



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 15, 2017 – 12:49 am GMT

PDB ID : 2D5N  
Title : Crystal structure of a bifunctional deaminase and reductase involved in riboflavin biosynthesis  
Authors : Liaw, S.H.; Chen, S.J.; Chang, Y.C.  
Deposited on : 2005-11-02  
Resolution : 2.97 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.

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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) : 1.9-1692  
EDS : trunk28620  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949



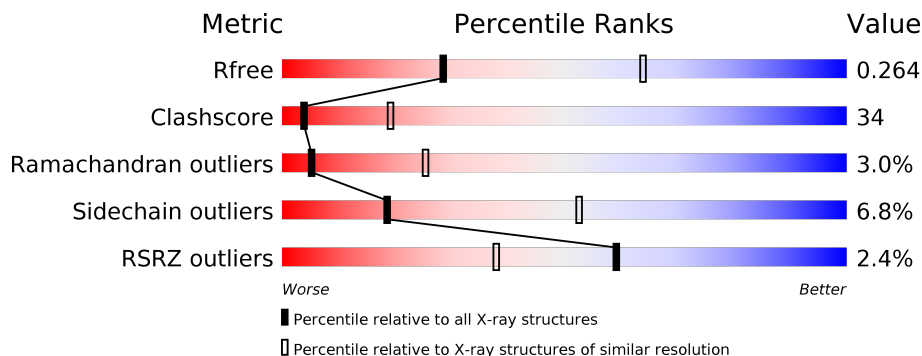
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.97 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))
$R_{free}$	100719	2168 (3.00-2.96)
Clashscore	112137	2535 (3.00-2.96)
Ramachandran outliers	110173	2451 (3.00-2.96)
Sidechain outliers	110143	2454 (3.00-2.96)
RSRZ outliers	101464	2192 (3.00-2.96)

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.

Mol	Chain	Length	Quality of chain
1	A	373	
1	B	373	
1	C	373	
1	D	373	



## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 11257 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 Riboflavin biosynthesis protein ribD.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	359	Total	C	N	O	S	0	0	0
			2741	1740	469	517	15			
1	B	359	Total	C	N	O	S	0	0	0
			2741	1740	469	517	15			
1	C	359	Total	C	N	O	S	0	0	0
			2741	1740	469	517	15			
1	D	360	Total	C	N	O	S	0	0	0
			2747	1743	470	519	15			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-11	MET	-	CLONING ARTIFACT	UNP P17618
A	-10	ARG	-	CLONING ARTIFACT	UNP P17618
A	-9	GLY	-	CLONING ARTIFACT	UNP P17618
A	-8	SER	-	CLONING ARTIFACT	UNP P17618
A	-7	HIS	-	CLONING ARTIFACT	UNP P17618
A	-6	HIS	-	CLONING ARTIFACT	UNP P17618
A	-5	HIS	-	CLONING ARTIFACT	UNP P17618
A	-4	HIS	-	CLONING ARTIFACT	UNP P17618
A	-3	HIS	-	CLONING ARTIFACT	UNP P17618
A	-2	HIS	-	CLONING ARTIFACT	UNP P17618
A	-1	GLY	-	CLONING ARTIFACT	UNP P17618
A	0	SER	-	CLONING ARTIFACT	UNP P17618
B	-11	MET	-	CLONING ARTIFACT	UNP P17618
B	-10	ARG	-	CLONING ARTIFACT	UNP P17618
B	-9	GLY	-	CLONING ARTIFACT	UNP P17618
B	-8	SER	-	CLONING ARTIFACT	UNP P17618
B	-7	HIS	-	CLONING ARTIFACT	UNP P17618
B	-6	HIS	-	CLONING ARTIFACT	UNP P17618
B	-5	HIS	-	CLONING ARTIFACT	UNP P17618
B	-4	HIS	-	CLONING ARTIFACT	UNP P17618
B	-3	HIS	-	CLONING ARTIFACT	UNP P17618

