



# wwPDB X-ray Structure Validation Summary Report ⓘ

Jan 31, 2016 – 06:55 PM GMT

PDB ID : 1D4F  
Title : CRYSTAL STRUCTURE OF RECOMBINANT RAT-LIVER D244E MUTANT S-ADENOSYLHOMOCYSTEINE HYDROLASE  
Authors : Komoto, J.; Huang, Y.; Takusagawa, F.; Gomi, T.; Ogawa, H.; Takata, Y.; Fujioka, M.  
Deposited on : 2000-06-22  
Resolution : 2.80 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](mailto: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 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

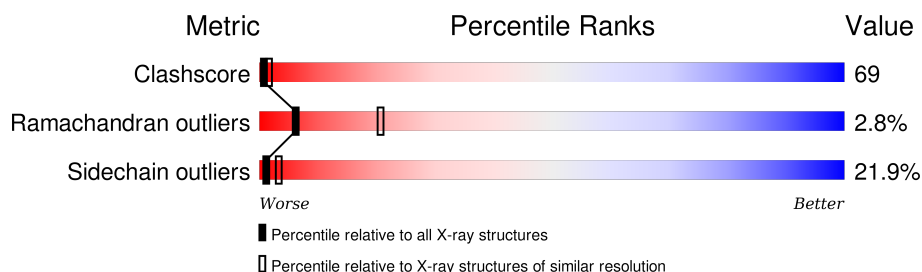
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)

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  $\geq 3$ , 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	431	<div> <div>31%</div> <div>55%</div> <div>14%</div> </div>
1	B	431	<div> <div>35%</div> <div>49%</div> <div>15%</div> </div>
1	C	431	<div> <div>27%</div> <div>55%</div> <div>16%</div> </div>
1	D	431	<div> <div>31%</div> <div>52%</div> <div>16%</div> </div>

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
2	NAD	A	501	-	-	X	-

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 14005 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.

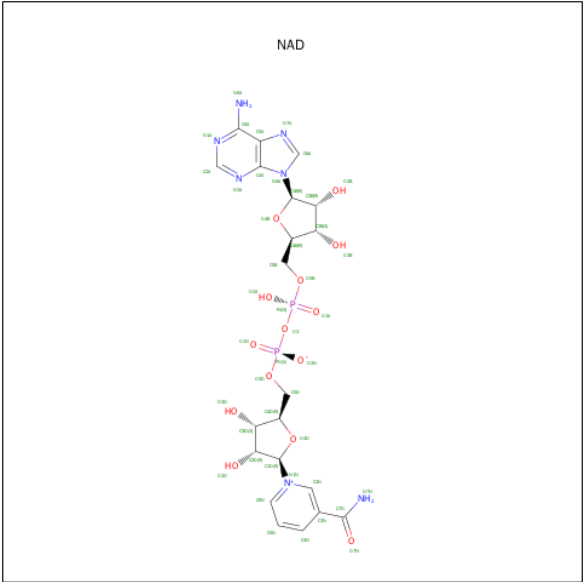
- Molecule 1 is a protein called S-ADENOSYLHOMOCYSTEINE HYDROLASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	430	Total	C	N	O	S	0	0	0
			3320	2109	571	615	25			
1	B	430	Total	C	N	O	S	0	0	0
			3320	2109	571	615	25			
1	C	430	Total	C	N	O	S	0	0	0
			3320	2109	571	615	25			
1	D	430	Total	C	N	O	S	0	0	0
			3320	2109	571	615	25			

There are 4 discrepancies between the modelled and reference sequences:

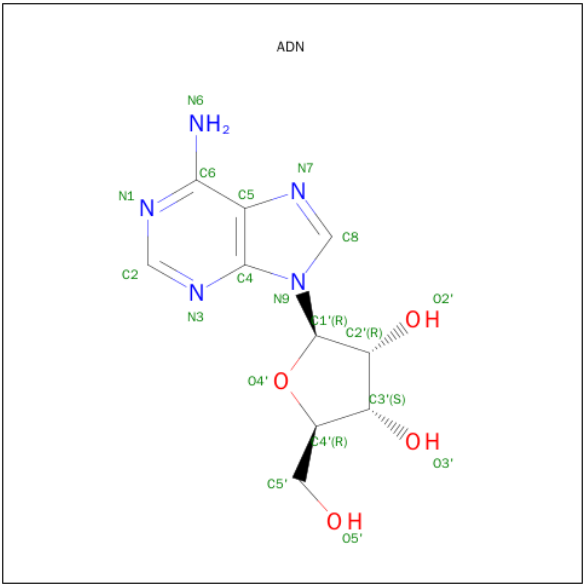
Chain	Residue	Modelled	Actual	Comment	Reference
A	244	GLU	ASP	ENGINEERED	UNP P10760
B	244	GLU	ASP	ENGINEERED	UNP P10760
C	244	GLU	ASP	ENGINEERED	UNP P10760
D	244	GLU	ASP	ENGINEERED	UNP P10760

