



Full wwPDB X-ray Structure Validation Report ⓘ

May 15, 2020 – 05:56 pm BST

PDB ID : 5BR4
Title : E. coli lactaldehyde reductase (FucO) M185C mutant
Authors : Cahn, J.K.B.; Brinkmann-Chen, S.; Arnold, F.H.
Deposited on : 2015-05-29
Resolution : 0.91 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 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 : 2.11
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) : 2.11

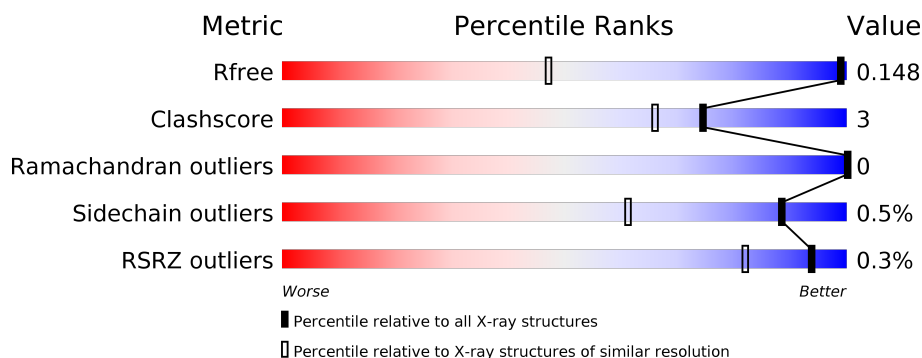
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 0.91 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	1039 (1.04-0.80)
Clashscore	141614	1108 (1.04-0.80)
Ramachandran outliers	138981	1035 (1.04-0.80)
Sidechain outliers	138945	1036 (1.04-0.80)
RSRZ outliers	127900	1009 (1.04-0.80)

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 on 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	391	 88% 9% ..
1	B	391	 90% 7% ..

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7097 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 Lactaldehyde reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	S	0	8	0
			2902	1838	501	546	17			
1	B	384	Total	C	N	O	S	0	12	0
			2916	1849	501	550	16			

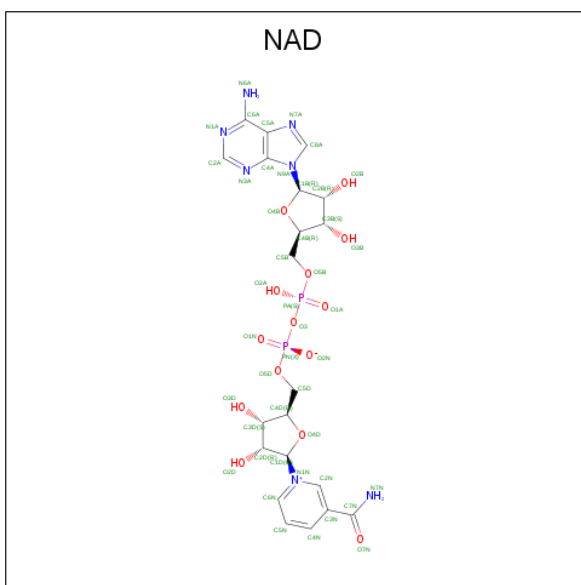
There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	initiating methionine	UNP P0A9S2
A	185	CYS	MET	engineered mutation	UNP P0A9S2
A	384	LEU	-	expression tag	UNP P0A9S2
A	385	GLU	-	expression tag	UNP P0A9S2
A	386	HIS	-	expression tag	UNP P0A9S2
A	387	HIS	-	expression tag	UNP P0A9S2
A	388	HIS	-	expression tag	UNP P0A9S2
A	389	HIS	-	expression tag	UNP P0A9S2
A	390	HIS	-	expression tag	UNP P0A9S2
A	391	HIS	-	expression tag	UNP P0A9S2
B	1	MET	-	initiating methionine	UNP P0A9S2
B	185	CYS	MET	engineered mutation	UNP P0A9S2
B	384	LEU	-	expression tag	UNP P0A9S2
B	385	GLU	-	expression tag	UNP P0A9S2
B	386	HIS	-	expression tag	UNP P0A9S2
B	387	HIS	-	expression tag	UNP P0A9S2
B	388	HIS	-	expression tag	UNP P0A9S2
B	389	HIS	-	expression tag	UNP P0A9S2
B	390	HIS	-	expression tag	UNP P0A9S2
B	391	HIS	-	expression tag	UNP P0A9S2

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total Zn 1 1	0	0
2	A	1	Total Zn 1 1	0	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $\text{C}_{21}\text{H}_{27}\text{N}_7\text{O}_{14}\text{P}_2$).



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 GLYCEROL (three-letter code: GOL) (formula: $\text{C}_3\text{H}_8\text{O}_3$).



