



wwPDB X-ray Structure Validation Summary Report ⓘ

Jul 3, 2017 – 05:43 PM EDT

PDB ID : 1E3W
Title : Rat brain 3-hydroxyacyl-CoA dehydrogenase binary complex with NADH and 3-keto butyrate
Authors : Powell, A.J.; Read, J.A.; Brady, R.L.
Deposited on : unknown
Resolution : 2.00 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : **NOT EXECUTED**
EDS : **NOT EXECUTED**
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20029824

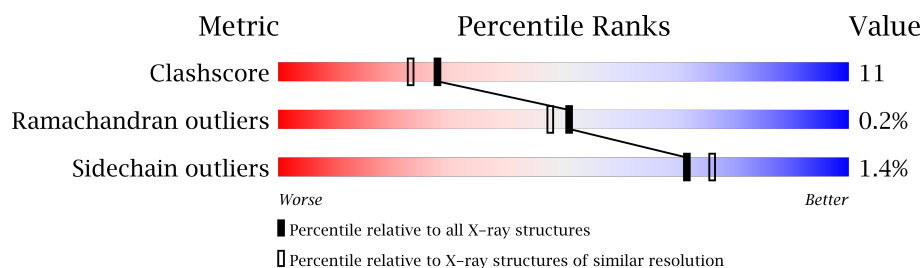
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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))
Clashscore	112137	7775 (2.00-2.00)
Ramachandran outliers	110173	7679 (2.00-2.00)
Sidechain outliers	110143	7678 (2.00-2.00)

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. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	261	
2	B	261	
2	C	261	
2	D	261	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	TRS	A	302	-	X	-	-
5	SO4	A	303	-	X	-	-
5	SO4	B	303	-	-	X	-

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 8558 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.

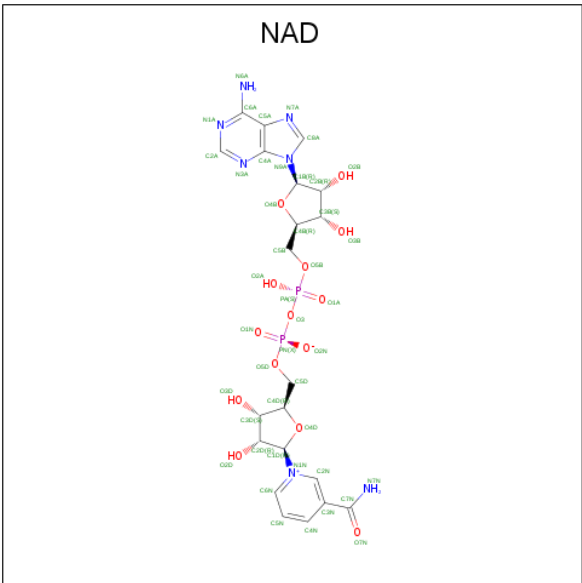
- Molecule 1 is a protein called SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	251	1868	1178	330	353	7	27	8	0

- Molecule 2 is a protein called SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE.

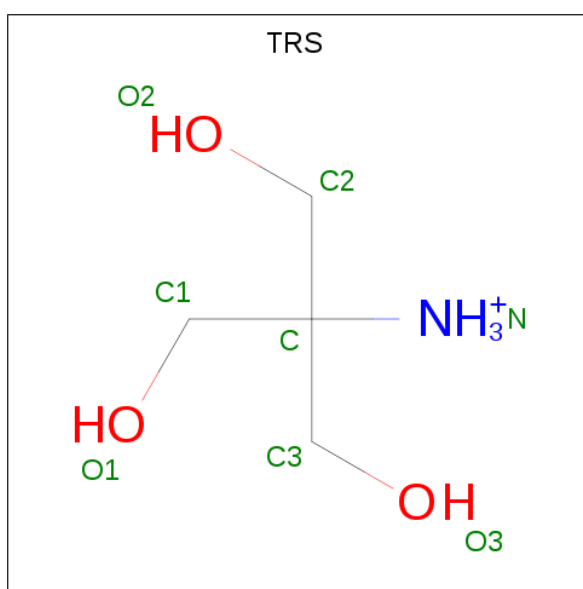
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	247	1852	1169	329	348	6	4	11	0
2	C	248	1838	1161	326	344	7	18	5	0
2	D	255	1879	1189	332	352	6	23	2	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: C₂₁H₂₇N₇O₁₄P₂).