- 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		
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 ADENOSINE (three-letter code: ADN) (formula: C<sub>10</sub>H<sub>13</sub>N<sub>5</sub>O<sub>4</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			19	10	5	4		
3	B	1	Total	C	N	O	0	0
			19	10	5	4		
3	C	1	Total	C	N	O	0	0
			19	10	5	4		
3	D	1	Total	C	N	O	0	0
			19	10	5	4		

- Molecule 4 is water.

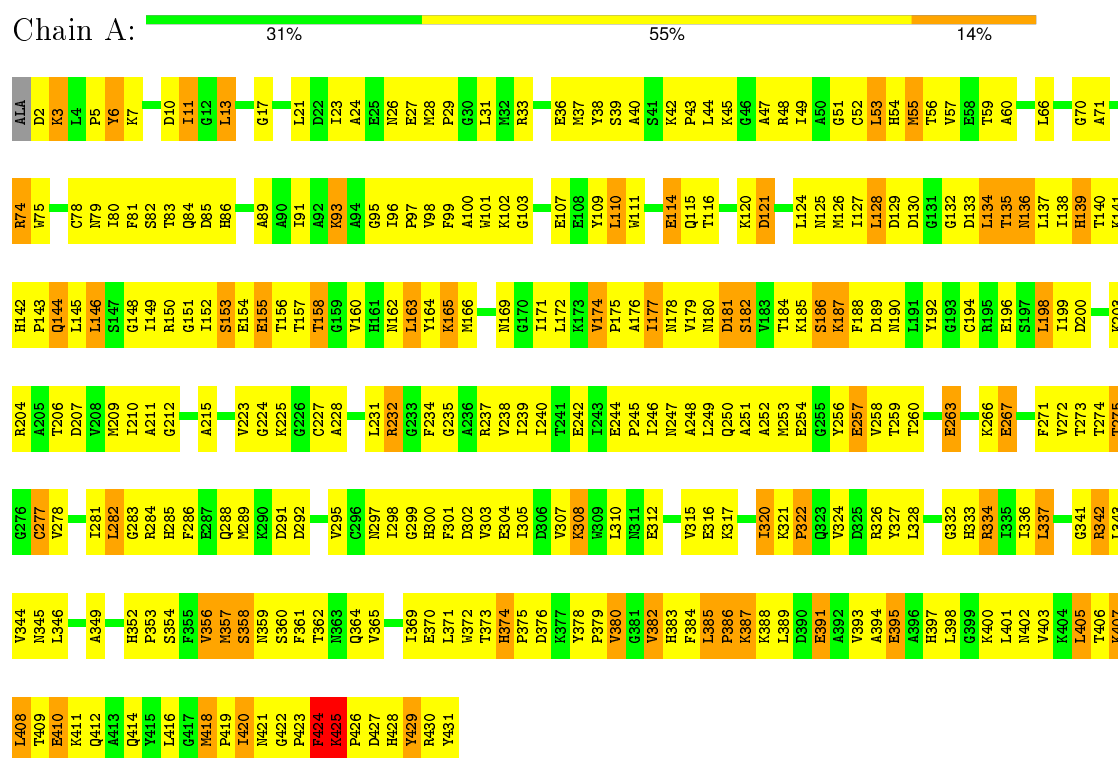
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	137	Total	O	0	0
			137	137		
4	B	118	Total	O	0	0
			118	118		
4	C	120	Total	O	0	0
			120	120		
4	D	98	Total	O	0	0
			98	98		