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

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Cl	0	0
			2	2		
5	A	2	Total	Cl	0	0
			2	2		

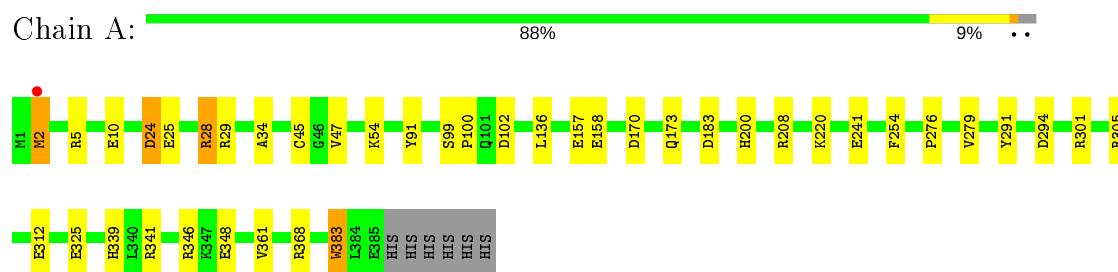
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	613	Total	O	0	0
			613	613		
6	B	554	Total	O	0	0
			554	554		

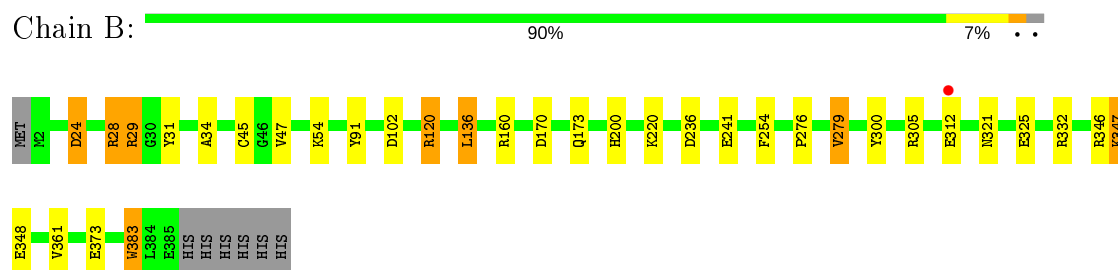
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Lactaldehyde reductase



- Molecule 1: Lactaldehyde reductase



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	69.70 Å 63.77 Å 91.67 Å 90.00° 111.15° 90.00°	Depositor
Resolution (Å)	85.50 – 0.91 36.53 – 0.91	Depositor EDS
% Data completeness (in resolution range)	91.6 (85.50-0.91) 91.6 (36.53-0.91)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.06	Depositor
$\langle I/\sigma(I) \rangle$ ¹	0.96 (at 0.91 Å)	Xtriage
Refinement program	REFMAC 5.8.0069	Depositor
R, R_{free}	0.129 , 0.147 0.130 , 0.148	Depositor DCC
R_{free} test set	24378 reflections (4.96%)	wwPDB-VP
Wilson B-factor (Å ²)	8.4	Xtriage
Anisotropy	0.677	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	0.018 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	7097	wwPDB-VP
Average B, all atoms (Å ²)	15.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.99% 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: GOL, ZN, NAD, CL

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	1.05	13/2980 (0.4%)	1.10	24/4054 (0.6%)
1	B	1.01	9/3006 (0.3%)	1.13	19/4091 (0.5%)
All	All	1.03	22/5986 (0.4%)	1.12	43/8145 (0.5%)

All (22) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	157	GLU	CG-CD	9.23	1.65	1.51
1	B	373	GLU	CD-OE1	8.19	1.34	1.25
1	A	325	GLU	CD-OE1	7.26	1.33	1.25
1	B	383	TRP	CE3-CZ3	-7.08	1.26	1.38
1	B	120	ARG	CB-CG	-6.95	1.33	1.52
1	A	368	ARG	CB-CG	-6.81	1.34	1.52
1	A	10[A]	GLU	CD-OE2	6.74	1.33	1.25
1	A	10[B]	GLU	CD-OE2	6.74	1.33	1.25
1	A	368	ARG	CA-CB	6.31	1.67	1.53
1	A	383	TRP	CD2-CE3	6.18	1.49	1.40
1	B	373	GLU	CG-CD	6.03	1.61	1.51
1	B	120	ARG	NE-CZ	-5.84	1.25	1.33
1	A	368	ARG	NE-CZ	-5.69	1.25	1.33
1	B	348	GLU	CD-OE1	-5.58	1.19	1.25
1	A	312	GLU	CG-CD	5.54	1.60	1.51
1	A	5	ARG	NE-CZ	-5.46	1.25	1.33
1	A	383	TRP	CG-CD2	-5.45	1.34	1.43
1	A	348	GLU	CD-OE1	-5.35	1.19	1.25
1	B	279[A]	VAL	CB-CG2	-5.26	1.41	1.52
1	B	279[B]	VAL	CB-CG2	-5.26	1.41	1.52
1	B	29	ARG	CZ-NH1	-5.24	1.26	1.33
1	A	158	GLU	CD-OE2	5.04	1.31	1.25

