



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 3, 2023 – 06:12 PM EDT

PDB ID : 3SXP
Title : Crystal Structure of Helicobacter pylori ADP-L-glycero-D-manno-heptose-6-e pimerase (rfaD, HP0859)
Authors : Shaik, M.M.; Zanotti, G.; Cendron, L.
Deposited on : 2011-07-15
Resolution : 2.55 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 : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

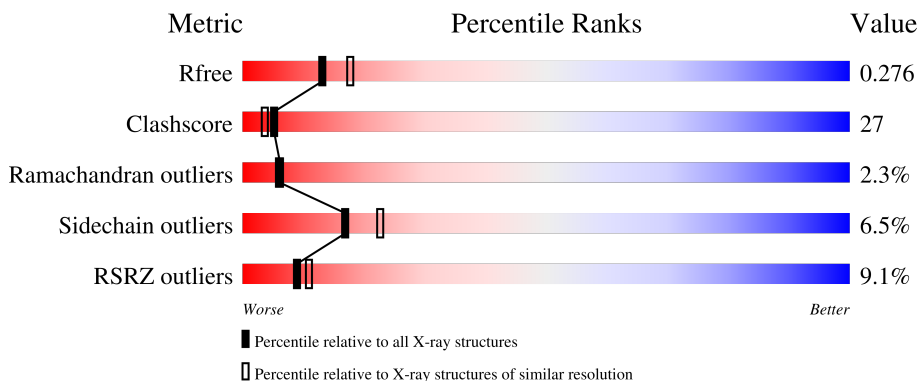
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	362	 7% 43% 38% 14%
1	B	362	 4% 43% 39% 14%
1	C	362	 12% 43% 39% 14%
1	D	362	 8% 45% 38% 13%
1	E	362	 9% 45% 36% 14%

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 12913 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 ADP-L-glycero-D-mannoheptose-6-epimerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	310	2480	1596	416	460	8	0	0	0
1	B	311	2489	1601	418	462	8	0	0	0
1	C	310	2480	1596	416	460	8	0	0	0
1	D	314	2519	1623	422	466	8	0	0	0
1	E	310	2480	1596	416	460	8	0	0	0

There are 165 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	7	GLU	GLY	engineered mutation	UNP B5Z7L9
A	331	LYS	-	expression tag	UNP B5Z7L9
A	332	GLY	-	expression tag	UNP B5Z7L9
A	333	GLU	-	expression tag	UNP B5Z7L9
A	334	LEU	-	expression tag	UNP B5Z7L9
A	335	ASN	-	expression tag	UNP B5Z7L9
A	336	SER	-	expression tag	UNP B5Z7L9
A	337	LYS	-	expression tag	UNP B5Z7L9
A	338	LEU	-	expression tag	UNP B5Z7L9
A	339	GLU	-	expression tag	UNP B5Z7L9
A	340	GLY	-	expression tag	UNP B5Z7L9
A	341	LYS	-	expression tag	UNP B5Z7L9
A	342	PRO	-	expression tag	UNP B5Z7L9
A	343	ILE	-	expression tag	UNP B5Z7L9
A	344	PRO	-	expression tag	UNP B5Z7L9
A	345	ASN	-	expression tag	UNP B5Z7L9
A	346	LEU	-	expression tag	UNP B5Z7L9
A	347	LEU	-	expression tag	UNP B5Z7L9
A	348	GLY	-	expression tag	UNP B5Z7L9

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Chain	Residue	Modelled	Actual	Comment	Reference
A	349	LEU	-	expression tag	UNP B5Z7L9
A	350	ASP	-	expression tag	UNP B5Z7L9
A	351	SER	-	expression tag	UNP B5Z7L9
A	352	THR	-	expression tag	UNP B5Z7L9
A	353	ARG	-	expression tag	UNP B5Z7L9
A	354	THR	-	expression tag	UNP B5Z7L9
A	355	GLY	-	expression tag	UNP B5Z7L9
A	356	HIS	-	expression tag	UNP B5Z7L9
A	357	HIS	-	expression tag	UNP B5Z7L9
A	358	HIS	-	expression tag	UNP B5Z7L9
A	359	HIS	-	expression tag	UNP B5Z7L9
A	360	HIS	-	expression tag	UNP B5Z7L9
A	361	HIS	-	expression tag	UNP B5Z7L9
A	362	HIS	-	expression tag	UNP B5Z7L9
B	7	GLU	GLY	engineered mutation	UNP B5Z7L9
B	331	LYS	-	expression tag	UNP B5Z7L9
B	332	GLY	-	expression tag	UNP B5Z7L9
B	333	GLU	-	expression tag	UNP B5Z7L9
B	334	LEU	-	expression tag	UNP B5Z7L9
B	335	ASN	-	expression tag	UNP B5Z7L9
B	336	SER	-	expression tag	UNP B5Z7L9
B	337	LYS	-	expression tag	UNP B5Z7L9
B	338	LEU	-	expression tag	UNP B5Z7L9
B	339	GLU	-	expression tag	UNP B5Z7L9
B	340	GLY	-	expression tag	UNP B5Z7L9
B	341	LYS	-	expression tag	UNP B5Z7L9
B	342	PRO	-	expression tag	UNP B5Z7L9
B	343	ILE	-	expression tag	UNP B5Z7L9
B	344	PRO	-	expression tag	UNP B5Z7L9
B	345	ASN	-	expression tag	UNP B5Z7L9
B	346	LEU	-	expression tag	UNP B5Z7L9
B	347	LEU	-	expression tag	UNP B5Z7L9
B	348	GLY	-	expression tag	UNP B5Z7L9
B	349	LEU	-	expression tag	UNP B5Z7L9
B	350	ASP	-	expression tag	UNP B5Z7L9
B	351	SER	-	expression tag	UNP B5Z7L9
B	352	THR	-	expression tag	UNP B5Z7L9
B	353	ARG	-	expression tag	UNP B5Z7L9
B	354	THR	-	expression tag	UNP B5Z7L9
B	355	GLY	-	expression tag	UNP B5Z7L9
B	356	HIS	-	expression tag	UNP B5Z7L9
B	357	HIS	-	expression tag	UNP B5Z7L9