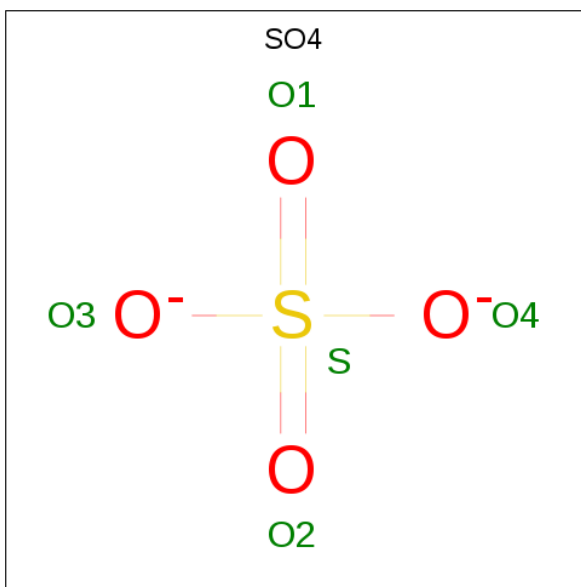
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	B	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	C	1	Total	C	N	O	P	0	0
			44	21	7	14	2		
3	D	1	Total	C	N	O	P	0	0
			44	21	7	14	2		

- Molecule 4 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: C₄H₁₂NO₃).



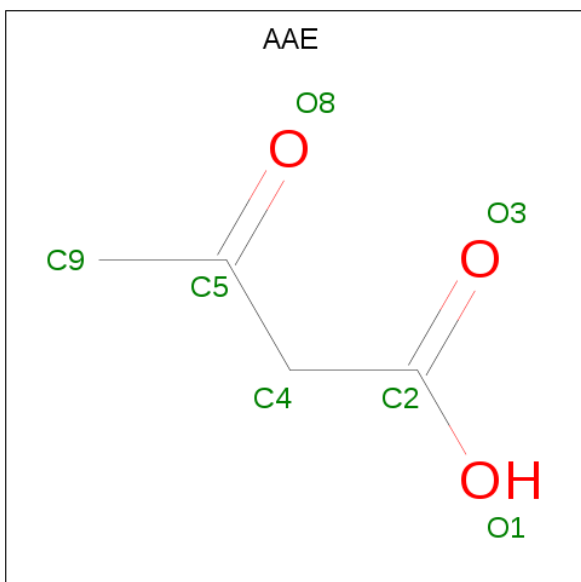
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			8	4	1	3		
4	B	1	Total	C	N	O	0	0
			8	4	1	3		
4	C	1	Total	C	N	O	0	0
			8	4	1	3		

- Molecule 5 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

- Molecule 6 is ACETOACETIC ACID (three-letter code: AAE) (formula: C₄H₆O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	D	1	Total	C	O	0	1
			7	4	3		

- Molecule 7 is water.