### 3 Residue-property plots

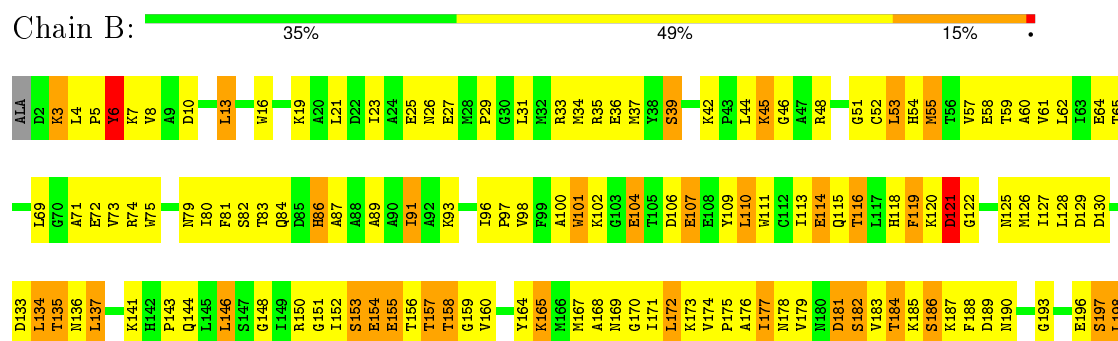
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according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

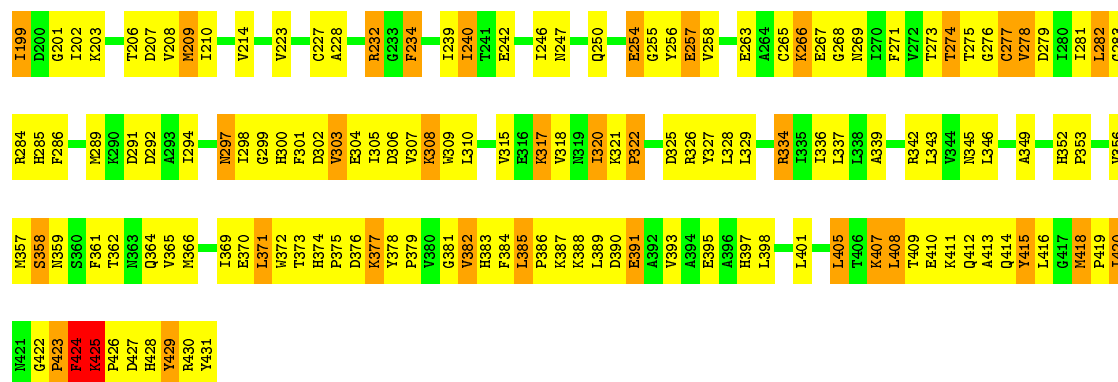
Note EDS was not executed.

#### • Molecule 1: S-ADENOSYLHOMOCYSTEINE HYDROLASE



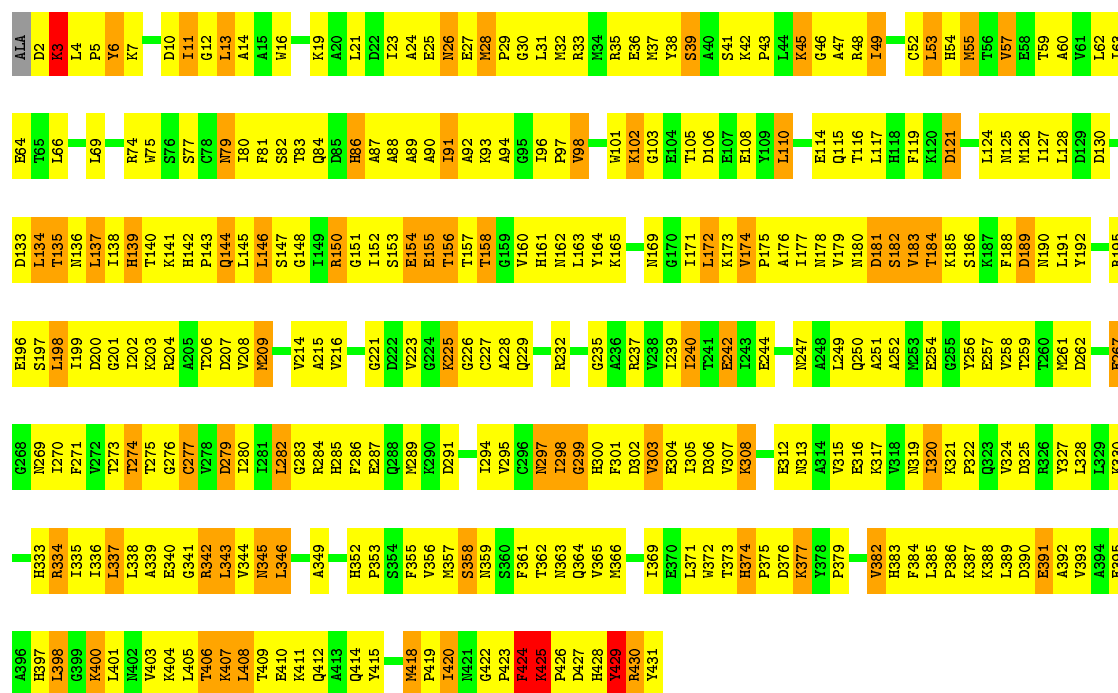
#### • Molecule 1: S-ADENOSYLHOMOCYSTEINE HYDROLASE