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Chain	Residue	Modelled	Actual	Comment	Reference
B	358	HIS	-	expression tag	UNP B5Z7L9
B	359	HIS	-	expression tag	UNP B5Z7L9
B	360	HIS	-	expression tag	UNP B5Z7L9
B	361	HIS	-	expression tag	UNP B5Z7L9
B	362	HIS	-	expression tag	UNP B5Z7L9
C	7	GLU	GLY	engineered mutation	UNP B5Z7L9
C	331	LYS	-	expression tag	UNP B5Z7L9
C	332	GLY	-	expression tag	UNP B5Z7L9
C	333	GLU	-	expression tag	UNP B5Z7L9
C	334	LEU	-	expression tag	UNP B5Z7L9
C	335	ASN	-	expression tag	UNP B5Z7L9
C	336	SER	-	expression tag	UNP B5Z7L9
C	337	LYS	-	expression tag	UNP B5Z7L9
C	338	LEU	-	expression tag	UNP B5Z7L9
C	339	GLU	-	expression tag	UNP B5Z7L9
C	340	GLY	-	expression tag	UNP B5Z7L9
C	341	LYS	-	expression tag	UNP B5Z7L9
C	342	PRO	-	expression tag	UNP B5Z7L9
C	343	ILE	-	expression tag	UNP B5Z7L9
C	344	PRO	-	expression tag	UNP B5Z7L9
C	345	ASN	-	expression tag	UNP B5Z7L9
C	346	LEU	-	expression tag	UNP B5Z7L9
C	347	LEU	-	expression tag	UNP B5Z7L9
C	348	GLY	-	expression tag	UNP B5Z7L9
C	349	LEU	-	expression tag	UNP B5Z7L9
C	350	ASP	-	expression tag	UNP B5Z7L9
C	351	SER	-	expression tag	UNP B5Z7L9
C	352	THR	-	expression tag	UNP B5Z7L9
C	353	ARG	-	expression tag	UNP B5Z7L9
C	354	THR	-	expression tag	UNP B5Z7L9
C	355	GLY	-	expression tag	UNP B5Z7L9
C	356	HIS	-	expression tag	UNP B5Z7L9
C	357	HIS	-	expression tag	UNP B5Z7L9
C	358	HIS	-	expression tag	UNP B5Z7L9
C	359	HIS	-	expression tag	UNP B5Z7L9
C	360	HIS	-	expression tag	UNP B5Z7L9
C	361	HIS	-	expression tag	UNP B5Z7L9
C	362	HIS	-	expression tag	UNP B5Z7L9
D	7	GLU	GLY	engineered mutation	UNP B5Z7L9
D	331	LYS	-	expression tag	UNP B5Z7L9
D	332	GLY	-	expression tag	UNP B5Z7L9
D	333	GLU	-	expression tag	UNP B5Z7L9

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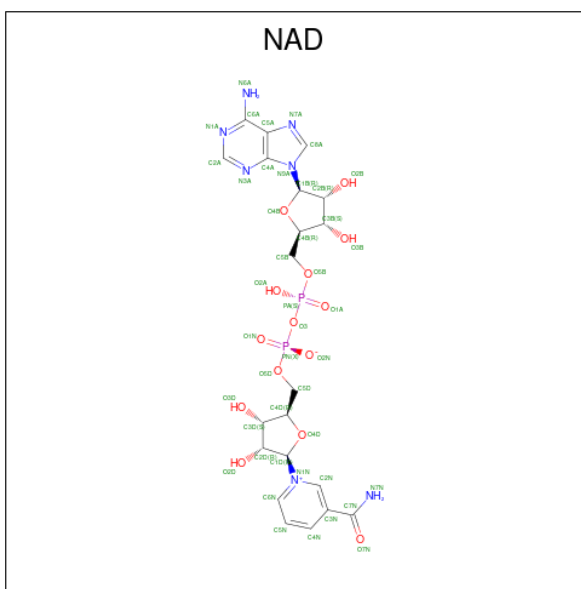
Chain	Residue	Modelled	Actual	Comment	Reference
D	334	LEU	-	expression tag	UNP B5Z7L9
D	335	ASN	-	expression tag	UNP B5Z7L9
D	336	SER	-	expression tag	UNP B5Z7L9
D	337	LYS	-	expression tag	UNP B5Z7L9
D	338	LEU	-	expression tag	UNP B5Z7L9
D	339	GLU	-	expression tag	UNP B5Z7L9
D	340	GLY	-	expression tag	UNP B5Z7L9
D	341	LYS	-	expression tag	UNP B5Z7L9
D	342	PRO	-	expression tag	UNP B5Z7L9
D	343	ILE	-	expression tag	UNP B5Z7L9
D	344	PRO	-	expression tag	UNP B5Z7L9
D	345	ASN	-	expression tag	UNP B5Z7L9
D	346	LEU	-	expression tag	UNP B5Z7L9
D	347	LEU	-	expression tag	UNP B5Z7L9
D	348	GLY	-	expression tag	UNP B5Z7L9
D	349	LEU	-	expression tag	UNP B5Z7L9
D	350	ASP	-	expression tag	UNP B5Z7L9
D	351	SER	-	expression tag	UNP B5Z7L9
D	352	THR	-	expression tag	UNP B5Z7L9
D	353	ARG	-	expression tag	UNP B5Z7L9
D	354	THR	-	expression tag	UNP B5Z7L9
D	355	GLY	-	expression tag	UNP B5Z7L9
D	356	HIS	-	expression tag	UNP B5Z7L9
D	357	HIS	-	expression tag	UNP B5Z7L9
D	358	HIS	-	expression tag	UNP B5Z7L9
D	359	HIS	-	expression tag	UNP B5Z7L9
D	360	HIS	-	expression tag	UNP B5Z7L9
D	361	HIS	-	expression tag	UNP B5Z7L9
D	362	HIS	-	expression tag	UNP B5Z7L9
E	7	GLU	GLY	engineered mutation	UNP B5Z7L9
E	331	LYS	-	expression tag	UNP B5Z7L9
E	332	GLY	-	expression tag	UNP B5Z7L9
E	333	GLU	-	expression tag	UNP B5Z7L9
E	334	LEU	-	expression tag	UNP B5Z7L9
E	335	ASN	-	expression tag	UNP B5Z7L9
E	336	SER	-	expression tag	UNP B5Z7L9
E	337	LYS	-	expression tag	UNP B5Z7L9
E	338	LEU	-	expression tag	UNP B5Z7L9
E	339	GLU	-	expression tag	UNP B5Z7L9
E	340	GLY	-	expression tag	UNP B5Z7L9
E	341	LYS	-	expression tag	UNP B5Z7L9
E	342	PRO	-	expression tag	UNP B5Z7L9

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Chain	Residue	Modelled	Actual	Comment	Reference
E	343	ILE	-	expression tag	UNP B5Z7L9
E	344	PRO	-	expression tag	UNP B5Z7L9
E	345	ASN	-	expression tag	UNP B5Z7L9
E	346	LEU	-	expression tag	UNP B5Z7L9
E	347	LEU	-	expression tag	UNP B5Z7L9
E	348	GLY	-	expression tag	UNP B5Z7L9
E	349	LEU	-	expression tag	UNP B5Z7L9
E	350	ASP	-	expression tag	UNP B5Z7L9
E	351	SER	-	expression tag	UNP B5Z7L9
E	352	THR	-	expression tag	UNP B5Z7L9
E	353	ARG	-	expression tag	UNP B5Z7L9
E	354	THR	-	expression tag	UNP B5Z7L9
E	355	GLY	-	expression tag	UNP B5Z7L9
E	356	HIS	-	expression tag	UNP B5Z7L9
E	357	HIS	-	expression tag	UNP B5Z7L9
E	358	HIS	-	expression tag	UNP B5Z7L9
E	359	HIS	-	expression tag	UNP B5Z7L9
E	360	HIS	-	expression tag	UNP B5Z7L9
E	361	HIS	-	expression tag	UNP B5Z7L9
E	362	HIS	-	expression tag	UNP B5Z7L9

