



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 07:07 AM UTC

PDB ID : 4I4B / pdb_00004i4b
Title : HMG-CoA Reductase from *Pseudomonas mevalonii* complexed with NAD and intermediate hemiacetal form of HMG-CoA
Authors : Stauffacher, C.V.; Steussy, C.N.; Critchelow, C.J.; Schmidt, T.; Min, J.; Wrensford, L.V.; Burgner, J.W.; Rodwell, V.W.
Deposited on : 2012-11-27
Resolution : 1.70 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 Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

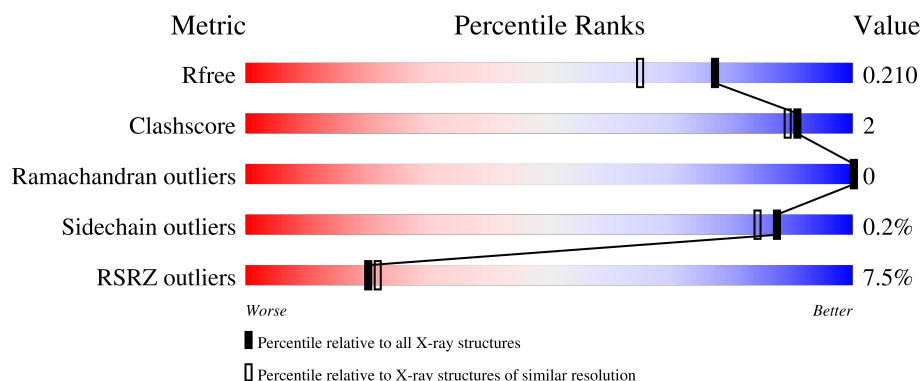
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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}	180053	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	428	8% 93%
1	B	428	6% 84% 12%

2 Entry composition [i](#)

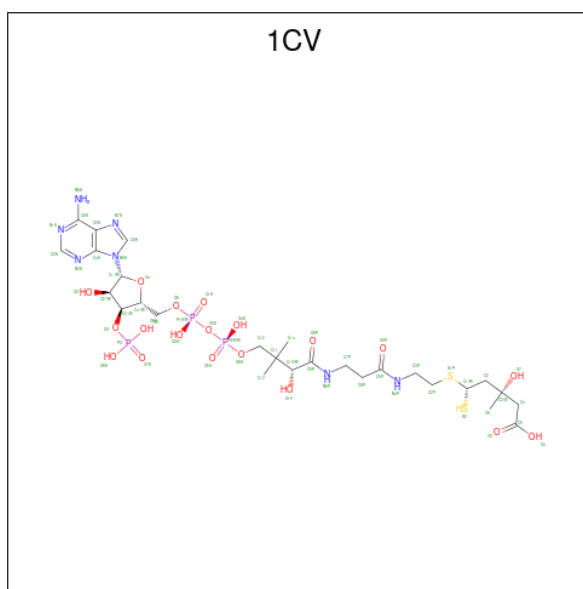
There are 7 unique types of molecules in this entry. The entry contains 6745 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 3-hydroxy-3-methylglutaryl-coenzyme A reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	410	Total	C	N	O	S	0	2	0
			3064	1916	562	569	17			
1	B	376	Total	C	N	O	S	0	0	0
			2791	1748	504	525	14			

- Molecule 2 is (3R,5R,9R,19R,21S)-1-[(2R,3S,4R,5R)-5-(6-amino-9H-purin-9-yl)-4-hydroxy-3-(phosphonooxy)tetrahydrofuran-2-yl]-3,5,9,21-tetrahydroxy-8,8,21-trimethyl-10,14-dioxo-19-sulfanyl-2,4,6-trioxa-18-thia-11,15-diaza-3,5-diphosphatricosan-23-oic acid 3,5-dioxide (CCD ID: 1CV) (formula: C₂₇H₄₆N₇O₁₉P₃S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P S	0	0
			58	27	7	19	3 2		