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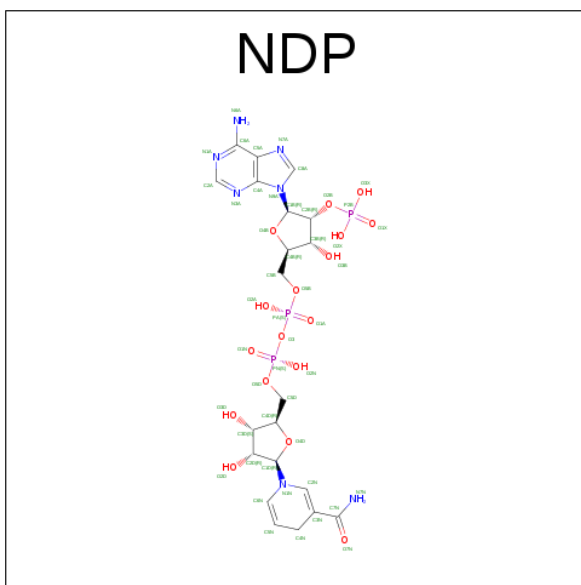
Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	HIS	-	CLONING ARTIFACT	UNP P17618
B	-1	GLY	-	CLONING ARTIFACT	UNP P17618
B	0	SER	-	CLONING ARTIFACT	UNP P17618
C	-11	MET	-	CLONING ARTIFACT	UNP P17618
C	-10	ARG	-	CLONING ARTIFACT	UNP P17618
C	-9	GLY	-	CLONING ARTIFACT	UNP P17618
C	-8	SER	-	CLONING ARTIFACT	UNP P17618
C	-7	HIS	-	CLONING ARTIFACT	UNP P17618
C	-6	HIS	-	CLONING ARTIFACT	UNP P17618
C	-5	HIS	-	CLONING ARTIFACT	UNP P17618
C	-4	HIS	-	CLONING ARTIFACT	UNP P17618
C	-3	HIS	-	CLONING ARTIFACT	UNP P17618
C	-2	HIS	-	CLONING ARTIFACT	UNP P17618
C	-1	GLY	-	CLONING ARTIFACT	UNP P17618
C	0	SER	-	CLONING ARTIFACT	UNP P17618
D	-11	MET	-	CLONING ARTIFACT	UNP P17618
D	-10	ARG	-	CLONING ARTIFACT	UNP P17618
D	-9	GLY	-	CLONING ARTIFACT	UNP P17618
D	-8	SER	-	CLONING ARTIFACT	UNP P17618
D	-7	HIS	-	CLONING ARTIFACT	UNP P17618
D	-6	HIS	-	CLONING ARTIFACT	UNP P17618
D	-5	HIS	-	CLONING ARTIFACT	UNP P17618
D	-4	HIS	-	CLONING ARTIFACT	UNP P17618
D	-3	HIS	-	CLONING ARTIFACT	UNP P17618
D	-2	HIS	-	CLONING ARTIFACT	UNP P17618
D	-1	GLY	-	CLONING ARTIFACT	UNP P17618
D	0	SER	-	CLONING ARTIFACT	UNP P17618

- 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
2	D	1	Total Zn 1 1	0	0
2	C	1	Total Zn 1 1	0	0

- Molecule 3 is NADPH DIHYDRO-NICOTINAMIDE-ADENINE-DINUCLEOTIDE PHOSPHATE (three-letter code: NDP) (formula: C<sub>21</sub>H<sub>30</sub>N<sub>7</sub>O<sub>17</sub>P<sub>3</sub>).





Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total 48	C 21	N 7	O 17	P 3	0	0

- Molecule 4 is water.

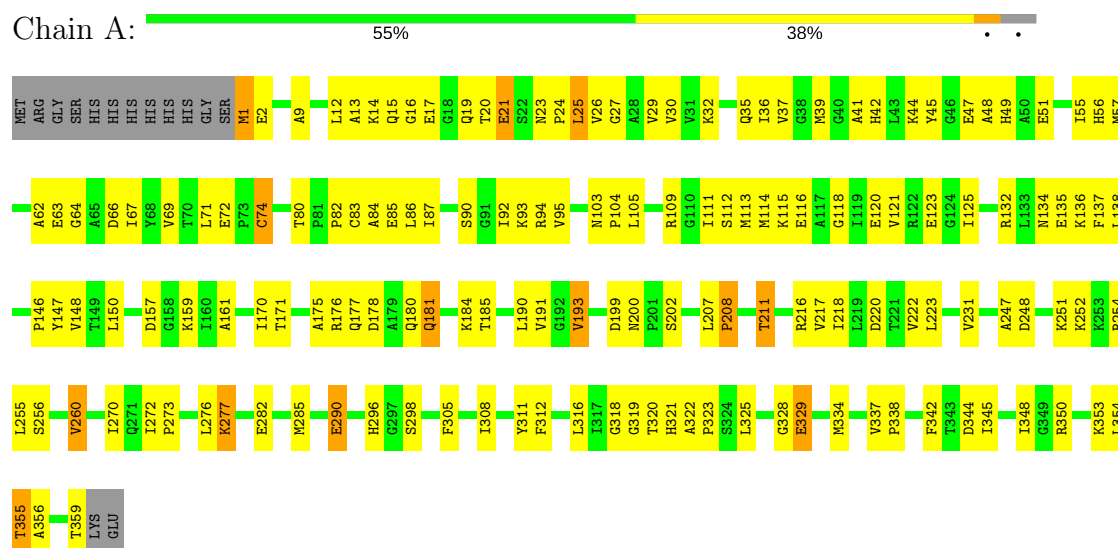
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	66	Total O 66 66	0	0
4	B	64	Total O 64 64	0	0
4	C	54	Total O 54 54	0	0
4	D	51	Total O 51 51	0	0