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



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

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

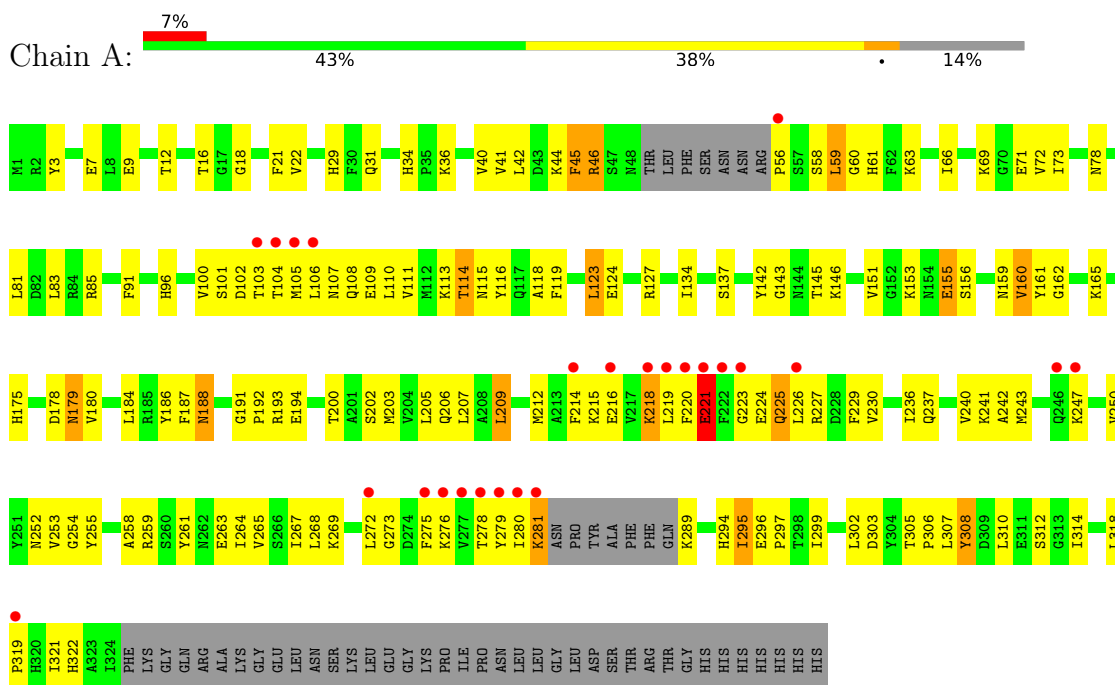
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	68	Total	O	0	0
			68	68		
3	B	56	Total	O	0	0
			56	56		
3	C	36	Total	O	0	0
			36	36		
3	D	43	Total	O	0	0
			43	43		
3	E	42	Total	O	0	0
			42	42		

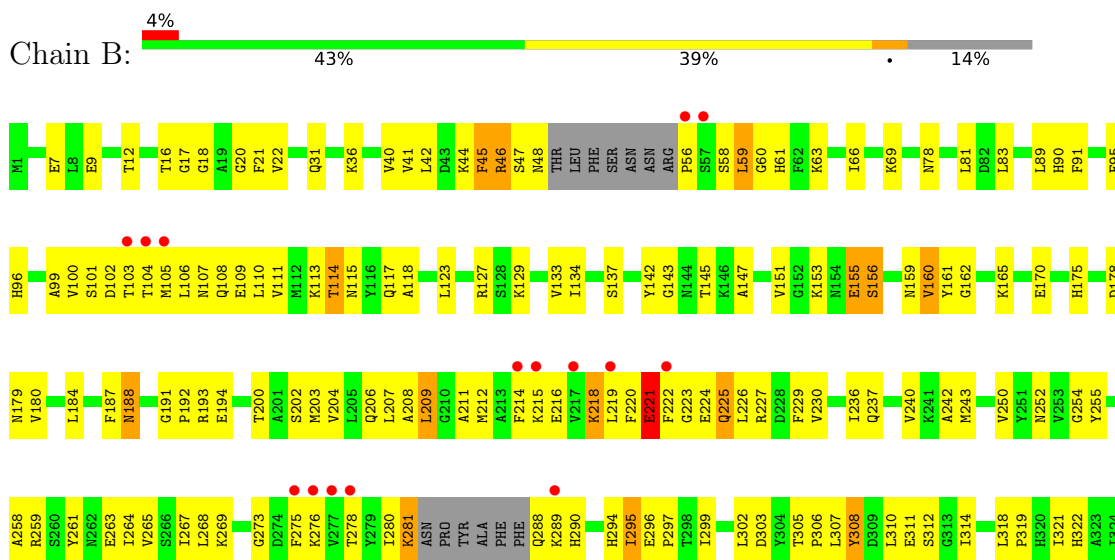
3 Residue-property plots [i](#)

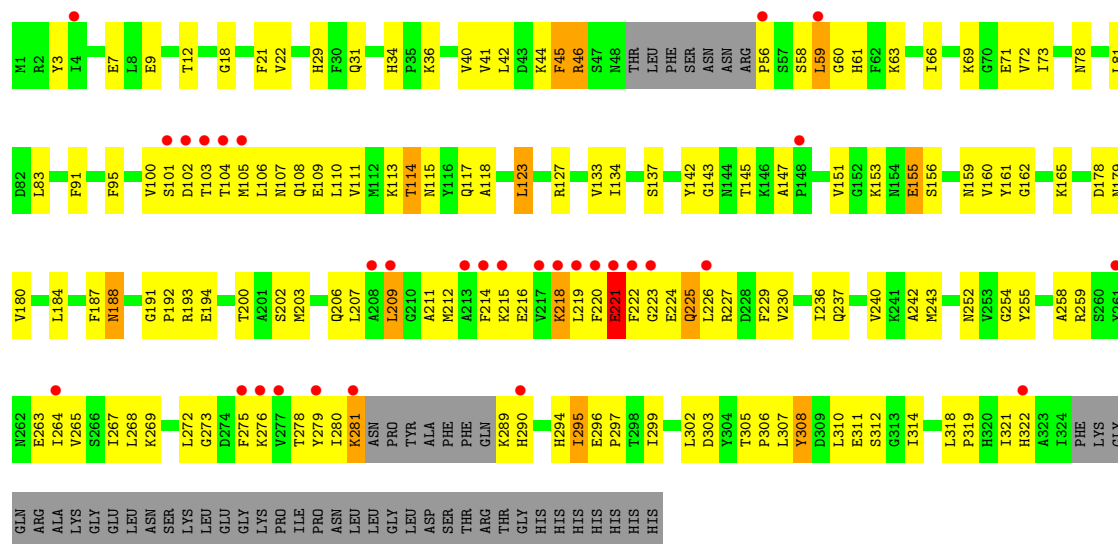
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: ADP-L-glycero-D-mannoheptose-6-epimerase



- Molecule 1: ADP-L-glycero-D-mannoheptose-6-epimerase





4 Data and refinement statistics

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	130.94Å 106.77Å 152.22Å 90.00° 108.35° 90.00°	Depositor
Resolution (Å)	53.39 – 2.55 53.38 – 2.55	Depositor EDS
% Data completeness (in resolution range)	85.6 (53.39-2.55) 85.6 (53.38-2.55)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.48 (at 2.55Å)	Xtrriage
Refinement program	CNS 1.3	Depositor
R, R_{free}	0.239 , 0.279 0.238 , 0.276	Depositor DCC
R_{free} test set	2808 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	46.0	Xtrriage
Anisotropy	0.080	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.36 , 76.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	12913	wwPDB-VP
Average B, all atoms (Å ²)	50.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.42% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality [i](#)