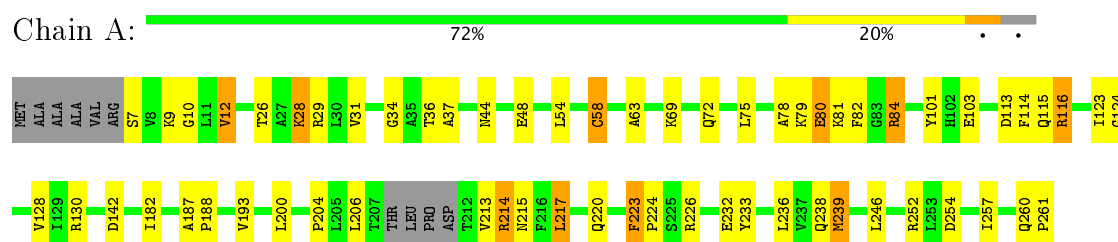
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	213	Total	O	0	0
			213	213		
7	B	226	Total	O	0	0
			226	226		
7	C	242	Total	O	0	0
			242	242		
7	D	208	Total	O	0	0
			208	208		

3 Residue-property plots

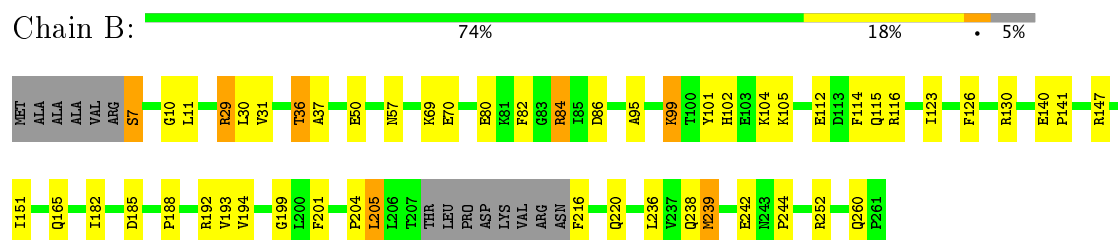
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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.

Note EDS was not executed.

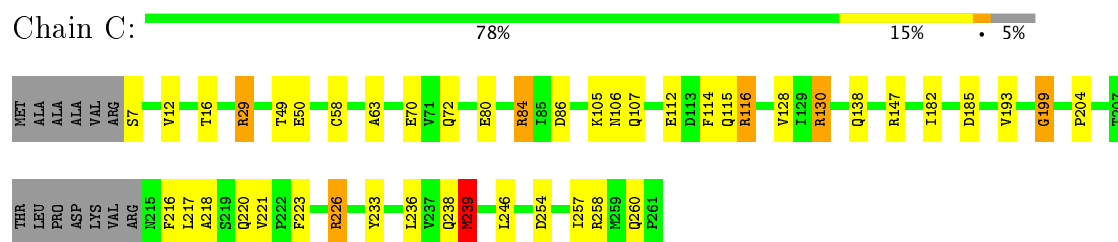
• Molecule 1: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE



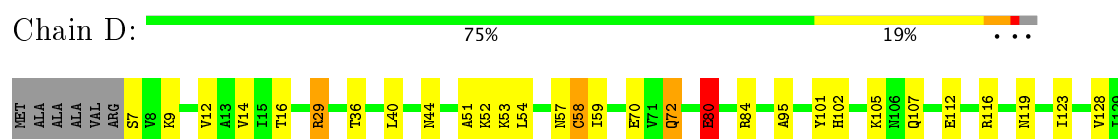
• Molecule 2: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE



• Molecule 2: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE



• Molecule 2: SHORT CHAIN 3-HYDROXYACYL-COA DEHYDROGENASE



R130	D142	Q143	R147	A154	K172	R184	D185	L186	A187	P188	R192	G199	T208	L209	P210	D211	V212	V213	R214	N215	F216	L217	V221	P222	F223	Y233	Q238	M239	R252	L253	D254	I257	Q260	P261
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4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	57.60 Å 67.43 Å 67.50 Å 65.22° 73.27° 75.67°	Depositor
Resolution (Å)	40.00 – 2.00	Depositor
% Data completeness (in resolution range)	94.9 (40.00-2.00)	Depositor
R_{merge}	0.06	Depositor
R_{sym}	0.06	Depositor
Refinement program	REFMAC	Depositor
R, R_{free}	0.189 , 0.226	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8558	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