- Molecule 3 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



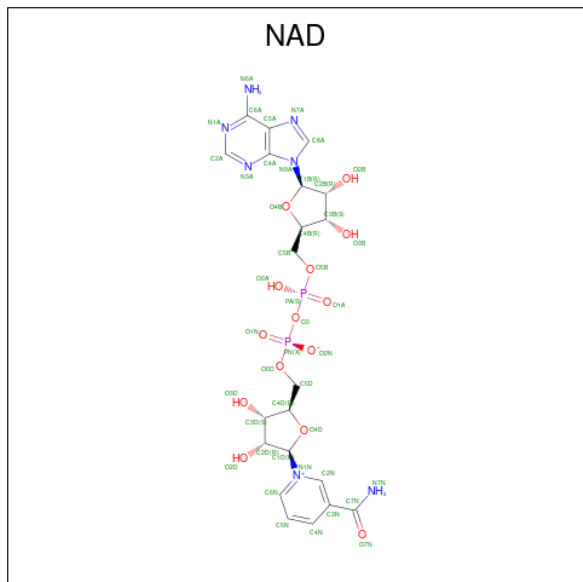
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



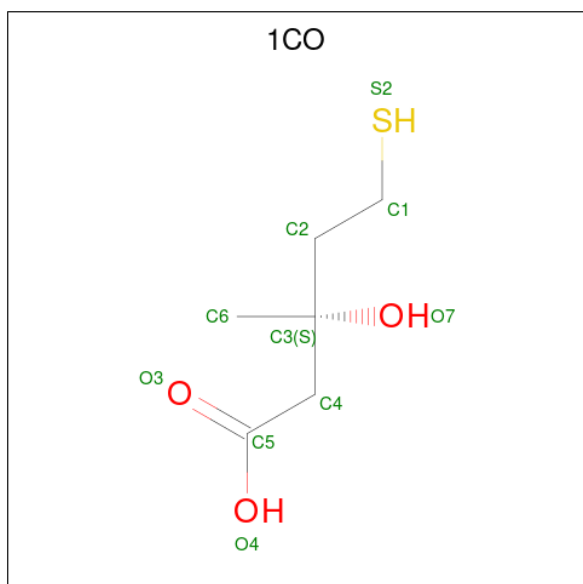
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 5 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (CCD ID: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).



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

- Molecule 6 is (3S)-3-hydroxy-3-methyl-5-sulfanylpentanoic acid (CCD ID: 1CO) (formula: $C_6H_{12}O_3S$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	B	1	Total	C	O	S	0	0
			10	6	3	1		

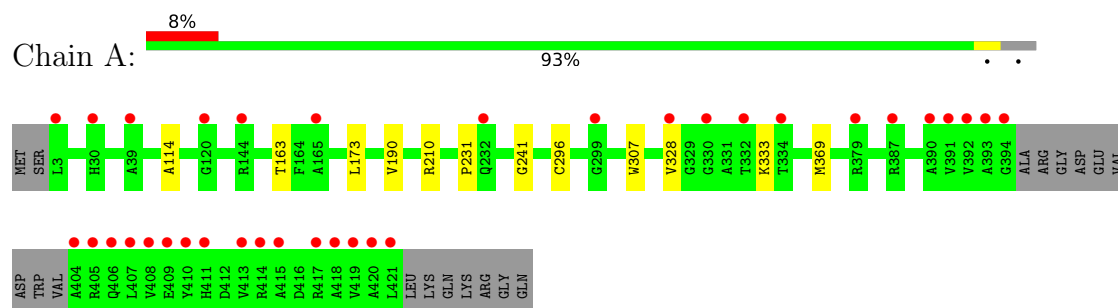
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	429	Total 429	O 429	0	0
7	B	326	Total 326	O 326	0	0