5.1 Standard geometry [i](#)

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

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	0.47	0/2532	0.66	1/3415 (0.0%)
1	B	0.47	0/2541	0.66	0/3427
1	C	0.48	0/2532	0.66	0/3415
1	D	0.47	0/2573	0.67	1/3470 (0.0%)
1	E	0.49	0/2532	0.67	0/3415
All	All	0.48	0/12710	0.66	2/17142 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	307	LEU	N-CA-C	-5.21	96.93	111.00
1	A	294	HIS	N-CA-C	-5.01	97.48	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	2480	0	2469	136	0
1	B	2489	0	2477	136	0
1	C	2480	0	2469	138	0
1	D	2519	0	2501	138	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	2480	0	2469	134	0
2	A	44	0	26	3	0
2	B	44	0	26	6	0
2	C	44	0	26	4	0
2	D	44	0	25	4	0
2	E	44	0	26	5	0
3	A	68	0	0	7	0
3	B	56	0	0	4	0
3	C	36	0	0	5	0
3	D	43	0	0	3	0
3	E	42	0	0	3	0
All	All	12913	0	12514	671	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 27.

The worst 5 of 671 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:59:LEU:HD21	1:C:101:SER:CB	1.61	1.31
1:B:59:LEU:CD2	1:B:101:SER:HB3	1.63	1.29
1:B:59:LEU:HD21	1:B:101:SER:CB	1.75	1.17
1:C:59:LEU:HD21	1:C:101:SER:HB3	1.28	1.14
1:C:59:LEU:HD21	1:C:101:SER:HB2	1.39	1.04

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	304/362 (84%)	267 (88%)	31 (10%)	6 (2%)	7 8

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	305/362 (84%)	269 (88%)	29 (10%)	7 (2%)	6	6
1	C	304/362 (84%)	268 (88%)	29 (10%)	7 (2%)	6	6
1	D	308/362 (85%)	271 (88%)	29 (9%)	8 (3%)	5	5
1	E	304/362 (84%)	267 (88%)	30 (10%)	7 (2%)	6	6
All	All	1525/1810 (84%)	1342 (88%)	148 (10%)	35 (2%)	6	6

5 of 35 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	45	PHE
1	A	221	GLU
1	B	45	PHE
1	B	221	GLU
1	C	45	PHE

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	268/313 (86%)	249 (93%)	19 (7%)	14	19
1	B	269/313 (86%)	251 (93%)	18 (7%)	16	21
1	C	268/313 (86%)	250 (93%)	18 (7%)	16	21
1	D	272/313 (87%)	255 (94%)	17 (6%)	18	23
1	E	268/313 (86%)	252 (94%)	16 (6%)	19	25
All	All	1345/1565 (86%)	1257 (94%)	88 (6%)	17	23

5 of 88 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	83	LEU
1	D	295	ILE
1	D	123	LEU
1	D	224	GLU

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Mol	Chain	Res	Type
1	E	83	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 80 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	181	GLN
1	E	159	ASN
1	D	237	GLN
1	D	290	HIS
1	E	239	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](#)

5 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	NAD	A	2402	-	42,48,48	1.28	4 (9%)	50,73,73	1.47	7 (14%)
2	NAD	C	2403	-	42,48,48	1.15	4 (9%)	50,73,73	1.55	8 (16%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	NAD	B	2401	-	42,48,48	1.44	5 (11%)	50,73,73	1.60	9 (18%)
2	NAD	E	2403	-	42,48,48	1.14	5 (11%)	50,73,73	1.51	8 (16%)
2	NAD	D	2401	-	42,48,48	1.22	5 (11%)	50,73,73	1.69	9 (18%)

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	A	2402	-	-	8/26/62/62	0/5/5/5
2	NAD	C	2403	-	-	6/26/62/62	0/5/5/5
2	NAD	B	2401	-	-	9/26/62/62	0/5/5/5
2	NAD	E	2403	-	-	7/26/62/62	0/5/5/5
2	NAD	D	2401	-	-	6/26/62/62	0/5/5/5

The worst 5 of 23 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	2401	NAD	O3D-C3D	5.74	1.56	1.43
2	E	2403	NAD	C2N-N1N	4.61	1.40	1.35
2	B	2401	NAD	C2N-N1N	4.57	1.40	1.35
2	C	2403	NAD	C2N-N1N	4.50	1.40	1.35
2	A	2402	NAD	C2N-N1N	4.45	1.40	1.35

The worst 5 of 41 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	2401	NAD	O4B-C1B-C2B	-5.65	98.67	106.93
2	C	2403	NAD	O3D-C3D-C2D	5.15	128.47	111.82
2	D	2401	NAD	O3D-C3D-C2D	5.00	127.99	111.82
2	B	2401	NAD	O4B-C1B-C2B	-4.56	100.26	106.93
2	E	2403	NAD	O3D-C3D-C2D	4.49	126.36	111.82

There are no chirality outliers.

5 of 36 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	2402	NAD	C5B-O5B-PA-O1A
2	A	2402	NAD	C5D-O5D-PN-O2N

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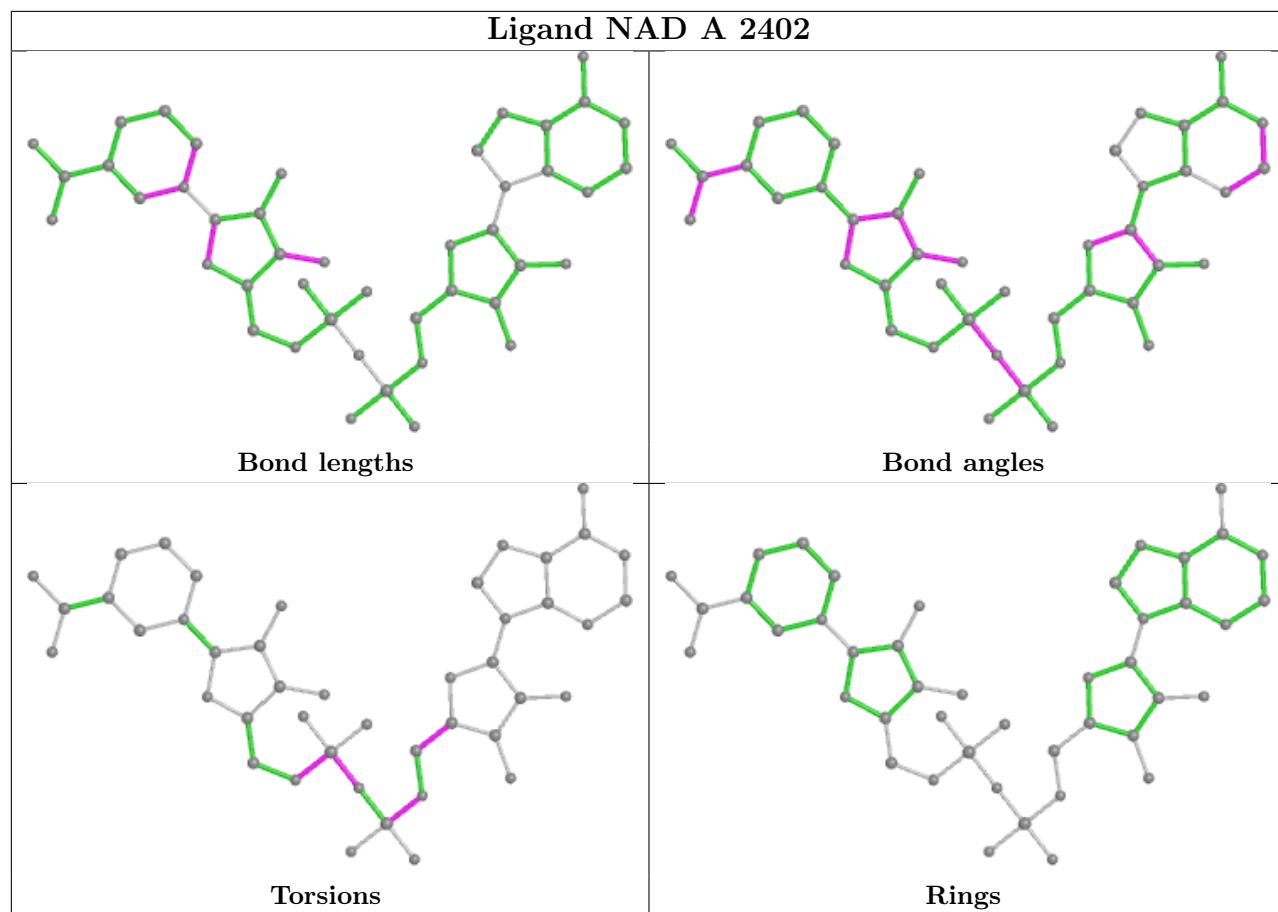
Mol	Chain	Res	Type	Atoms
2	B	2401	NAD	C5B-O5B-PA-O2A
2	B	2401	NAD	C5D-O5D-PN-O2N
2	C	2403	NAD	C5D-O5D-PN-O1N

