W O R L D W I D E
wwPDB
PROTEIN DATA BANK

wwPDB X-ray Structure Validation Summary Report (i)

Jun 14, 2020 – 10:30 am BST

PDB ID	:	2CFC
Title	:	structural basis for stereo selectivity in the (R)- and (S)- hydroxypropylethane thiosulfonate dehydrogenases
Authors	:	Krishnakumar, A.M.; Nocek, B.P.; Clark, D.D.; Ensign, S.A.; Peters, J.W.
Deposited on	:	2006-02-19
Resolution	:	1.80 Å(reported)

The following versions of software and data (see references (1)) were used in the production of this report:

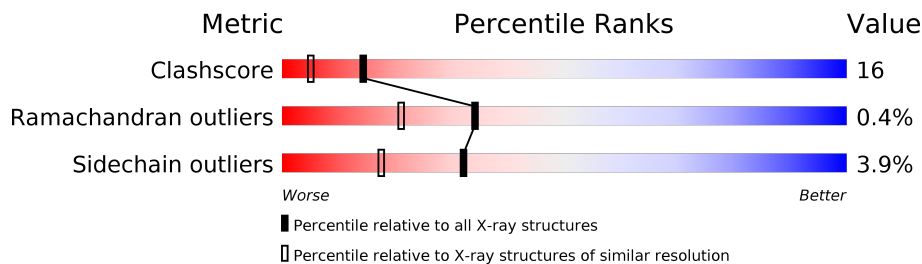|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (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 1.80 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	Percentile Ranks	Value
Clashscore		16
Ramachandran outliers		0.4%
Sidechain outliers		3.9%

Worse   *Better*

■ Percentile relative to all X-ray structures
▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	141614	6793 (1.80-1.80)
Ramachandran outliers	138981	6697 (1.80-1.80)
Sidechain outliers	138945	6696 (1.80-1.80)

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 <=5%

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	250	80% 18% •
1	B	250	78% 20% •
1	C	250	76% 22% •
1	D	250	78% 19% •

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:

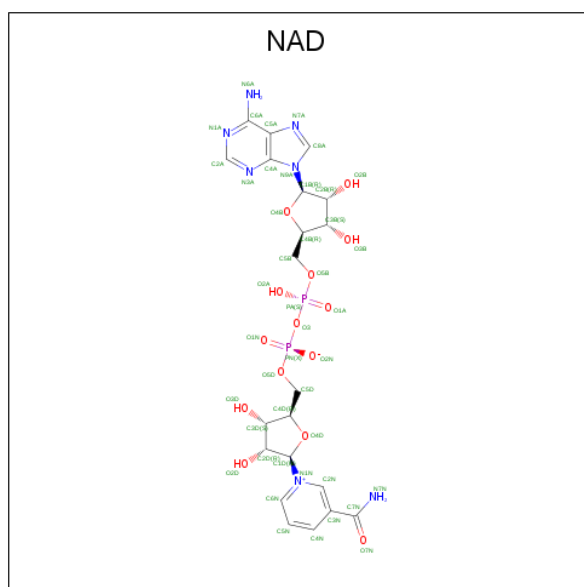| Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	KPC	A	1252	-	-	X	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 8463 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 2-(R)-HYDROXYPROPYL-COM DEHYDROGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	250	Total	C	N	O	S	0	0	0
			1832	1144	325	352	11			
1	B	250	Total	C	N	O	S	0	0	0
			1832	1144	325	352	11			
1	C	250	Total	C	N	O	S	0	0	0
			1832	1144	325	352	11			
1	D	250	Total	C	N	O	S	0	0	0
			1832	1144	325	352	11			

- Molecule 2 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).