All (43) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	28	ARG	NE-CZ-NH1	15.65	128.12	120.30
1	B	29	ARG	NE-CZ-NH2	15.30	127.95	120.30
1	A	28	ARG	NE-CZ-NH1	13.32	126.96	120.30
1	B	28	ARG	NE-CZ-NH2	-12.99	113.81	120.30
1	A	368	ARG	NE-CZ-NH2	-10.27	115.17	120.30
1	B	24	ASP	CB-CG-OD1	10.05	127.34	118.30
1	B	29	ARG	NE-CZ-NH1	-9.47	115.56	120.30
1	B	24	ASP	CB-CG-OD2	-9.42	109.82	118.30
1	B	346	ARG	NE-CZ-NH1	8.62	124.61	120.30
1	A	208	ARG	NE-CZ-NH1	8.55	124.58	120.30
1	B	346	ARG	NE-CZ-NH2	-8.30	116.15	120.30
1	A	301	ARG	NE-CZ-NH2	-8.07	116.27	120.30
1	A	24	ASP	CB-CG-OD2	8.07	125.56	118.30
1	B	120	ARG	NE-CZ-NH2	-8.04	116.28	120.30
1	A	346	ARG	NE-CZ-NH1	7.08	123.84	120.30
1	B	160	ARG	NE-CZ-NH2	-7.00	116.80	120.30
1	B	300	TYR	CB-CG-CD1	6.89	125.14	121.00
1	A	24	ASP	CB-CG-OD1	-6.58	112.38	118.30
1	B	29	ARG	CD-NE-CZ	-6.58	114.39	123.60
1	B	136	LEU	CB-CG-CD1	6.46	121.99	111.00
1	A	170	ASP	CB-CG-OD1	6.32	123.98	118.30
1	A	305	ARG	NE-CZ-NH2	-6.30	117.15	120.30
1	A	2	MET	CA-CB-CG	6.09	123.65	113.30
1	B	160	ARG	NE-CZ-NH1	6.02	123.31	120.30
1	B	120	ARG	N-CA-CB	6.00	121.41	110.60
1	A	136	LEU	CB-CG-CD1	5.97	121.15	111.00
1	B	241	GLU	OE1-CD-OE2	-5.85	116.28	123.30
1	A	383	TRP	CB-CG-CD1	5.73	134.45	127.00
1	A	368	ARG	CG-CD-NE	-5.72	99.80	111.80
1	A	341	ARG	NE-CZ-NH1	-5.62	117.49	120.30
1	A	301	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	A	241	GLU	OE1-CD-OE2	-5.50	116.70	123.30
1	A	291	TYR	CB-CG-CD2	-5.50	117.70	121.00
1	B	332	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	170	ASP	CB-CG-OD2	-5.41	113.43	118.30
1	A	183	ASP	CB-CG-OD2	-5.24	113.58	118.30
1	B	236	ASP	CB-CG-OD2	5.20	122.98	118.30
1	A	361	VAL	CG1-CB-CG2	5.15	119.14	110.90
1	B	170	ASP	CB-CG-OD2	-5.13	113.69	118.30
1	A	28	ARG	NE-CZ-NH2	-5.12	117.74	120.30
1	A	294	ASP	CB-CG-OD1	5.07	122.86	118.30
1	A	383	TRP	CG-CD1-NE1	5.04	115.14	110.10
1	A	294	ASP	CB-CG-OD2	-5.01	113.79	118.30

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	2902	0	2929	18	0
1	B	2916	0	2945	20	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	44	0	26	1	0
3	B	44	0	26	1	0
4	A	12	0	16	0	0
4	B	6	0	8	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
6	A	613	0	0	10	3
6	B	554	0	0	10	3
All	All	7097	0	5950	38	3

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 3.