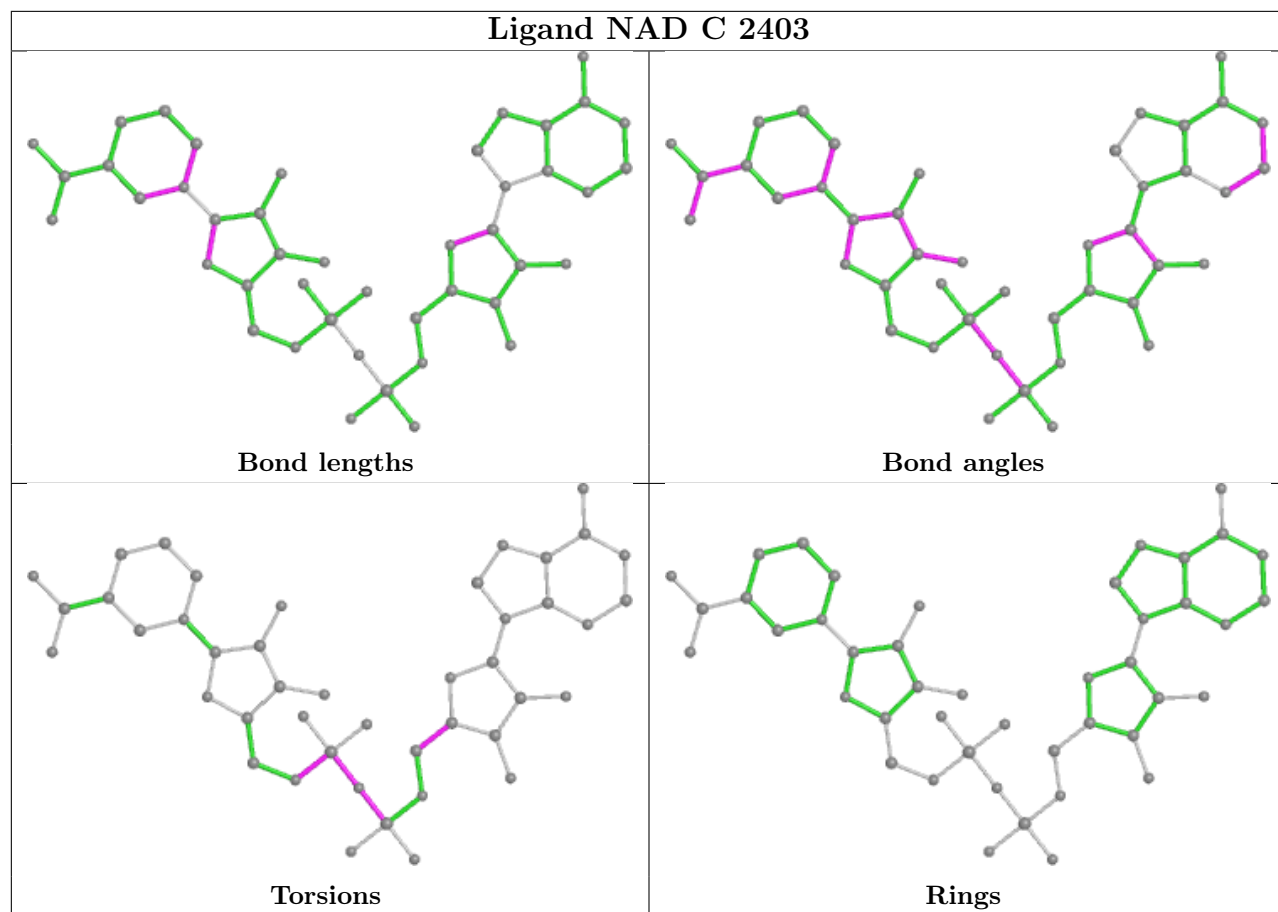
There are no ring outliers.