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

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
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		

- Molecule 3 is (2-[2-KETOPROPYLTHIO]ETHANESULFONATE (three-letter code: KPC) (formula: $C_5H_{10}O_4S_2$).
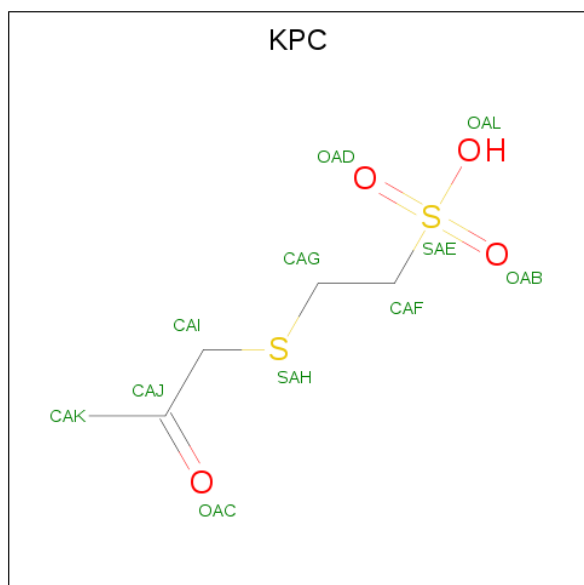
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	O	S	0	0
			11	5	4	2		
3	B	1	Total	C	O	S	0	0
			11	5	4	2		
3	C	1	Total	C	O	S	0	0
			11	5	4	2		
3	D	1	Total	C	O	S	0	0
			11	5	4	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	246	Total	O	0	0
			246	246		
4	B	243	Total	O	0	0
			243	243		
4	C	201	Total	O	0	0
			201	201		

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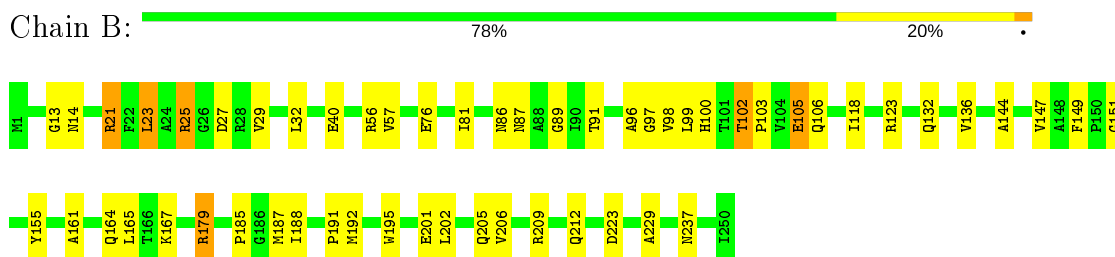| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	D	225	Total 225	O 225	0	0

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. 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. 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.
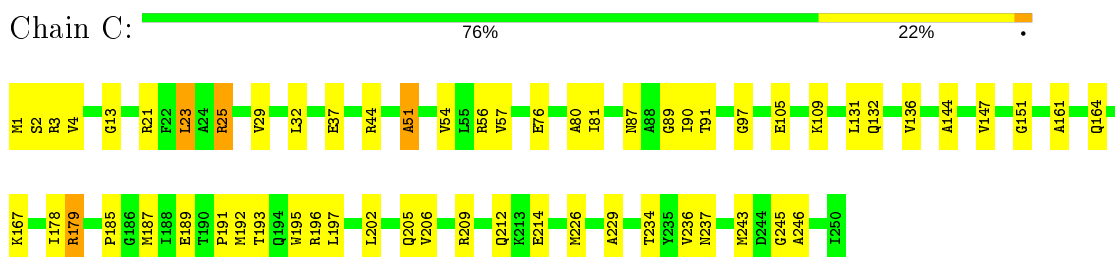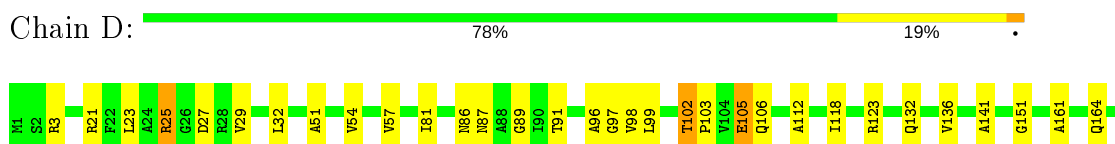
Note EDS was not executed.