All (38) 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:45[B]:CYS:SG	1:B:47:VAL:HG23	1.89	1.12
1:B:321[B]:ASN:OD1	6:B:501:HOH:O	1.85	0.92
1:A:29[A]:ARG:NH1	6:A:502:HOH:O	2.10	0.85
1:A:24:ASP:OD2	6:A:501:HOH:O	2.08	0.71
1:B:45[B]:CYS:SG	1:B:47:VAL:CG2	2.73	0.71
1:A:28:ARG:HD2	6:A:501:HOH:O	1.93	0.68
1:A:25:GLU:OE1	1:A:29[B]:ARG:NH1	2.28	0.65
1:A:54[B]:LYS:NZ	6:A:503:HOH:O	2.18	0.65
1:A:45[B]:CYS:SG	1:A:47:VAL:HG23	2.39	0.63
1:B:173:GLN:OE1	6:B:502:HOH:O	2.16	0.62
1:B:325[B]:GLU:HG2	6:B:501:HOH:O	2.01	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:361[A]:VAL:HG21	6:B:1019:HOH:O	2.05	0.56
1:B:24:ASP:HB3	1:B:28:ARG:NH1	2.21	0.56
1:B:276:PRO:HB2	1:B:279[A]:VAL:HG22	1.88	0.55
1:B:29:ARG:NH1	6:B:509:HOH:O	2.43	0.53
1:B:54[B]:LYS:NZ	6:B:507:HOH:O	2.41	0.51
1:A:2:MET:HE2	6:A:657:HOH:O	2.10	0.49
1:A:173:GLN:NE2	6:A:504:HOH:O	2.46	0.49
1:B:276:PRO:O	1:B:279[A]:VAL:HG22	2.15	0.47
1:A:2:MET:HB3	6:A:657:HOH:O	2.15	0.46
1:B:200:HIS:HB3	1:B:254:PHE:CD2	2.51	0.46
1:B:347:LYS:HE2	1:B:383:TRP:CZ3	2.52	0.45
1:B:312:GLU:HG3	6:B:846:HOH:O	2.16	0.44
1:A:28:ARG:NE	6:A:501:HOH:O	2.51	0.44
1:A:28:ARG:CD	6:A:501:HOH:O	2.59	0.43
1:B:305[A]:ARG:NH2	6:B:510:HOH:O	2.44	0.43
1:B:102:ASP:OD2	3:B:402:NAD:H2N	2.18	0.43
1:B:31:TYR:HB3	1:B:91:TYR:CD1	2.54	0.43
1:A:102:ASP:OD2	3:A:402:NAD:H2N	2.18	0.42
1:B:220:LYS:HD2	6:B:504:HOH:O	2.19	0.42
1:B:220:LYS:NZ	6:B:504:HOH:O	2.32	0.42
1:A:220:LYS:HE2	6:A:895:HOH:O	2.20	0.42
1:A:200:HIS:HB3	1:A:254:PHE:CD2	2.55	0.41
1:A:339:HIS:HB3	1:A:383:TRP:O	2.20	0.41
1:A:34:ALA:HB2	1:A:91:TYR:CZ	2.55	0.41
1:B:34:ALA:HB2	1:B:91:TYR:CZ	2.57	0.40
1:A:276:PRO:O	1:A:279[A]:VAL:HG22	2.20	0.40
1:A:99:SER:HB2	1:A:100:PRO:HD3	2.02	0.40

All (3) 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:A:508:HOH:O	6:B:665:HOH:O[1_455]	1.73	0.47
6:A:766:HOH:O	6:B:769:HOH:O[2_655]	2.09	0.11
6:A:854:HOH:O	6:B:791:HOH:O[1_455]	2.18	0.02

5.3 Torsion angles

5.3.1 Protein backbone

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	391/391 (100%)	386 (99%)	5 (1%)	0	100	100
1	B	394/391 (101%)	388 (98%)	6 (2%)	0	100	100
All	All	785/782 (100%)	774 (99%)	11 (1%)	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	300/300 (100%)	300 (100%)	0	100	100
1	B	303/300 (101%)	300 (99%)	3 (1%)	76	44
All	All	603/600 (100%)	600 (100%)	3 (0%)	88	61

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	120	ARG
1	B	136	LEU
1	B	347	LYS

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

Mol	Chain	Res	Type
1	A	173	GLN

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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 11 ligands modelled in this entry, 6 are monoatomic - leaving 5 for Mogul analysis.

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	$\# Z > 2$
4	GOL	A	404	-	5,5,5	0.82	0	5,5,5	0.89	0
3	NAD	A	402	-	42,48,48	1.19	4 (9%)	50,73,73	1.01	4 (8%)
4	GOL	B	403	-	5,5,5	1.57	1 (20%)	5,5,5	2.20	2 (40%)
4	GOL	A	403	-	5,5,5	2.35	2 (40%)	5,5,5	2.35	1 (20%)
3	NAD	B	402	-	42,48,48	1.44	7 (16%)	50,73,73	1.15	5 (10%)

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
4	GOL	A	404	-	-	2/4/4/4	-
3	NAD	A	402	-	-	5/26/62/62	0/5/5/5
4	GOL	B	403	-	-	1/4/4/4	-
4	GOL	A	403	-	-	1/4/4/4	-
3	NAD	B	402	-	-	5/26/62/62	0/5/5/5