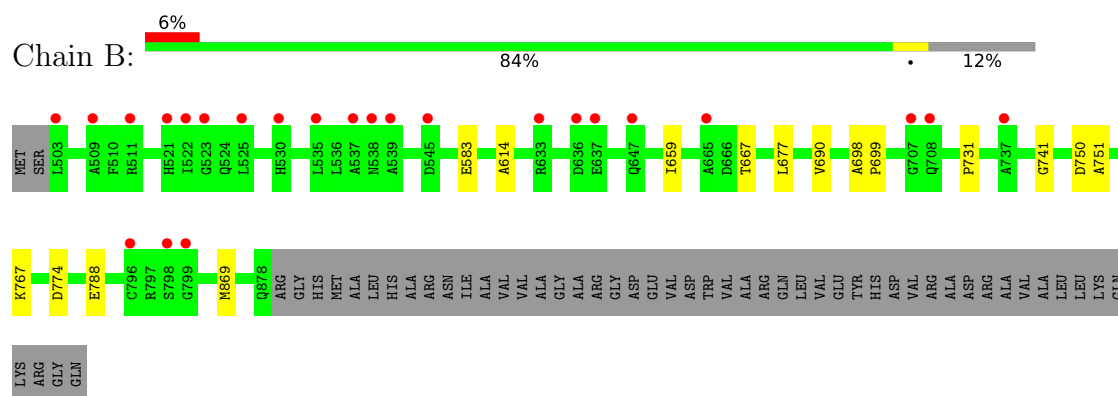
3 Residue-property plots [i](#)

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: 3-hydroxy-3-methylglutaryl-coenzyme A reductase



- Molecule 1: 3-hydroxy-3-methylglutaryl-coenzyme A reductase



4 Data and refinement statistics

Property	Value	Source
Space group	I 41 3 2	Depositor
Cell constants a, b, c, α , β , γ	226.08 Å 226.08 Å 226.08 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.83 – 1.70 27.83 – 1.70	Depositor EDS
% Data completeness (in resolution range)	96.3 (27.83-1.70) 96.3 (27.83-1.70)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	0.04	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.71 (at 1.70 Å)	Xtriage
Refinement program	REFMAC 5.5.0109, CNS	Depositor
R, R_{free}	0.178 , 0.202 0.188 , 0.210	Depositor DCC
R_{free} test set	7679 reflections (7.21%)	wwPDB-VP
Wilson B-factor (Å ²)	25.0	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 44.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6745	wwPDB-VP
Average B, all atoms (Å ²)	30.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 1.85% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: SO4, GOL, NAD, 1CO, 1CV

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	0.46	0/3113	0.71	0/4230
1	B	0.45	0/2834	0.71	0/3855
All	All	0.46	0/5947	0.71	0/8085

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3064	0	3112	8	0
1	B	2791	0	2833	10	0
2	A	58	0	41	2	0
3	A	6	0	8	0	0
3	B	12	0	16	0	0
4	A	5	0	0	0	0
5	B	44	0	26	2	0
6	B	10	0	11	3	0
7	A	429	0	0	1	0
7	B	326	0	0	0	0
All	All	6745	0	6047	20	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 2.

All (20) 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:328:VAL:HG12	1:A:333:LYS:HE2	1.80	0.64
1:B:583:GLU:OE2	6:B:1002:1CO:S2	2.51	0.61
1:A:163:THR:HG22	1:A:173:LEU:HD13	1.83	0.60
2:A:501:1CV:S2	5:B:1001:NAD:C4N	2.89	0.60
7:A:762:HOH:O	6:B:1002:1CO:H4	2.04	0.58
2:A:501:1CV:S2	5:B:1001:NAD:C3N	2.95	0.54
1:A:114:ALA:HB2	1:A:190:VAL:HB	1.90	0.53
1:B:767:LYS:NZ	6:B:1002:1CO:S2	2.78	0.52
1:A:163:THR:HG22	1:A:173:LEU:CD1	2.41	0.50
1:B:614:ALA:HB2	1:B:690:VAL:HB	1.94	0.50
1:A:210:ARG:NH1	1:B:750:ASP:OD2	2.40	0.50
1:B:659:ILE:HD12	1:B:677:LEU:HD23	1.96	0.46
1:B:731:PRO:O	1:B:741:GLY:HA3	2.15	0.45
1:A:307:TRP:CD1	1:A:369[B]:MET:HE1	2.52	0.45
1:B:659:ILE:HD12	1:B:677:LEU:CD2	2.47	0.44
1:B:751:ALA:HB3	1:B:869:MET:HE2	2.00	0.44
1:A:231:PRO:O	1:A:241:GLY:HA3	2.17	0.43
1:B:774:ASP:OD2	1:B:788:GLU:OE2	2.37	0.42
1:B:698:ALA:HB3	1:B:699:PRO:HD3	2.01	0.41
1:A:296[A]:CYS:SG	1:A:296[A]:CYS:O	2.79	0.40