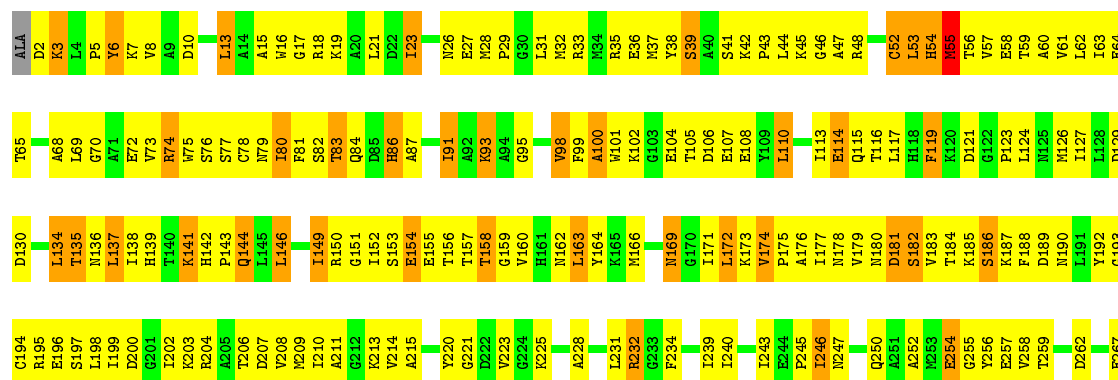
• Molecule 1: S-ADENOSYLHOMOCYSTEINE HYDROLASE

Chain C: 27% 55% 16%



• Molecule 1: S-ADENOSYLHOMOCYSTEINE HYDROLASE

Chain D: 31% 52% 16%







## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	91.00 Å   223.00 Å   91.23 Å 90.00°   90.00°   90.00°	Depositor
Resolution (Å)	8.00 – 2.80	Depositor
% Data completeness (in resolution range)	100.0 (8.00-2.80)	Depositor
$R_{merge}$	0.10	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	X-PLOR 3.843	Depositor
R, $R_{free}$	0.197 , 0.248	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	14005	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	11.0	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: ADN, 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	0.31	0/3385	0.59	0/4580
1	B	0.31	0/3385	0.59	0/4580
1	C	0.32	0/3385	0.59	0/4580
1	D	0.32	0/3385	0.58	0/4580
All	All	0.32	0/13540	0.59	0/18320

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	3320	0	3343	465	0
1	B	3320	0	3343	480	0
1	C	3320	0	3343	497	0
1	D	3320	0	3343	513	0
2	A	44	0	26	22	0
2	B	44	0	26	16	0
2	C	44	0	26	7	0
2	D	44	0	26	9	0
3	A	19	0	13	3	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	B	19	0	13	2	0
3	C	19	0	13	1	0
3	D	19	0	13	1	0
4	A	137	0	0	3	0
4	B	118	0	0	8	0
4	C	120	0	0	7	0
4	D	98	0	0	3	0
All	All	14005	0	13528	1856	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 69.