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: AAE, TRS, SO4, 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	1.37	11/1933 (0.6%)	1.85	31/2621 (1.2%)
2	B	1.19	5/1932 (0.3%)	1.95	35/2617 (1.3%)
2	C	1.10	3/1888 (0.2%)	1.69	27/2559 (1.1%)
2	D	1.24	9/1918 (0.5%)	1.78	33/2603 (1.3%)
All	All	1.23	28/7671 (0.4%)	1.82	126/10400 (1.2%)

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	A	0	3
2	B	0	2
2	C	0	3
2	D	0	2
All	All	0	10

The worst 5 of 28 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	58	CYS	CB-SG	22.30	2.20	1.82
2	D	211	ASP	CB-CG	13.19	1.79	1.51
1	A	261	PRO	N-CD	8.22	1.59	1.47
2	D	217	LEU	CB-CG	7.70	1.74	1.52
2	C	217	LEU	CA-CB	7.33	1.70	1.53

The worst 5 of 126 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	84	ARG	CD-NE-CZ	36.43	174.60	123.60
2	B	84[A]	ARG	CD-NE-CZ	28.50	163.49	123.60
2	B	84[B]	ARG	CD-NE-CZ	28.50	163.49	123.60
1	A	84	ARG	NE-CZ-NH2	24.80	132.70	120.30
2	D	211	ASP	CB-CG-OD1	-23.07	97.54	118.30

There are no chirality outliers.

5 of 10 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	214	ARG	Sidechain
1	A	34	GLY	Mainchain
1	A	80	GLU	Mainchain
2	B	199	GLY	Mainchain
2	B	95	ALA	Mainchain

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	1868	0	1931	48	0
2	B	1852	0	1922	56	1
2	C	1838	0	1901	47	0
2	D	1879	0	1942	52	1
3	A	44	0	26	0	0
3	B	44	0	26	0	0
3	C	44	0	26	1	0
3	D	44	0	26	1	0
4	A	8	0	12	0	0
4	B	8	0	12	0	0
4	C	8	0	12	0	0
5	A	10	0	0	0	0
5	B	5	0	0	2	0
5	C	5	0	0	0	0
5	D	5	0	0	0	0
6	D	7	0	5	2	0
7	A	213	0	0	9	0
7	B	226	0	0	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	C	242	0	0	8	0
7	D	208	0	0	6	0
All	All	8558	0	7841	172	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 11.

The worst 5 of 172 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)
2:B:239:MET:CE	2:B:239:MET:SD	2.17	1.33
1:A:58:CYS:SG	1:A:58:CYS:CB	2.20	1.30
2:D:210:PRO:HG2	2:D:213:VAL:CB	1.74	1.18
2:D:210:PRO:HG2	2:D:213:VAL:HB	1.11	1.07
1:A:239[A]:MET:CG	2:C:239[A]:MET:HG3	1.85	1.04

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)
2:B:112[B]:GLU:OE2	2:D:52:LYS:NZ[1_645]	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	255/261 (98%)	249 (98%)	6 (2%)	0	100	100
2	B	254/261 (97%)	248 (98%)	6 (2%)	0	100	100
2	C	249/261 (95%)	241 (97%)	8 (3%)	0	100	100
2	D	255/261 (98%)	245 (96%)	8 (3%)	2 (1%)	22	15

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	1013/1044 (97%)	983 (97%)	28 (3%)	2 (0%)	51 48

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	D	211	ASP
2	D	210	PRO

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	201/200 (100%)	198 (98%)	3 (2%)	70 74
2	B	200/200 (100%)	197 (98%)	3 (2%)	70 74
2	C	195/200 (98%)	193 (99%)	2 (1%)	80 84
2	D	199/200 (100%)	195 (98%)	4 (2%)	60 64
All	All	795/800 (99%)	783 (98%)	12 (2%)	71 74