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	408/428 (95%)	394 (97%)	14 (3%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	B	374/428 (87%)	365 (98%)	9 (2%)	0	100	100
All	All	782/856 (91%)	759 (97%)	23 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	314/327 (96%)	314 (100%)	0	100	100
1	B	288/327 (88%)	287 (100%)	1 (0%)	86	83
All	All	602/654 (92%)	601 (100%)	1 (0%)	87	84

All (1) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	667	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	67	ASN
1	A	150	ASN
1	B	600	ASN
1	B	626	ASN

5.3.3 RNA ⓘ

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](#)

7 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	1CV	A	501	-	55,60,60	1.03	5 (9%)	78,90,90	1.54	16 (20%)
4	SO4	A	503	-	4,4,4	0.47	0	6,6,6	0.41	0
3	GOL	B	1004	-	5,5,5	0.40	0	5,5,5	0.25	0
3	GOL	B	1003	-	5,5,5	0.30	0	5,5,5	0.37	0
3	GOL	A	502	-	5,5,5	0.27	0	5,5,5	0.31	0
5	NAD	B	1001	-	46,48,48	1.44	7 (15%)	64,73,73	1.57	12 (18%)
6	1CO	B	1002	-	8,9,9	0.95	0	7,12,12	3.04	1 (14%)

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	1CV	A	501	-	-	5/58/77/77	0/3/3/3
3	GOL	B	1004	-	-	4/4/4/4	-
3	GOL	B	1003	-	-	2/4/4/4	-
3	GOL	A	502	-	-	0/4/4/4	-
5	NAD	B	1001	-	-	7/30/62/62	0/5/5/5
6	1CO	B	1002	-	-	3/9/9/9	-

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	B	1001	NAD	C5A-C4A	4.73	1.47	1.39
5	B	1001	NAD	PN-O3	4.24	1.64	1.59
5	B	1001	NAD	PA-O3	4.01	1.63	1.59
2	A	501	1CV	P1A-O3A	2.90	1.62	1.59
2	A	501	1CV	C2P-S1P	-2.79	1.77	1.81
5	B	1001	NAD	C5A-C6A	2.62	1.48	1.41
5	B	1001	NAD	C8A-N7A	2.57	1.36	1.31
5	B	1001	NAD	C5A-N7A	-2.19	1.35	1.39
2	A	501	1CV	C1-S1P	-2.18	1.78	1.82
5	B	1001	NAD	O4D-C1D	2.11	1.43	1.40
2	A	501	1CV	C8A-N7A	2.03	1.35	1.31
2	A	501	1CV	C4A-N9A	-2.02	1.33	1.37