• Molecule 1: 2-(R)-HYDROXYPROPYL-COM DEHYDROGENASE
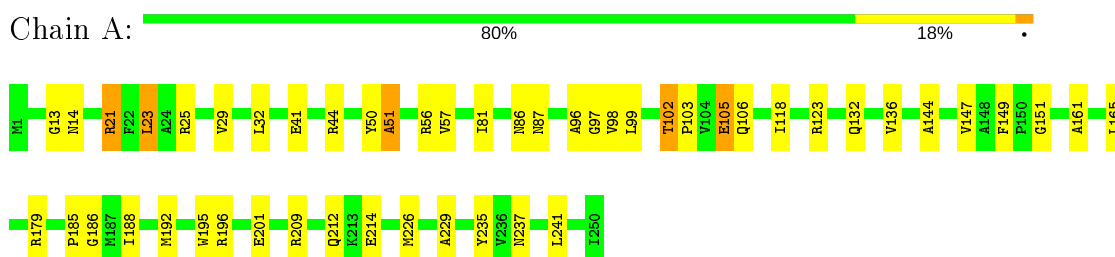
• Molecule 1: 2-(R)-HYDROXYPROPYL-COM DEHYDROGENASE

• Molecule 1: 2-(R)-HYDROXYPROPYL-COM DEHYDROGENASE

• Molecule 1: 2-(R)-HYDROXYPROPYL-COM DEHYDROGENASE

K167 R179 P185 G186 M187 I188 E189 T190 P191 M192 T193 Q194 W195 R196 L197 P200 R203 D204 Q205 V206 Q212 A229 V236 N237 L241 I250

4 Data and refinement statistics (i)

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	64.44Å 110.28Å 68.98Å 90.00° 93.88° 90.00°	Depositor
Resolution (Å)	50.00 – 1.80	Depositor
% Data completeness (in resolution range)	76.1 (50.00-1.80)	Depositor
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	CNS	Depositor
R, R_{free}	0.197 , 0.227	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	8463	wwPDB-VP
Average B, all atoms (Å^2)	21.0	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: KPC, 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	0.57	0/1857	0.72	0/2526
1	B	0.57	0/1857	0.74	0/2526
1	C	0.51	0/1857	0.71	0/2526
1	D	0.51	0/1857	0.72	0/2526
All	All	0.54	0/7428	0.72	0/10104

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 (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	1832	0	1845	59	0
1	B	1832	0	1845	51	0
1	C	1832	0	1845	60	0
1	D	1832	0	1845	55	0
2	A	44	0	26	11	0
2	B	44	0	26	17	0
2	C	44	0	26	11	0
2	D	44	0	26	17	0
3	A	11	0	10	7	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	11	0	10	5	0
3	C	11	0	10	4	0
3	D	11	0	10	5	0
4	A	246	0	0	4	0
4	B	243	0	0	4	0
4	C	201	0	0	4	0
4	D	225	0	0	6	0
All	All	8463	0	7524	234	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 16.

The worst 5 of 234 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)
3:D:1252:KPC:HAG1	3:D:1252:KPC:HAK1	1.49	0.92
1:B:21:ARG:NH2	1:B:223:ASP:OD1	2.04	0.91
1:D:87:ASN:O	2:D:1251:NAD:H4D	1.73	0.89
3:C:1252:KPC:HAG1	3:C:1252:KPC:HAK1	1.54	0.88
1:A:179:ARG:HG3	1:A:179:ARG:HH11	1.43	0.83

There are no symmetry-related clashes.