All (14) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	402	NAD	O7N-C7N	4.35	1.32	1.24
4	A	403	GOL	C1-C2	4.19	1.69	1.51
3	B	402	NAD	C7N-N7N	-3.75	1.25	1.33
3	A	402	NAD	O4D-C1D	3.74	1.46	1.41
3	B	402	NAD	O4D-C1D	3.72	1.46	1.41
3	B	402	NAD	C4N-C3N	2.72	1.44	1.39
3	A	402	NAD	C4N-C3N	2.56	1.43	1.39
4	B	403	GOL	C1-C2	2.39	1.61	1.51
3	B	402	NAD	C2B-C1B	-2.25	1.50	1.53
3	A	402	NAD	C2B-C1B	-2.19	1.50	1.53
3	A	402	NAD	C2N-N1N	2.18	1.37	1.35
3	B	402	NAD	C2N-N1N	2.14	1.37	1.35
3	B	402	NAD	C2D-C1D	-2.11	1.50	1.53
4	A	403	GOL	O2-C2	-2.01	1.37	1.43

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	403	GOL	C3-C2-C1	-4.94	92.50	111.70
4	B	403	GOL	C3-C2-C1	-3.51	98.06	111.70
3	B	402	NAD	C2N-C3N-C4N	3.49	122.21	118.26
3	B	402	NAD	C5N-C4N-C3N	-3.15	116.62	120.34
3	A	402	NAD	O4D-C1D-C2D	-3.08	102.42	106.93
3	B	402	NAD	C5A-C6A-N6A	3.00	124.91	120.35
3	A	402	NAD	C6N-N1N-C2N	-2.59	119.61	121.97
4	B	403	GOL	O2-C2-C1	2.51	120.18	109.12
3	A	402	NAD	C5A-C6A-N6A	2.37	123.95	120.35
3	B	402	NAD	O4D-C1D-C2D	-2.30	103.57	106.93
3	A	402	NAD	C5N-C4N-C3N	-2.16	117.79	120.34
3	B	402	NAD	C6N-N1N-C2N	-2.03	120.12	121.97

There are no chirality outliers.

All (14) torsion outliers are listed below:

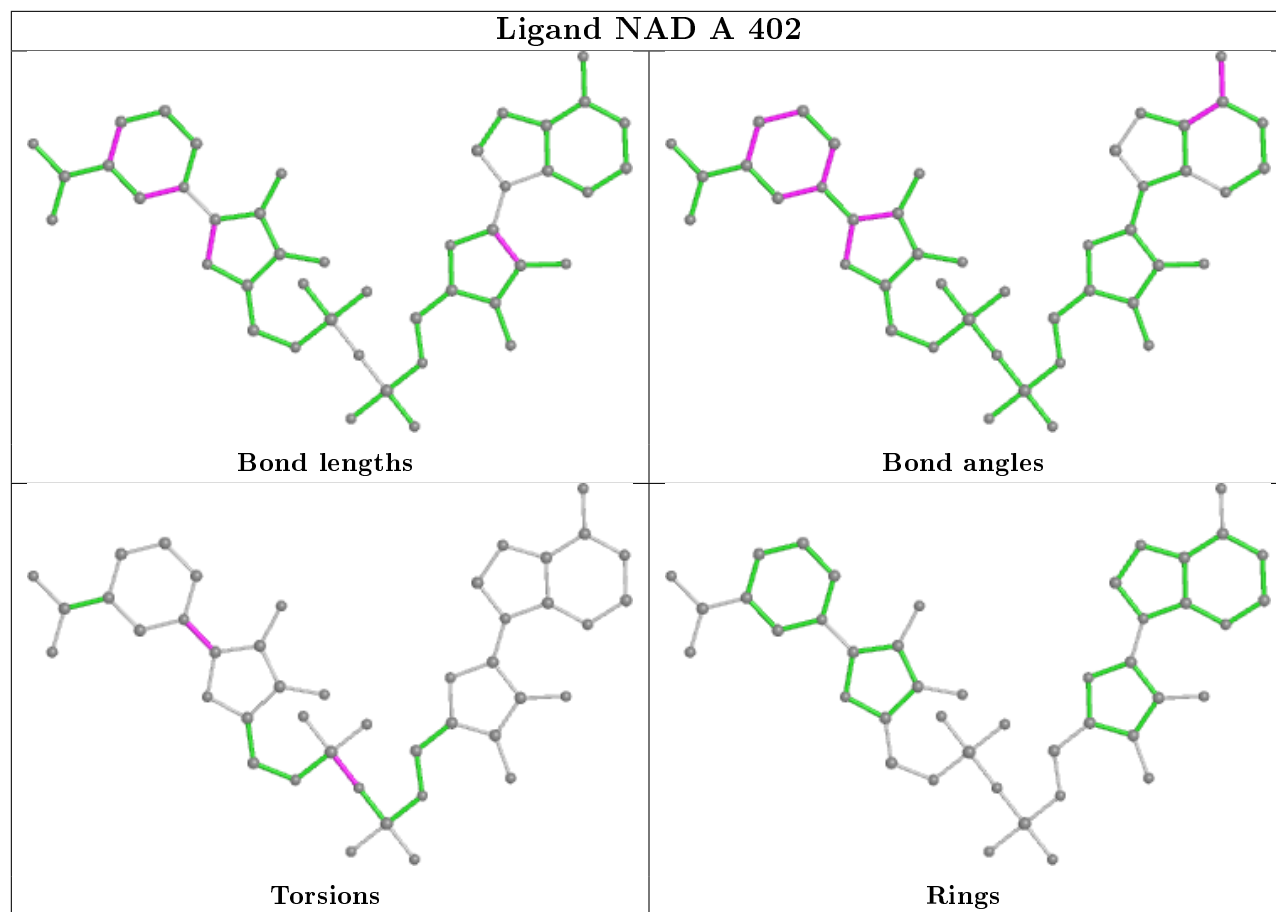
Mol	Chain	Res	Type	Atoms
3	A	402	NAD	O4D-C1D-N1N-C2N
3	A	402	NAD	O4D-C1D-N1N-C6N
3	A	402	NAD	C2D-C1D-N1N-C2N
3	B	402	NAD	O4D-C1D-N1N-C2N
3	B	402	NAD	O4D-C1D-N1N-C6N
3	B	402	NAD	C2D-C1D-N1N-C2N
3	B	402	NAD	C2D-C1D-N1N-C6N
3	A	402	NAD	PA-O3-PN-O5D
3	B	402	NAD	PA-O3-PN-O5D
4	A	404	GOL	O1-C1-C2-O2
4	A	403	GOL	O1-C1-C2-O2
4	B	403	GOL	O1-C1-C2-O2
3	A	402	NAD	C2D-C1D-N1N-C6N
4	A	404	GOL	C1-C2-C3-O3