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1002	1CO	C2-C1-S2	-7.54	105.89	113.74
5	B	1001	NAD	C5A-C4A-N3A	-5.32	119.39	126.72
2	A	501	1CV	N3A-C2A-N1A	-4.84	121.26	128.58
2	A	501	1CV	C5A-C4A-N3A	-4.49	120.53	126.72
5	B	1001	NAD	N3A-C4A-N9A	4.35	134.56	127.17
5	B	1001	NAD	C2A-N3A-C4A	3.42	120.19	111.83
2	A	501	1CV	N9A-C8A-N7A	-3.31	109.25	113.94
2	A	501	1CV	C2A-N3A-C4A	3.18	119.61	111.83
5	B	1001	NAD	N3A-C2A-N1A	-3.18	123.78	128.58
2	A	501	1CV	C6P-C7P-N8P	-3.14	105.31	112.00
5	B	1001	NAD	C4A-C5A-N7A	-3.12	107.02	110.58
5	B	1001	NAD	C4A-N9A-C8A	3.02	108.91	105.74
2	A	501	1CV	C2P-S1P-C1	2.90	108.67	101.50
2	A	501	1CV	C4A-C5A-N7A	-2.83	107.35	110.58
2	A	501	1CV	O3A-P1A-O1A	-2.52	103.11	110.70
2	A	501	1CV	N3A-C4A-N9A	2.52	131.46	127.17
2	A	501	1CV	C2P-C3P-N4P	-2.51	107.17	112.41
2	A	501	1CV	C7P-N8P-C9P	2.47	126.98	122.55
2	A	501	1CV	C3-C2-C1	-2.45	113.77	117.48
2	A	501	1CV	C5A-N7A-C8A	2.40	107.22	103.45
5	B	1001	NAD	C5A-N7A-C8A	2.39	107.21	103.45
2	A	501	1CV	C4A-N9A-C8A	2.32	108.18	105.74
5	B	1001	NAD	N9A-C8A-N7A	-2.21	110.81	113.94
5	B	1001	NAD	C6N-N1N-C1D	-2.02	115.76	119.73
2	A	501	1CV	O2A-P1A-O1A	2.02	121.82	112.44
5	B	1001	NAD	C2A-N1A-C6A	2.01	122.04	118.73

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	501	1CV	C5A-C4A-N9A	2.01	108.00	105.81
5	B	1001	NAD	C4D-O4D-C1D	-2.01	108.09	109.92
5	B	1001	NAD	O3-PN-O1N	-2.00	104.67	110.70

There are no chirality outliers.

All (21) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	501	1CV	C12-O6A-P2A-O3A
2	A	501	1CV	C12-O6A-P2A-O4A
3	B	1003	GOL	C1-C2-C3-O3
3	B	1004	GOL	O1-C1-C2-C3
5	B	1001	NAD	O4D-C1D-N1N-C2N
5	B	1001	NAD	O4D-C1D-N1N-C6N
5	B	1001	NAD	C2D-C1D-N1N-C6N
3	B	1004	GOL	C1-C2-C3-O3
3	B	1003	GOL	O2-C2-C3-O3
3	B	1004	GOL	O1-C1-C2-O2
3	B	1004	GOL	O2-C2-C3-O3
5	B	1001	NAD	PN-O3-PA-O1A
5	B	1001	NAD	PN-O3-PA-O2A
5	B	1001	NAD	C2D-C1D-N1N-C2N
2	A	501	1CV	C3'-O3'-P3'-O7A
2	A	501	1CV	P2A-O3A-P1A-O1A
2	A	501	1CV	P2A-O3A-P1A-O2A
6	B	1002	1CO	C3-C4-C5-O4
6	B	1002	1CO	C3-C4-C5-O3
6	B	1002	1CO	S2-C1-C2-C3
5	B	1001	NAD	O4B-C1B-N9A-C8A