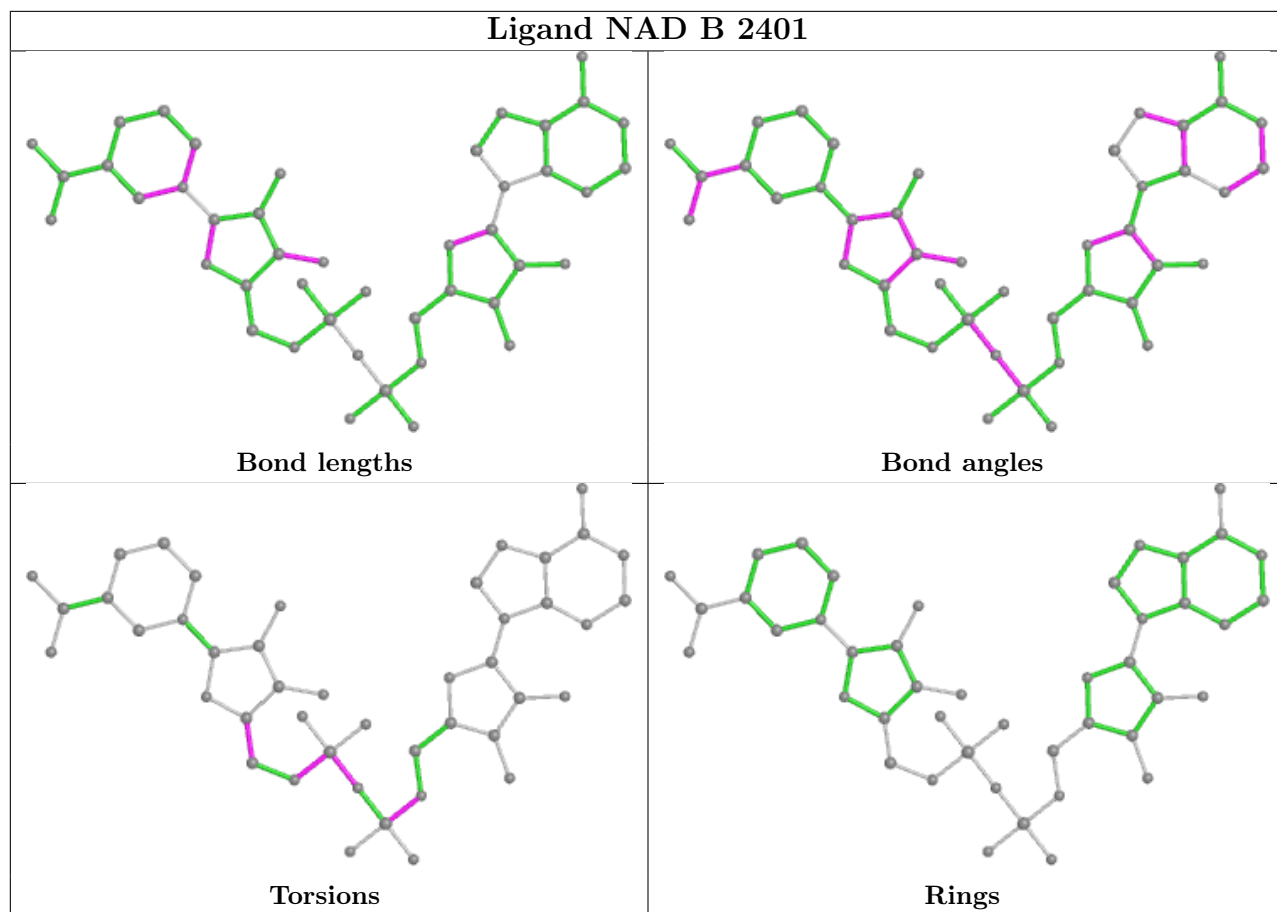
5 monomers are involved in 22 short contacts:

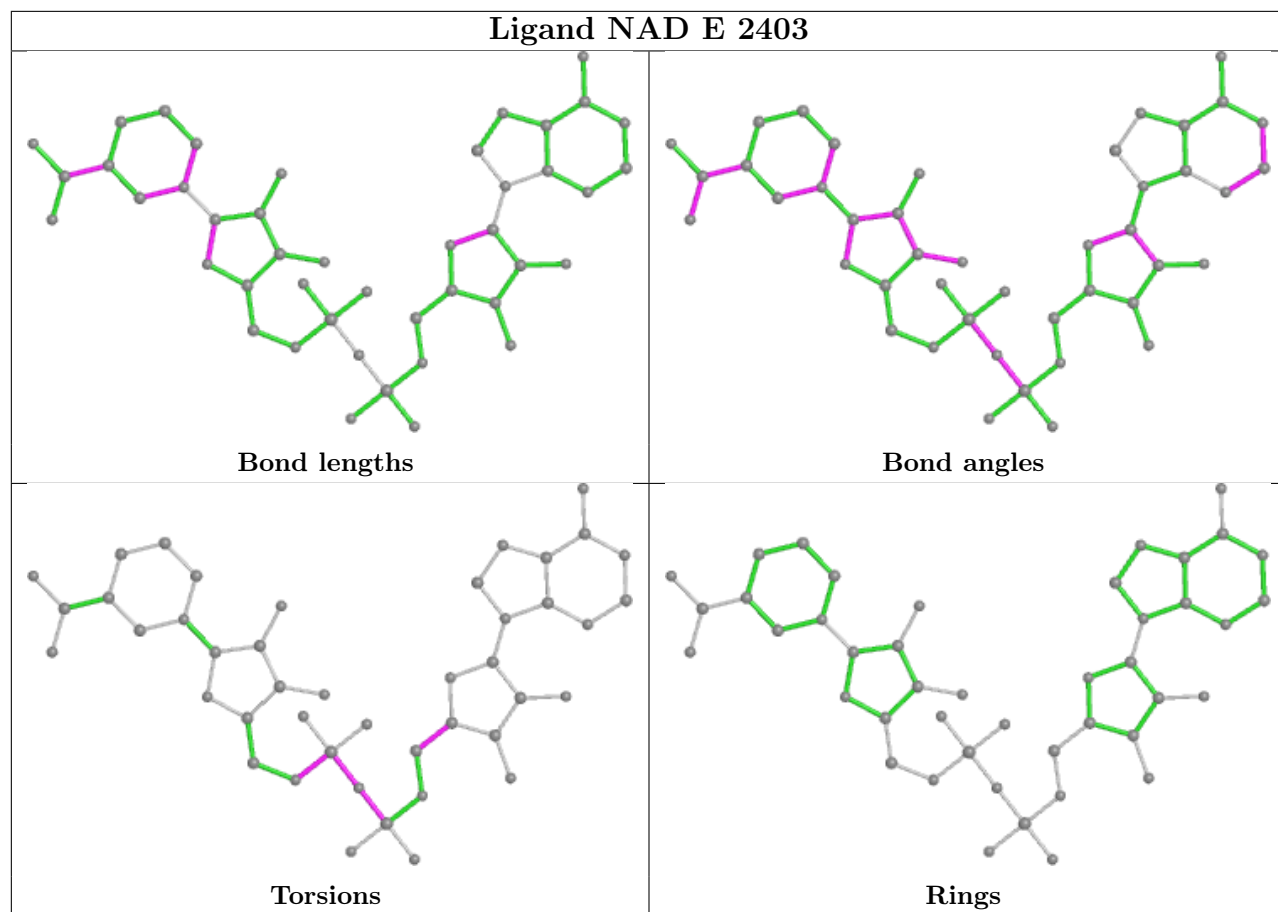
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	2402	NAD	3	0
2	C	2403	NAD	4	0
2	B	2401	NAD	6	0
2	E	2403	NAD	5	0
2	D	2401	NAD	4	0