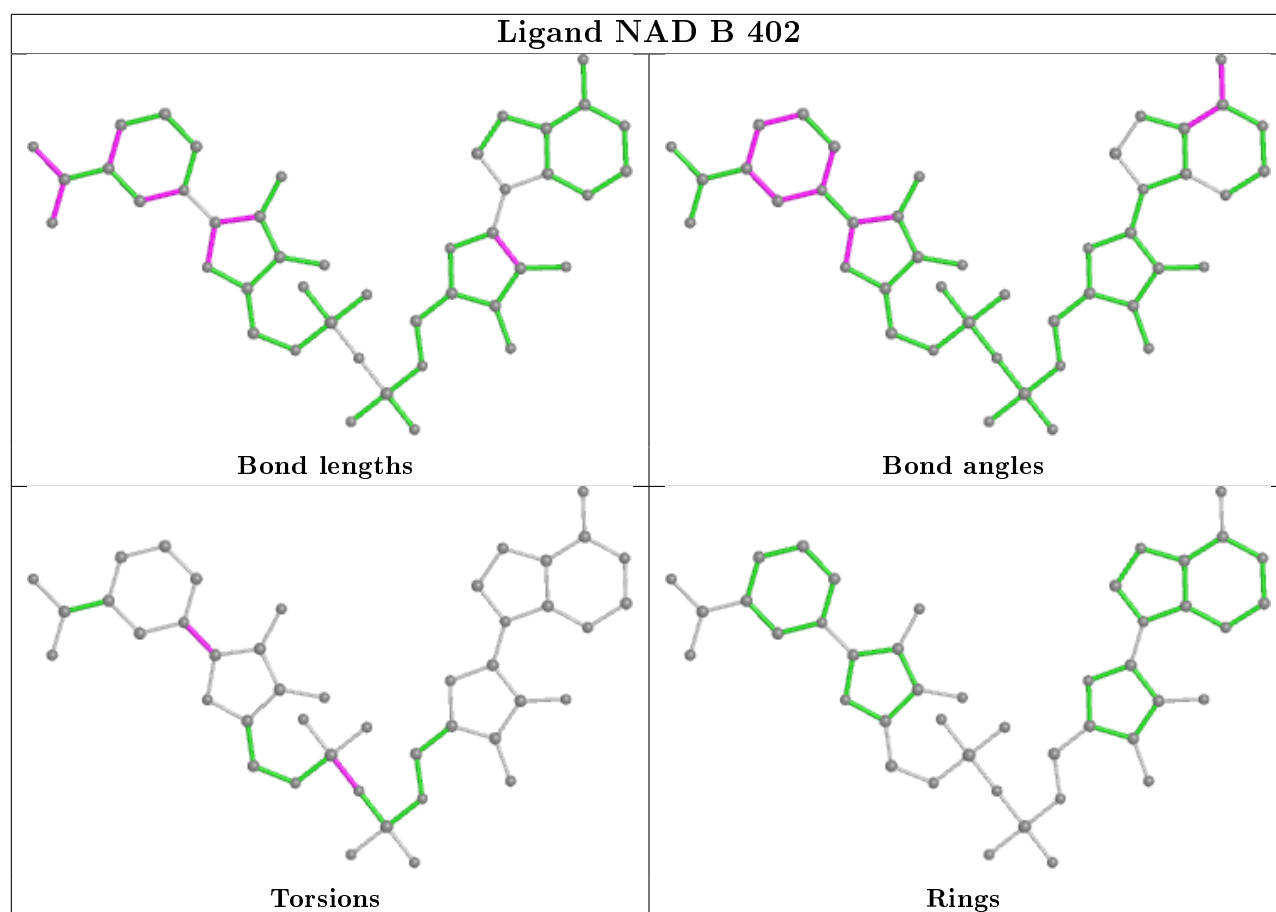
There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	402	NAD	1	0
3	B	402	NAD	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 [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	385/391 (98%)	-0.52	1 (0%) 94 82	7, 9, 25, 76	0
1	B	384/391 (98%)	-0.54	1 (0%) 94 82	7, 11, 25, 96	0
All	All	769/782 (98%)	-0.53	2 (0%) 94 82	7, 10, 25, 96	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	312	GLU	2.5
1	A	2	MET	2.1