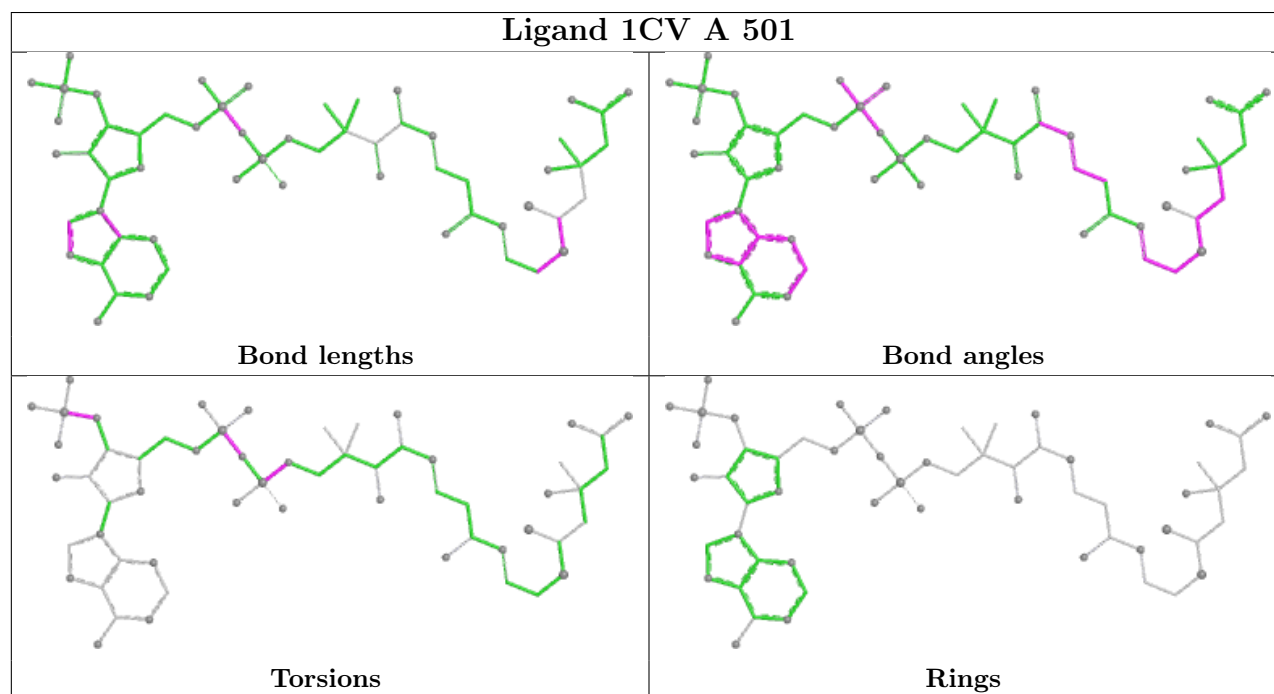
There are no ring outliers.

