0.22	80,90,95,97	0
5	ACY	A	404	4/4	0.66	0.24	59,82,83,86	0
4	IMD	B	404	5/5	0.70	0.32	81,84,89,98	0
3	OXM	C	402	6/6	0.72	0.20	81,95,98,101	0

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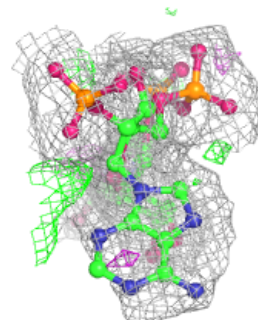
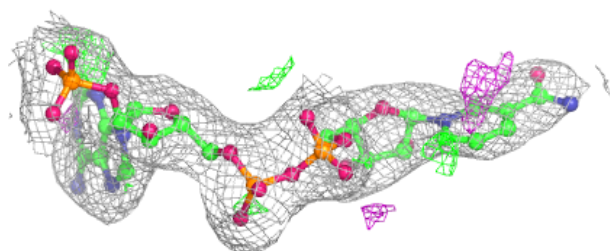
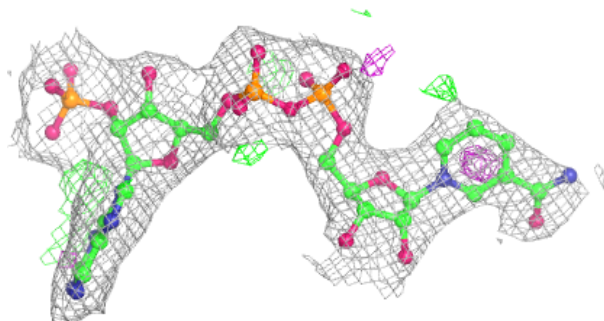
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
4	IMD	B	405	5/5	0.75	0.26	82,82,86,99	0
3	OXM	C	403	6/6	0.81	0.14	56,81,88,88	0
3	OXM	B	402	6/6	0.85	0.17	73,84,85,87	0
4	IMD	A	403	5/5	0.88	0.18	71,74,86,92	0
4	IMD	B	403	5/5	0.88	0.22	58,61,65,69	0
5	ACY	B	406	4/4	0.88	0.17	60,61,63,78	0
4	IMD	C	404	5/5	0.89	0.17	62,62,71,71	0
2	NAP	C	401	48/48	0.90	0.10	56,76,90,92	0
2	NAP	B	401	48/48	0.93	0.10	59,68,82,88	0
2	NAP	A	401	48/48	0.95	0.07	53,65,74,84	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.

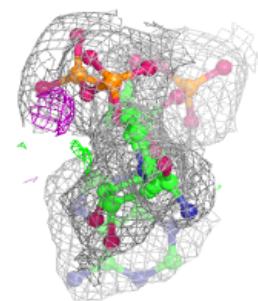
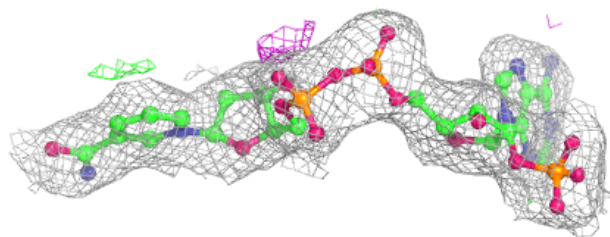
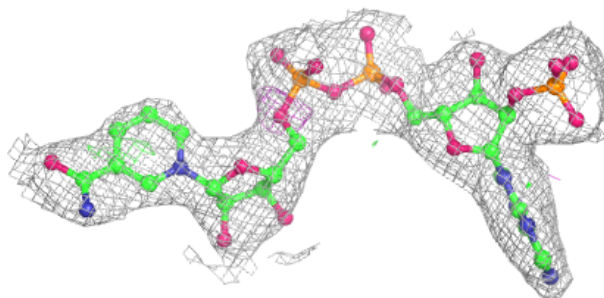


Electron density around NAP B 401:

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

**Electron density around NAP 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.