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 carbohydrates 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.

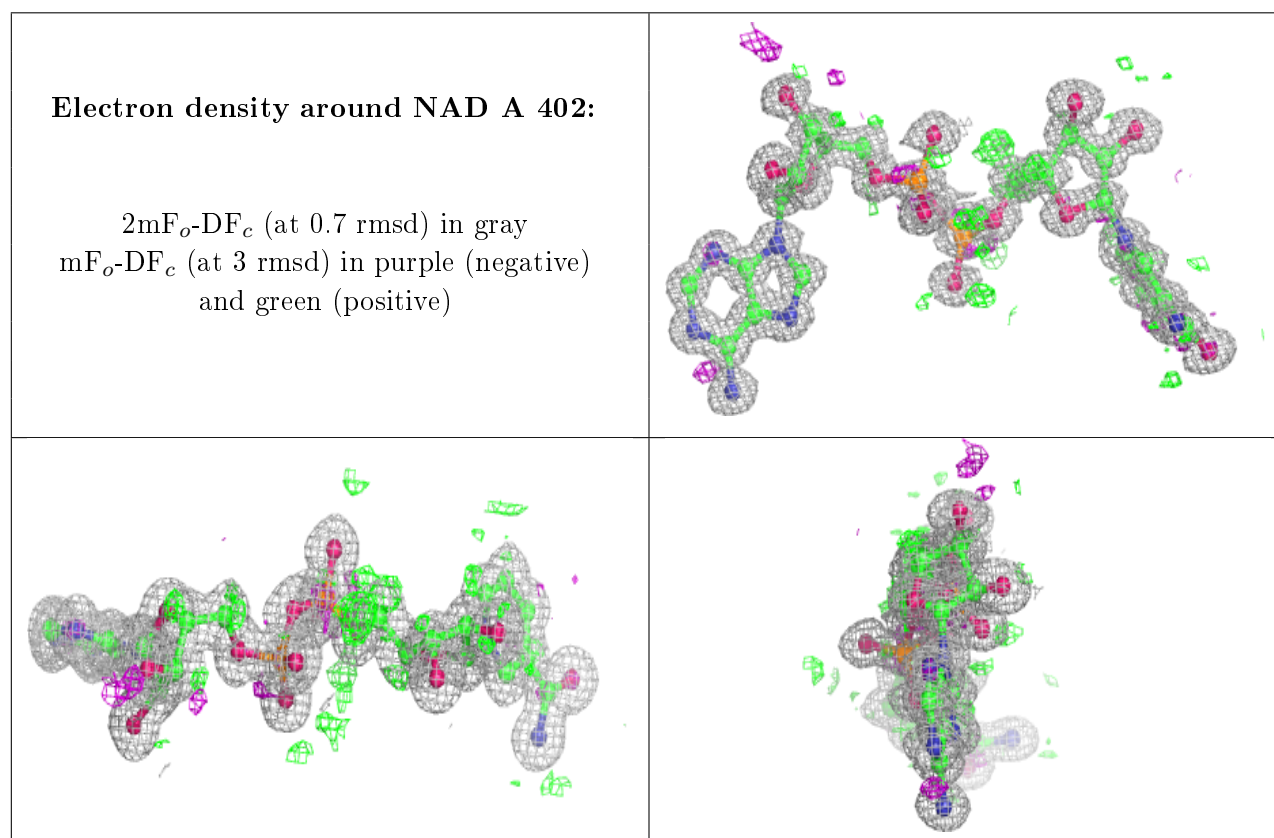
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	GOL	A	404	6/6	0.90	0.20	30,32,44,50	0
4	GOL	B	403	6/6	0.92	0.09	18,26,30,39	0
4	GOL	A	403	6/6	0.94	0.10	14,23,25,30	0