The worst 5 of 1856 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:419:PRO:CG	1:A:422:GLY:HA3	1.36	1.53
1:A:419:PRO:HG2	1:A:422:GLY:C	1.23	1.52
1:A:419:PRO:HG2	1:A:422:GLY:CA	1.40	1.51
1:D:419:PRO:HG2	1:D:422:GLY:C	1.31	1.45
1:A:419:PRO:CG	1:A:422:GLY:CA	1.91	1.40

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	428/431 (99%)	367 (86%)	50 (12%)	11 (3%)	7	22
1	B	428/431 (99%)	373 (87%)	43 (10%)	12 (3%)	6	21
1	C	428/431 (99%)	374 (87%)	42 (10%)	12 (3%)	6	21
1	D	428/431 (99%)	358 (84%)	57 (13%)	13 (3%)	5	18

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	1712/1724 (99%)	1472 (86%)	192 (11%)	48 (3%)	6	21

5 of 48 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	3	LYS
1	A	425	LYS
1	B	425	LYS
1	C	184	THR
1	D	415	TYR

### 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	353/353 (100%)	282 (80%)	71 (20%)	1	4
1	B	353/353 (100%)	271 (77%)	82 (23%)	1	3
1	C	353/353 (100%)	269 (76%)	84 (24%)	1	2
1	D	353/353 (100%)	281 (80%)	72 (20%)	1	4
All	All	1412/1412 (100%)	1103 (78%)	309 (22%)	1	3

5 of 309 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	390	ASP
1	C	110	LEU
1	D	321	LYS
1	B	407	LYS
1	C	26	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	428	HIS
1	C	269	ASN
1	D	374	HIS
1	C	26	ASN
1	C	178	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 ⓘ

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	A	501	-	38,48,48	1.48	3 (7%)	47,73,73	2.56	16 (34%)
3	ADN	A	601	-	16,21,21	0.91	1 (6%)	16,31,31	2.27	4 (25%)
2	NAD	B	502	-	38,48,48	1.46	4 (10%)	47,73,73	2.24	10 (21%)
3	ADN	B	602	-	16,21,21	0.87	1 (6%)	16,31,31	2.60	4 (25%)
2	NAD	C	503	-	38,48,48	1.19	3 (7%)	47,73,73	2.10	11 (23%)
3	ADN	C	603	-	16,21,21	0.80	1 (6%)	16,31,31	2.61	6 (37%)
2	NAD	D	504	-	38,48,48	1.01	3 (7%)	47,73,73	2.04	10 (21%)
3	ADN	D	604	-	16,21,21	0.86	0	16,31,31	2.82	5 (31%)

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	501	-	-	0/22/62/62	0/5/5/5
3	ADN	A	601	-	-	0/2/22/22	0/3/3/3
2	NAD	B	502	-	-	0/22/62/62	0/5/5/5
3	ADN	B	602	-	-	0/2/22/22	0/3/3/3
2	NAD	C	503	-	-	0/22/62/62	0/5/5/5
3	ADN	C	603	-	-	0/2/22/22	0/3/3/3
2	NAD	D	504	-	-	0/22/62/62	0/5/5/5
3	ADN	D	604	-	-	0/2/22/22	0/3/3/3

The worst 5 of 16 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	502	NAD	C5A-N7A	-2.11	1.32	1.39
2	A	501	NAD	C5A-N7A	-2.06	1.32	1.39
3	C	603	ADN	C5-N7	-2.06	1.32	1.39
3	B	602	ADN	C5-N7	-2.04	1.32	1.39
2	D	504	NAD	C5A-N7A	-2.02	1.32	1.39

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	C	603	ADN	N3-C2-N1	-7.67	123.03	128.89
3	D	604	ADN	N3-C2-N1	-7.47	123.17	128.89
3	B	602	ADN	N3-C2-N1	-7.00	123.53	128.89
2	C	503	NAD	N3A-C2A-N1A	-6.83	123.67	128.89
2	D	504	NAD	N3A-C2A-N1A	-6.71	123.75	128.89

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

8 monomers are involved in 57 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	501	NAD	22	0
3	A	601	ADN	3	0
2	B	502	NAD	16	0
3	B	602	ADN	2	0

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	503	NAD	7	0
3	C	603	ADN	1	0
2	D	504	NAD	9	0
3	D	604	ADN	1	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 [i](#)

### 6.1 Protein, DNA and RNA chains [i](#)

EDS was not executed - this section will therefore be empty.

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

EDS was not executed - this section will therefore be empty.

### 6.3 Carbohydrates [i](#)

EDS was not executed - this section will therefore be empty.

### 6.4 Ligands [i](#)

EDS was not executed - this section will therefore be empty.

### 6.5 Other polymers [i](#)

EDS was not executed - this section will therefore be empty.