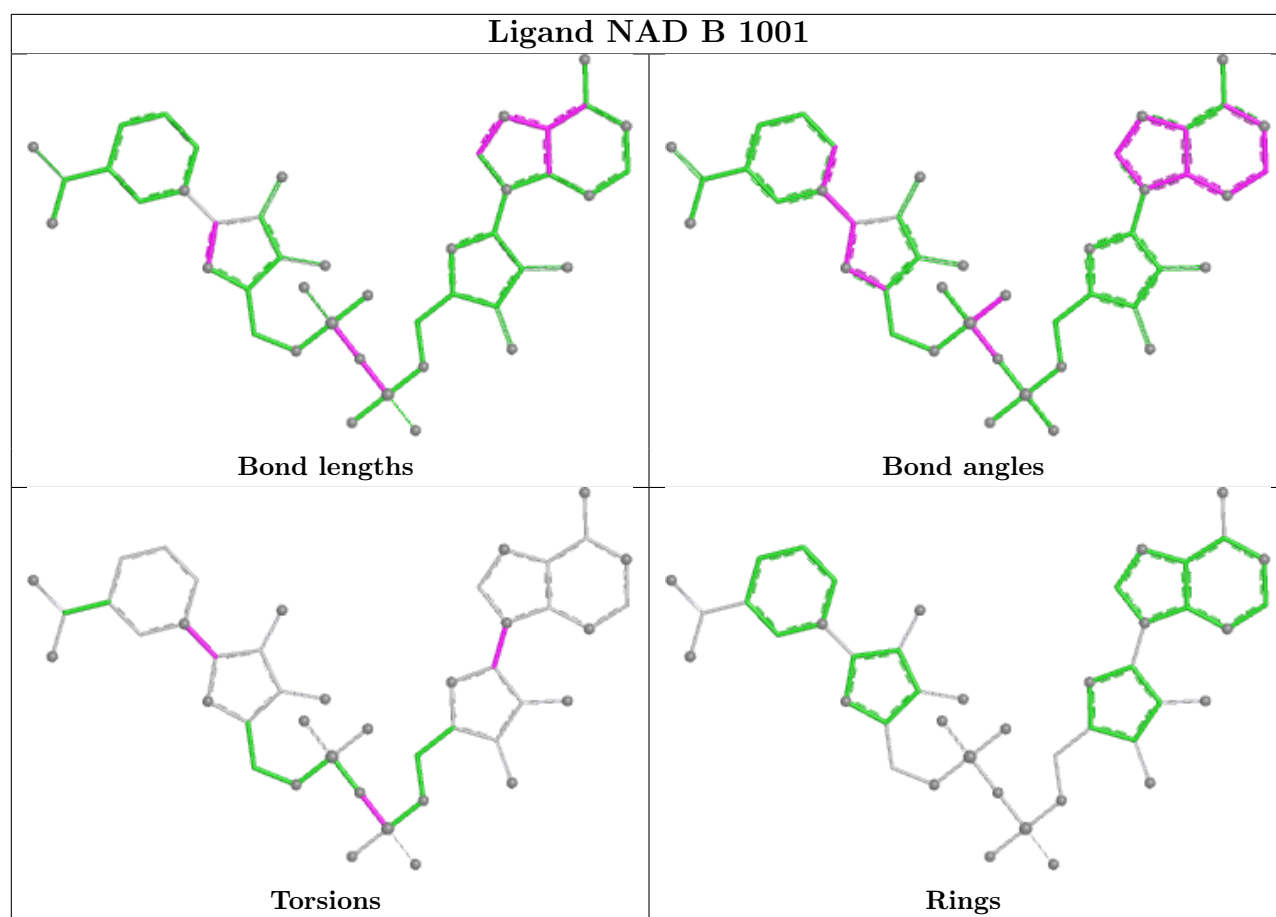
3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	1CV	2	0
5	B	1001	NAD	2	0
6	B	1002	1CO	3	0

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

also be included. For torsion angles, if less 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	410/428 (95%)	0.55	35 (8%) 16 17	13, 26, 47, 79	14 (3%)
1	B	376/428 (87%)	0.45	24 (6%) 25 27	19, 27, 39, 50	13 (3%)
All	All	786/856 (91%)	0.50	59 (7%) 20 22	13, 26, 41, 79	27 (3%)

All (59) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	410	TYR	8.8
1	A	408	VAL	5.4
1	A	409	GLU	4.7
1	A	404	ALA	4.6
1	A	391	VAL	4.3
1	A	407	LEU	4.3
1	A	390	ALA	4.3
1	B	523	GLY	4.2
1	A	419	VAL	4.2
1	B	537	ALA	4.2
1	A	420	ALA	4.1
1	A	405	ARG	3.9
1	A	165	ALA	3.9
1	B	665	ALA	3.5
1	A	394	GLY	3.4
1	A	415	ALA	3.4
1	A	332	THR	3.2
1	A	413	VAL	3.1
1	B	707	GLY	3.0
1	B	538	ASN	3.0
1	A	299	GLY	2.9
1	A	328	VAL	2.9
1	B	530	HIS	2.8
1	A	392	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
1	B	799	GLY	2.7
1	B	737	ALA	2.7
1	B	539	ALA	2.7
1	A	406	GLN	2.6
1	B	535	LEU	2.6
1	A	387	ARG	2.6
1	A	393	ALA	2.5
1	A	334	THR	2.5
1	B	636	ASP	2.5
1	A	411	HIS	2.5
1	B	522	ILE	2.5
1	A	379	ARG	2.5
1	A	417	ARG	2.4
1	A	120	GLY	2.4
1	B	503	LEU	2.4
1	A	421	LEU	2.3
1	B	545	ASP	2.3
1	A	232	GLN	2.3
1	B	708	GLN	2.3
1	A	3	LEU	2.3
1	B	798	SER	2.3
1	B	637	GLU	2.2
1	A	144	ARG	2.2
1	B	633	ARG	2.2
1	B	525	LEU	2.2
1	A	39	ALA	2.2
1	B	647	GLN	2.1
1	B	509	ALA	2.1
1	A	414	ARG	2.1
1	A	418	ALA	2.1
1	A	30	HIS	2.1
1	B	796	CYS	2.1
1	B	521	HIS	2.1
1	A	330	GLY	2.0
1	B	511	ARG	2.0