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	248/250 (99%)	240 (97%)	7 (3%)	1 (0%)	34	21
1	B	248/250 (99%)	242 (98%)	6 (2%)	0	100	100
1	C	248/250 (99%)	239 (96%)	7 (3%)	2 (1%)	19	7
1	D	248/250 (99%)	239 (96%)	8 (3%)	1 (0%)	34	21

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	992/1000 (99%)	960 (97%)	28 (3%)	4 (0%)	34 21

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	51	ALA
1	C	51	ALA
1	C	2	SER
1	D	51	ALA

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	186/186 (100%)	180 (97%)	6 (3%)	39 25
1	B	186/186 (100%)	177 (95%)	9 (5%)	25 11
1	C	186/186 (100%)	180 (97%)	6 (3%)	39 25
1	D	186/186 (100%)	178 (96%)	8 (4%)	29 14
All	All	744/744 (100%)	715 (96%)	29 (4%)	32 17

5 of 29 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	179	ARG
1	C	25	ARG
1	D	179	ARG
1	B	195	TRP
1	C	56	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	164	GLN

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Mol	Chain	Res	Type
1	C	14	ASN
1	D	199	GLN
1	B	205	GLN
1	B	212	GLN

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 ⓘ

8 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	D	1251	-	42,48,48	1.51	5 (11%)	50,73,73	1.35	4 (8%)
3	KPC	C	1252	-	10,10,10	1.71	1 (10%)	9,13,13	1.32	2 (22%)
3	KPC	B	1252	-	10,10,10	1.70	1 (10%)	9,13,13	1.32	2 (22%)
3	KPC	A	1252	-	10,10,10	1.71	1 (10%)	9,13,13	1.39	2 (22%)
2	NAD	B	1251	-	42,48,48	1.51	5 (11%)	50,73,73	1.36	5 (10%)
2	NAD	A	1251	-	42,48,48	1.50	5 (11%)	50,73,73	1.39	5 (10%)
3	KPC	D	1252	-	10,10,10	1.71	1 (10%)	9,13,13	1.34	2 (22%)
2	NAD	C	1251	-	42,48,48	1.51	5 (11%)	50,73,73	1.33	4 (8%)

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	D	1251	-	-	8/26/62/62	0/5/5/5
3	KPC	C	1252	-	-	0/8/8/8	-
3	KPC	B	1252	-	-	1/8/8/8	-
3	KPC	A	1252	-	-	1/8/8/8	-
2	NAD	B	1251	-	-	8/26/62/62	0/5/5/5
2	NAD	A	1251	-	-	9/26/62/62	0/5/5/5
3	KPC	D	1252	-	-	0/8/8/8	-
2	NAD	C	1251	-	-	8/26/62/62	0/5/5/5

The worst 5 of 24 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1251	NAD	O7N-C7N	6.46	1.36	1.24
2	D	1251	NAD	O7N-C7N	6.46	1.36	1.24
2	A	1251	NAD	O7N-C7N	6.46	1.36	1.24
2	C	1251	NAD	O7N-C7N	6.45	1.36	1.24
2	C	1251	NAD	C2N-N1N	4.72	1.40	1.35

The worst 5 of 26 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1251	NAD	N3A-C2A-N1A	-4.88	121.05	128.68
2	A	1251	NAD	N3A-C2A-N1A	-4.82	121.14	128.68
2	D	1251	NAD	N3A-C2A-N1A	-4.81	121.16	128.68
2	C	1251	NAD	N3A-C2A-N1A	-4.68	121.37	128.68
2	A	1251	NAD	O4B-C1B-C2B	-4.31	100.62	106.93

There are no chirality outliers.