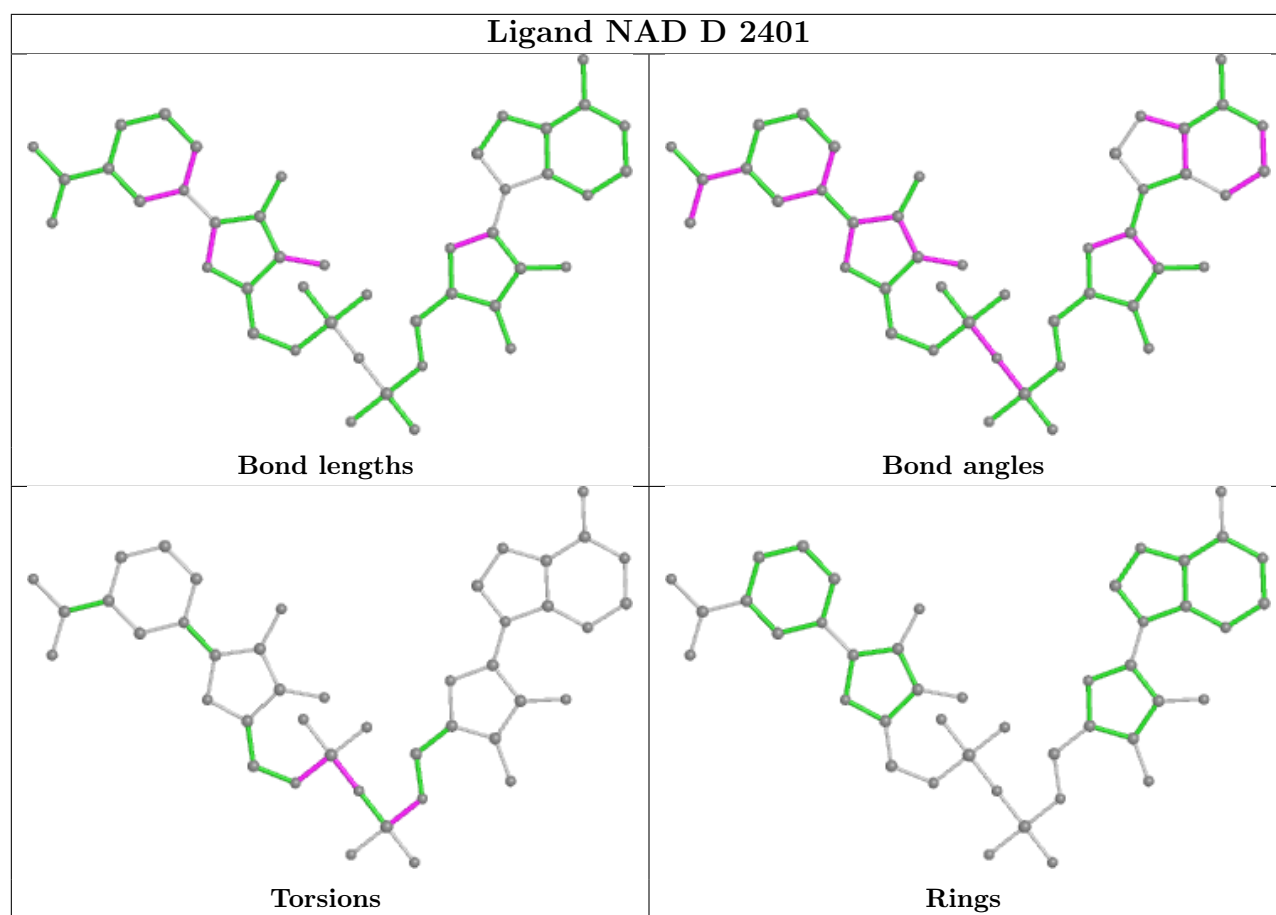
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 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	310/362 (85%)	0.65	25 (8%) 12 15	27, 46, 86, 100	0
1	B	311/362 (85%)	0.49	15 (4%) 30 37	26, 46, 87, 100	0
1	C	310/362 (85%)	0.71	43 (13%) 2 3	29, 48, 87, 102	0
1	D	314/362 (86%)	0.62	28 (8%) 9 11	27, 47, 88, 101	0
1	E	310/362 (85%)	0.61	31 (10%) 7 9	30, 48, 87, 101	0
All	All	1555/1810 (85%)	0.62	142 (9%) 9 11	26, 47, 88, 102	0

The worst 5 of 142 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	104	THR	7.8
1	D	222	PHE	7.6
1	A	104	THR	7.4
1	A	56	PRO	6.5
1	E	220	PHE	6.3

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.

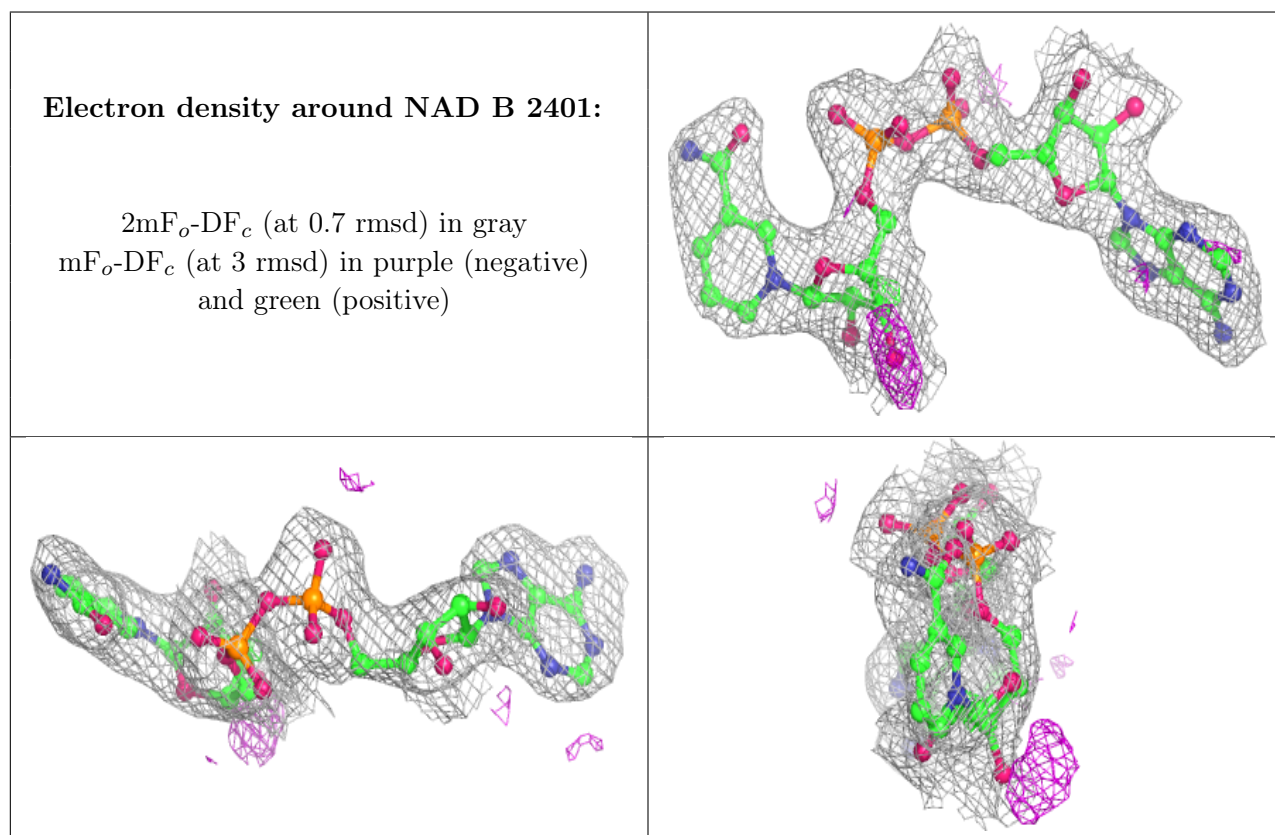
6.4 Ligands [i](#)

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, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