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

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

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

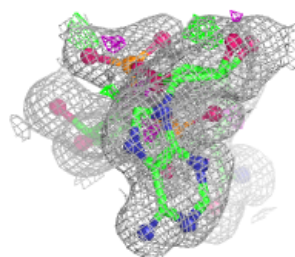
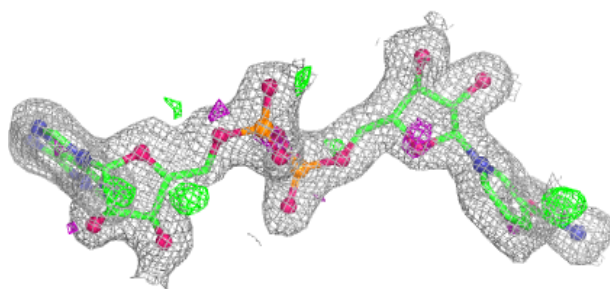
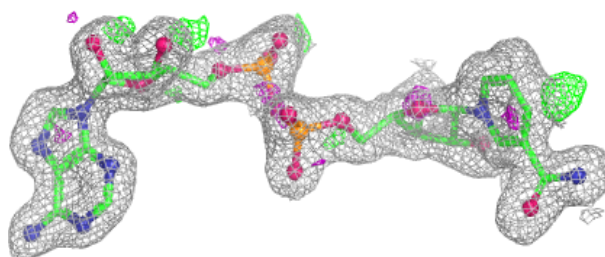
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	GOL	B	1003	6/6	0.70	0.24	52,54,54,57	0
3	GOL	A	502	6/6	0.81	0.16	40,42,42,43	0
3	GOL	B	1004	6/6	0.84	0.11	51,51,52,52	0
6	1CO	B	1002	10/10	0.88	0.12	27,33,35,37	0
4	SO4	A	503	5/5	0.94	0.12	32,34,35,36	0
5	NAD	B	1001	44/44	0.95	0.08	22,28,32,33	0
2	1CV	A	501	58/58	0.95	0.08	20,27,34,37	0

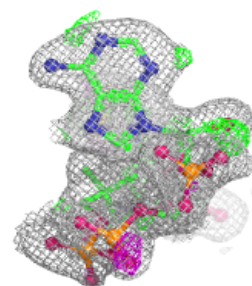
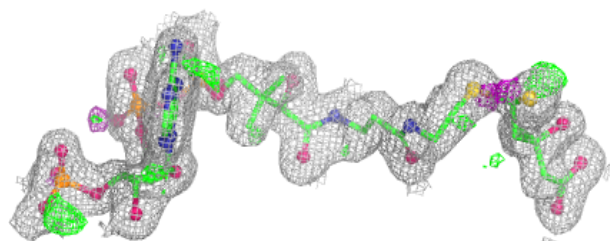
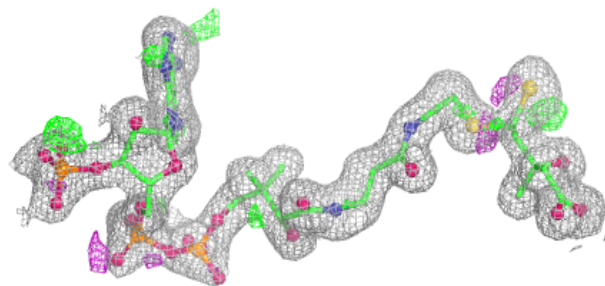
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around NAD B 1001:

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

**Electron density around 1CV A 501:**

$2mF_o-DF_c$ (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.