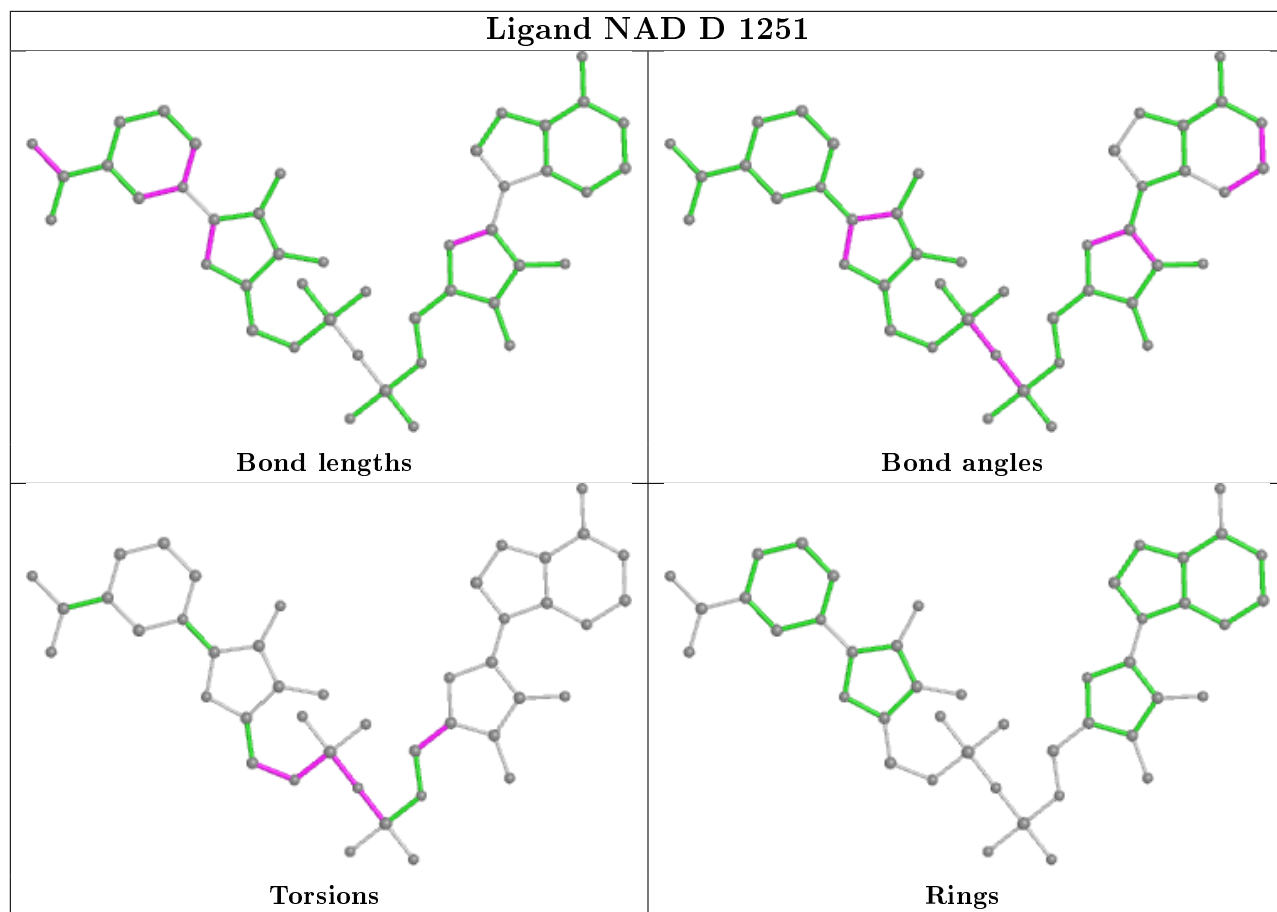5 of 35 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	D	1251	NAD	C5D-O5D-PN-O1N
3	B	1252	KPC	SAH-CAI-CAJ-CAK
2	B	1251	NAD	PA-O3-PN-O5D
2	B	1251	NAD	C5D-O5D-PN-O1N
2	A	1251	NAD	C5B-O5B-PA-O2A