5 of 12 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	216	PHE
2	C	239[A]	MET
2	D	80	GLU
2	B	205	LEU
2	D	72	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 8 such sidechains are listed below:

Mol	Chain	Res	Type
2	C	72	GLN
2	D	107	GLN
2	C	138	GLN

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Mol	Chain	Res	Type
2	B	260	GLN
2	C	106	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

13 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	NAD	A	301	-	41,48,48	1.38	6 (14%)	43,73,73	2.45	14 (32%)
4	TRS	A	302	-	7,7,7	2.71	4 (57%)	9,9,9	4.72	6 (66%)
5	SO4	A	303	-	4,4,4	1.39	1 (25%)	6,6,6	1.56	3 (50%)
5	SO4	A	304	-	4,4,4	0.61	0	6,6,6	0.40	0
3	NAD	B	301	-	41,48,48	1.61	8 (19%)	43,73,73	2.39	13 (30%)
4	TRS	B	302	-	7,7,7	1.85	3 (42%)	9,9,9	3.15	4 (44%)
5	SO4	B	303	-	4,4,4	1.75	1 (25%)	6,6,6	0.87	0
3	NAD	C	301	-	41,48,48	1.46	5 (12%)	43,73,73	2.36	10 (23%)
5	SO4	C	302	-	4,4,4	0.86	0	6,6,6	0.66	0
4	TRS	C	303	-	7,7,7	1.01	0	9,9,9	1.16	2 (22%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	NAD	D	301	-	41,48,48	1.25	4 (9%)	43,73,73	2.62	13 (30%)
6	AAE	D	302[L]	-	2,6,6	1.14	0	2,7,7	2.73	1 (50%)
5	SO4	D	303	-	4,4,4	0.81	0	6,6,6	1.02	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	NAD	A	301	-	-	0/22/62/62	0/5/5/5
4	TRS	A	302	-	-	0/9/9/9	0/0/0/0
5	SO4	A	303	-	-	0/0/0/0	0/0/0/0
5	SO4	A	304	-	-	0/0/0/0	0/0/0/0
3	NAD	B	301	-	-	0/22/62/62	0/5/5/5
4	TRS	B	302	-	-	0/9/9/9	0/0/0/0
5	SO4	B	303	-	-	0/0/0/0	0/0/0/0
3	NAD	C	301	-	-	0/22/62/62	0/5/5/5
5	SO4	C	302	-	-	0/0/0/0	0/0/0/0
4	TRS	C	303	-	-	0/9/9/9	0/0/0/0
3	NAD	D	301	-	-	0/22/62/62	0/5/5/5
6	AAE	D	302[L]	-	-	0/2/4/4	0/0/0/0
5	SO4	D	303	-	-	0/0/0/0	0/0/0/0

The worst 5 of 32 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	302	TRS	C3-C	-2.86	1.46	1.52
3	A	301	NAD	O7N-C7N	-2.44	1.19	1.24
3	B	301	NAD	C2N-C3N	-2.33	1.35	1.39
4	A	302	TRS	C2-C	-2.03	1.48	1.52
3	D	301	NAD	O3B-C3B	2.03	1.47	1.43

The worst 5 of 66 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	302	TRS	C1-C-N	-9.01	88.58	107.73
3	B	301	NAD	C5N-C4N-C3N	-7.49	111.54	120.35
3	C	301	NAD	C5N-C4N-C3N	-7.44	111.60	120.35
3	D	301	NAD	C5N-C4N-C3N	-7.43	111.61	120.35
3	C	301	NAD	C4B-O4B-C1B	-6.81	102.52	109.77

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	B	303	SO4	2	0
3	C	301	NAD	1	0
3	D	301	NAD	1	0
6	D	302[L]	AAE	2	0

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 ⓘ

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates ⓘ

EDS was not executed - this section is therefore empty.

6.4 Ligands ⓘ

EDS was not executed - this section is therefore empty.

6.5 Other polymers ⓘ

EDS was not executed - this section is therefore empty.