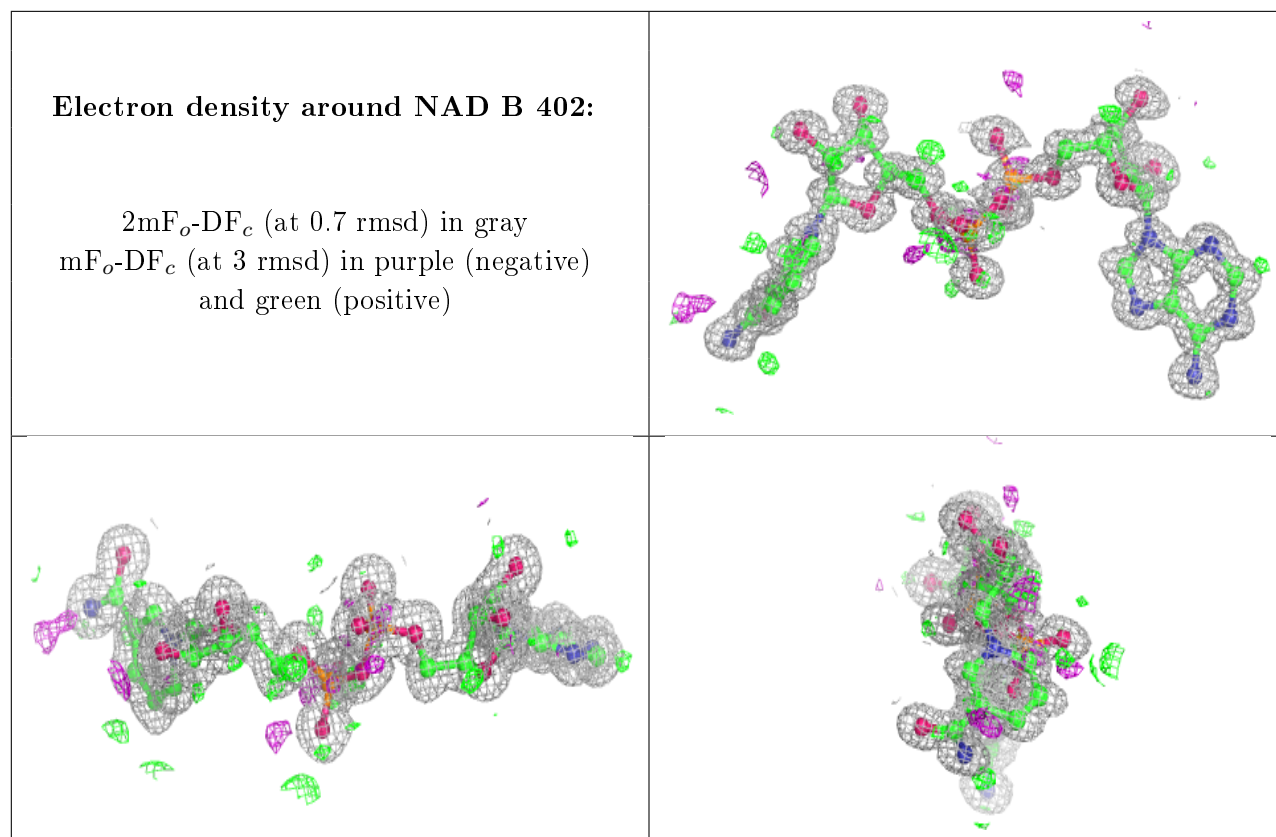
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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	NAD	A	402	44/44	0.99	0.05	7,8,9,11	0
3	NAD	B	402	44/44	0.99	0.04	8,9,11,13	0
5	CL	A	405	1/1	1.00	0.01	10,10,10,10	0
5	CL	B	404	1/1	1.00	0.03	12,12,12,12	0
5	CL	A	406	1/1	1.00	0.02	9,9,9,9	0
2	ZN	A	401	1/1	1.00	0.04	7,7,7,7	0
5	CL	B	405	1/1	1.00	0.05	13,13,13,13	0
2	ZN	B	401	1/1	1.00	0.03	8,8,8,8	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.





6.5 Other polymers [i](#)

There are no such residues in this entry.