There are no ring outliers.
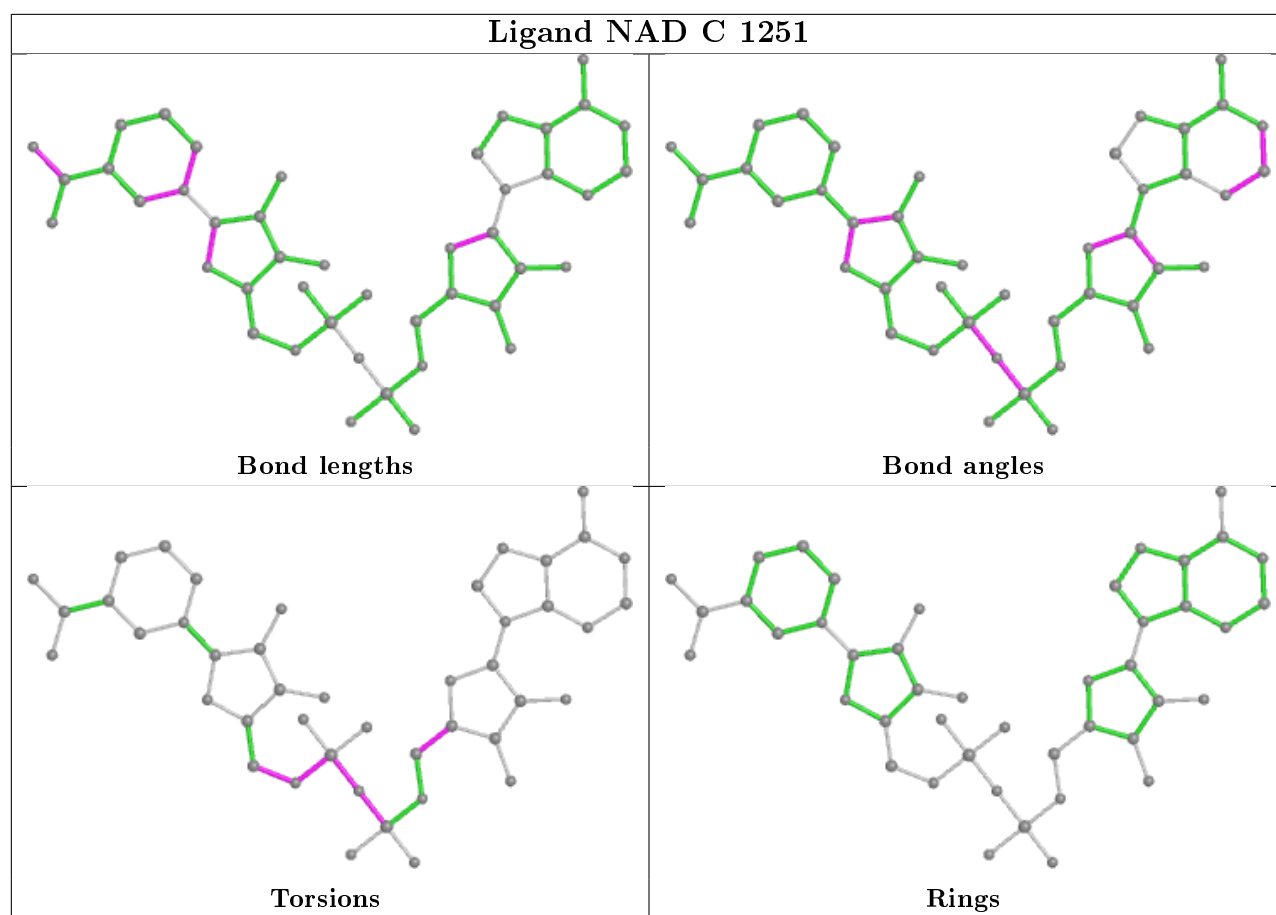
8 monomers are involved in 77 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	1251	NAD	17	0
3	C	1252	KPC	4	0
3	B	1252	KPC	5	0
3	A	1252	KPC	7	0
2	B	1251	NAD	17	0
2	A	1251	NAD	11	0
3	D	1252	KPC	5	0
2	C	1251	NAD	11	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 then 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.