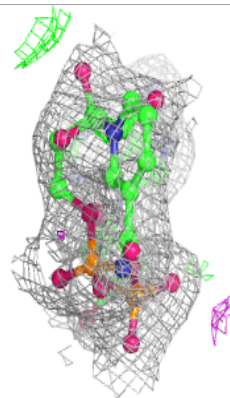
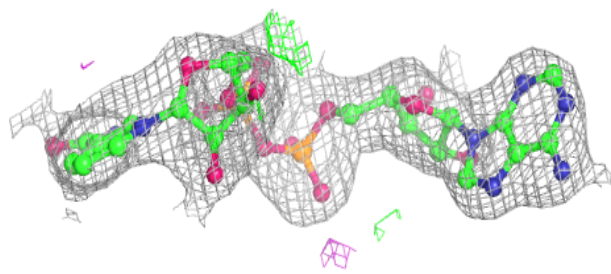
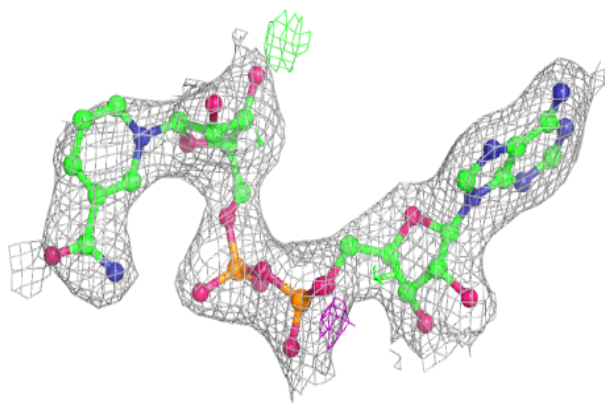
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	NAD	B	2401	44/44	0.96	0.17	35,39,51,53	0
2	NAD	C	2403	44/44	0.96	0.18	40,51,62,63	0
2	NAD	D	2401	44/44	0.96	0.17	27,35,45,49	0
2	NAD	E	2403	44/44	0.96	0.14	43,47,57,58	0
2	NAD	A	2402	44/44	0.97	0.15	30,35,44,49	0

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.

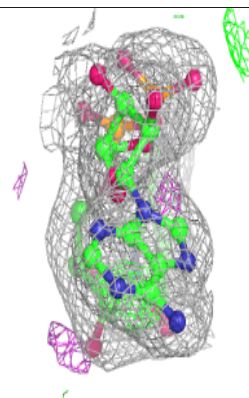
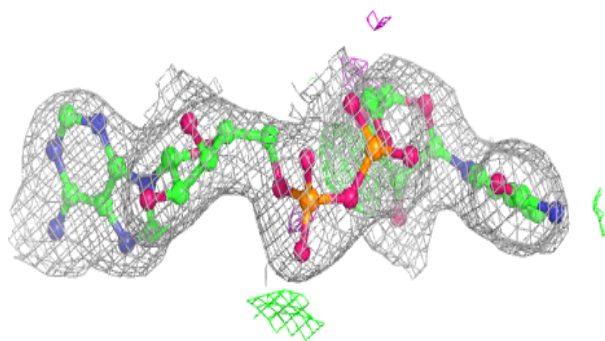
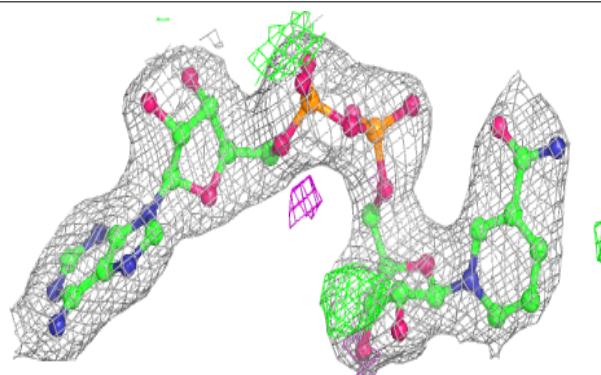


Electron density around NAD C 2403:

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

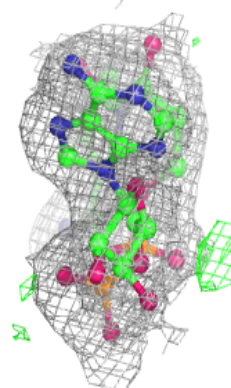
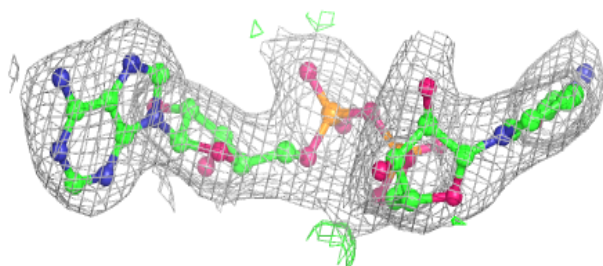
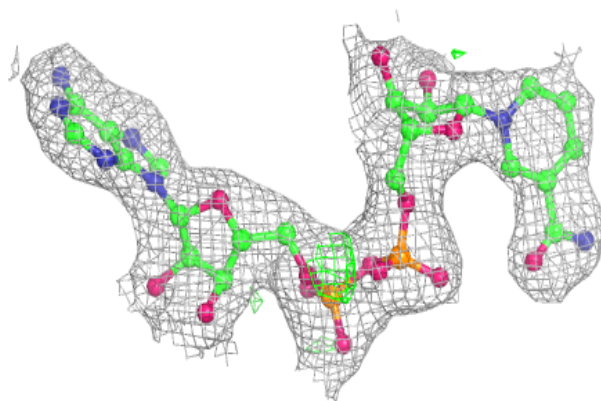
**Electron density around NAD D 2401:**

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

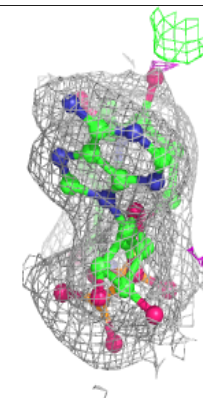
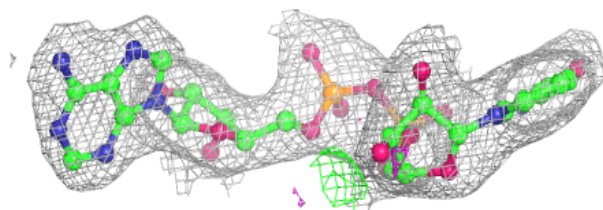
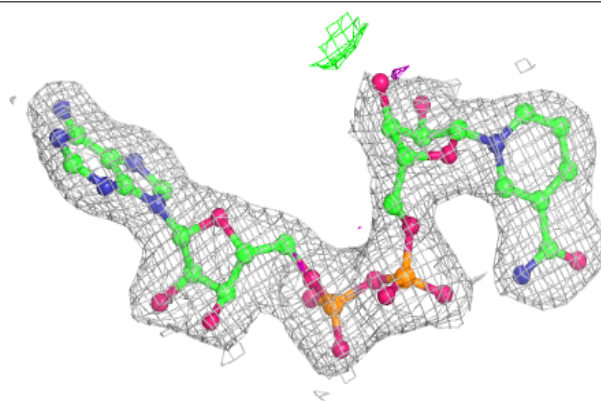


Electron density around NAD E 2403:

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

**Electron density around NAD A 2402:**

$2mF_o-DF_c$ (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.