Ligand NAD D 1251

Bond lengths

Bond angles

Torsions

Rings

Ligand NAD B 1251

Bond lengths

Bond angles

Torsions

Rings

Ligand NAD A 1251

Bond lengths

Bond angles

Torsions

Rings

Ligand NAD C 1251

Bond lengths

Bond angles

Torsions

Rings
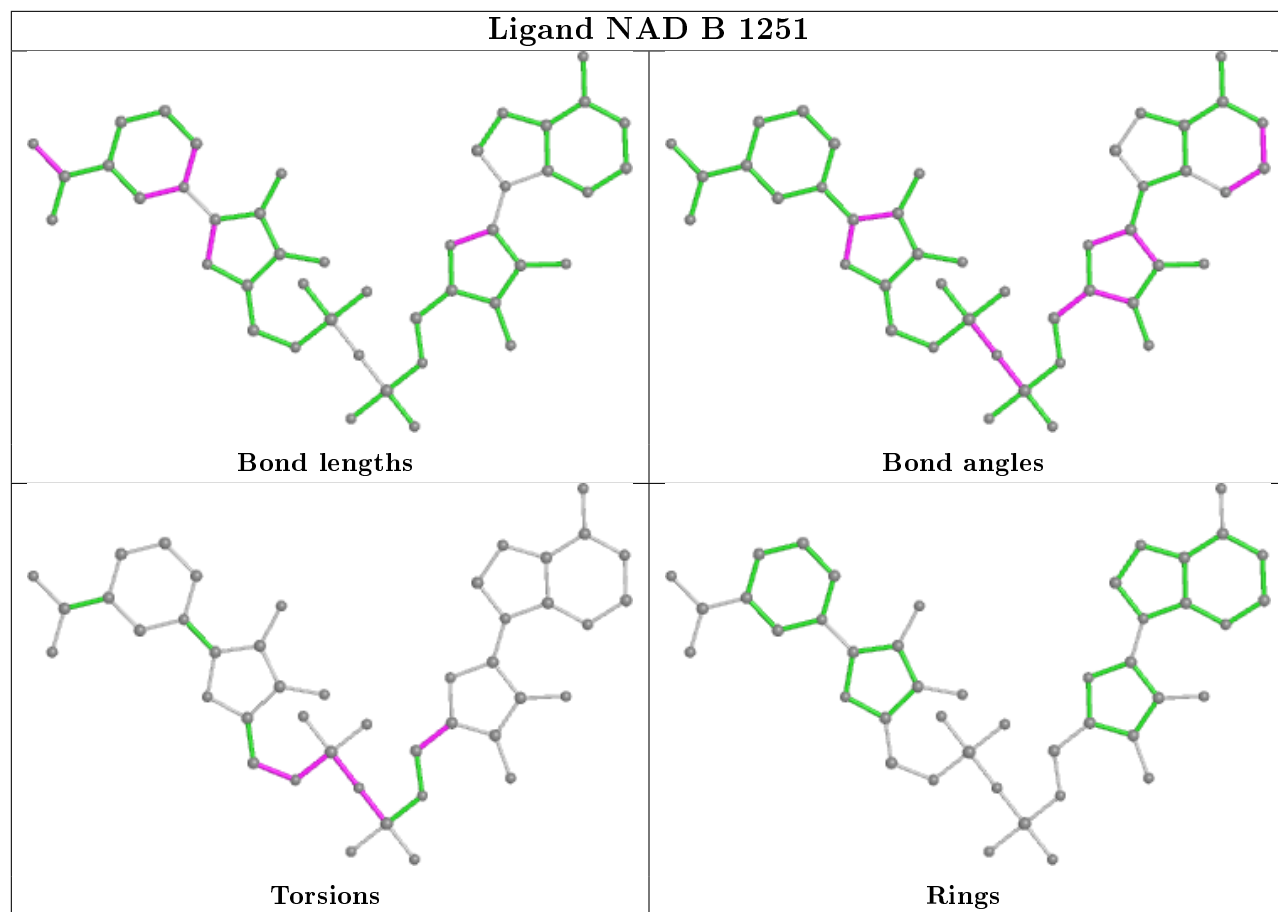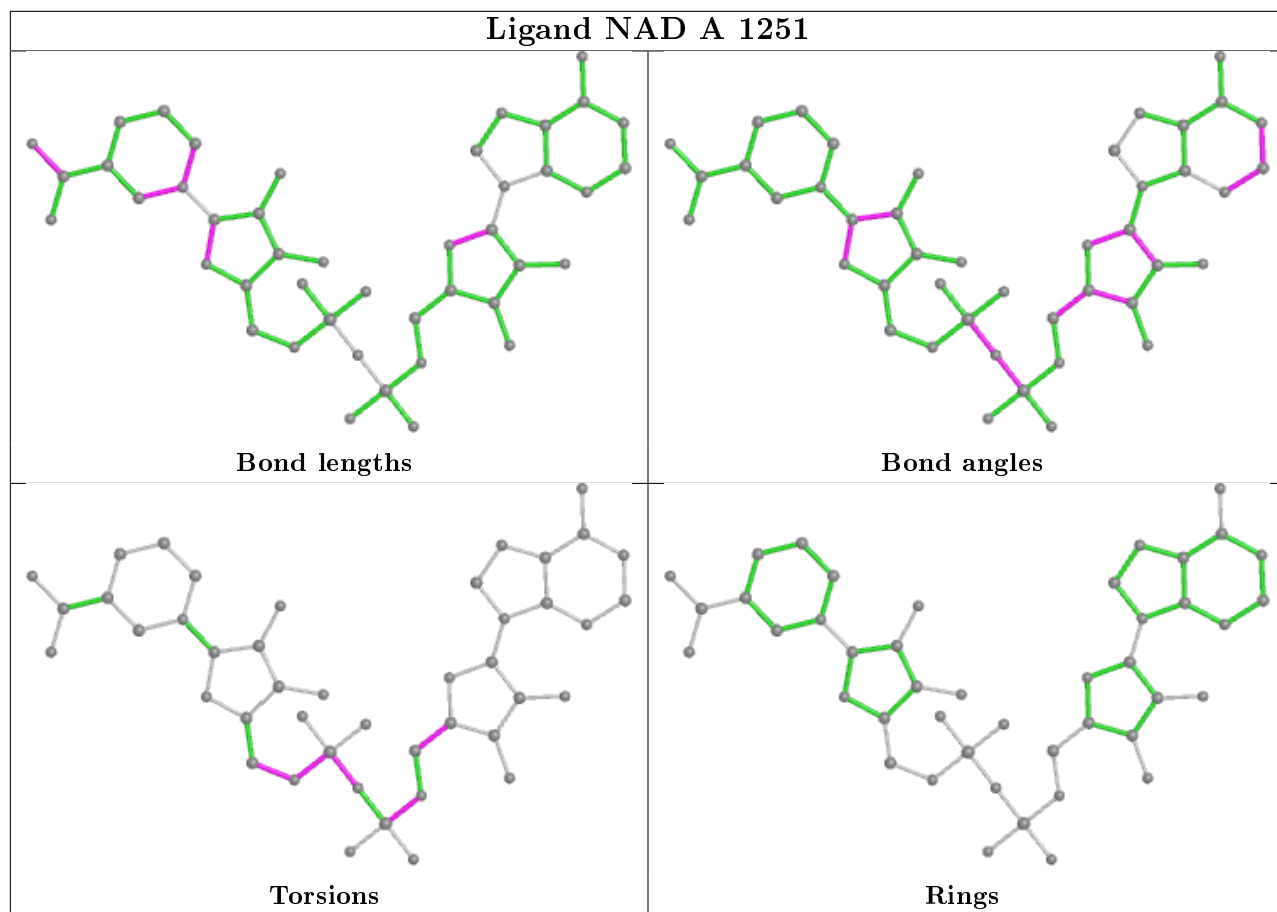
5.7 Other polymers (i)

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)

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates (i)

EDS was not executed - this section is therefore empty.

6.4 Ligands (i)

EDS was not executed - this section is therefore empty.

6.5 Other polymers (i)

EDS was not executed - this section is therefore empty.