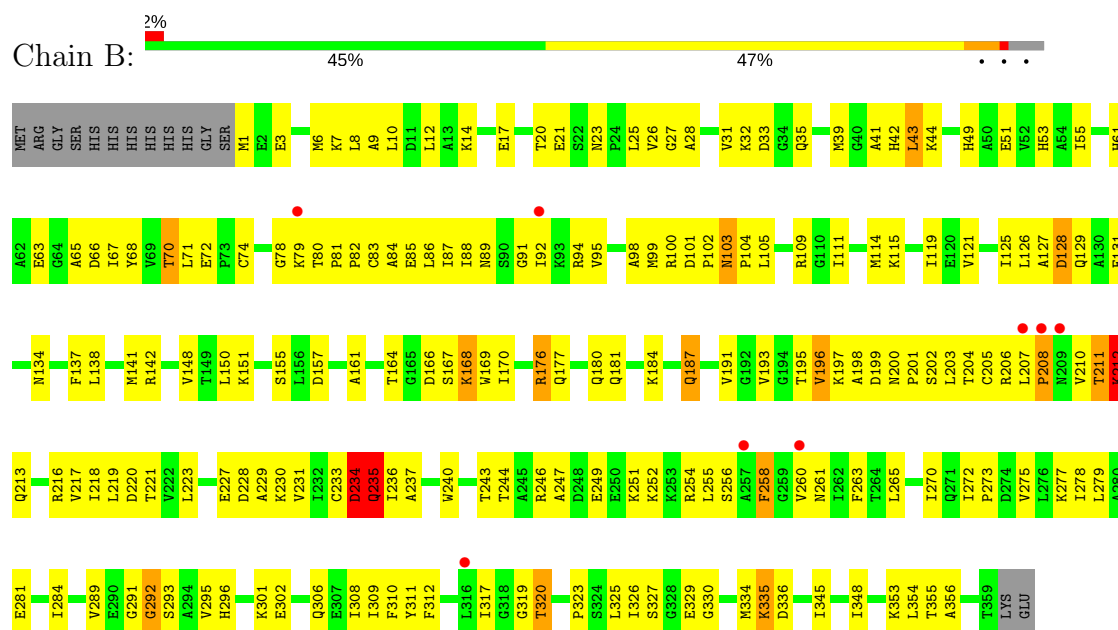
### 3 Residue-property plots

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.

#### • Molecule 1: Riboflavin biosynthesis protein ribD



#### • Molecule 1: Riboflavin biosynthesis protein ribD





Chain C:

5% 43% 47% 6%

MET ARG GLY SER HIS HIS HIS HIS HIS GLY SER M1 Y5 M6 K7 L8 A9 L10 L11 D12 A13 K14 E17 E21 S22 N23 P24 V26 G27 A28 V29 V30 V31 K32 G33 D34 Q35 V37 G38 N39 L43 K44 H49 A50 E51 V52 H53 A54 H55 H56 A57 A58 E123 H61 A62 E63 D66 I67 Y68 V69 T70 L71 E72 P73 C74 S75 H76 Y77 G78 K79 T80 L81 P82 C83 A84 E85 L86 T87 T88 N89 S90 G91 I92 K93 R94 V95 F96 Y97 A98 N99 R100 L103 P104 L105 V106 A107 G108 I111 S112 M113 K114 L115 E116 A117 G118 I119 T120 V121 R122 G192 V193 G194 T195 T204 C205 R206 L207 P208 S209 V210 T211 K212 Q213 R216 V217 L218 K219 D220 T221 V222 L223 C232 T233 D234 Q235 T236 A237 T238 T239 V240 K251 R252 K253 R254 L255 S256 V260 N261 K265 L266 S266 T267 E268 Q271 L272 T273 K274 V275 L276 K277 A280 V281 M285 Y288 V289 E290 H296 F305 Q306 E307 I308 K309 F310 Y311 F312 A313 F314 K315 L316 I317 P323 S324 G328 F331 Q332 S333 K336 V337 P338 D344 I345 K346 Q347 I348 D351 I352 K353 L354 T355 A356 K357 P358 T359 LYS GLU

Chain D:

3% 47% 43% 5%

MET ARG GLY SER HIS HIS HIS HIS HIS GLY SO M1 E2 Y5 A9 K14 E17 G18 Q19 T20 S21 S22 N23 P24 L25 V29 Q35 T36 V37 K44 A48 H49 H53 M57 H61 A62 E63 G64 I67 Y68 L71 E72 P73 C74 S75 F76

T149 L150 K151 S155 L156 I160 A161 D166 S167 K168 W169 I170 T171 S172 Q177 D178 K184 T185 H186 Q187 S188 T189 K190 G192 V191 G194 T195 N200 P201 S202 T203 T204 L207 P208 N209 Q213 R216 V217 L218 L219 D220 T221 V222 L223 S224 L225 P226 E227 D228 F229 K230 V231 T232 C233 D234 Q235 T239 W240 I241 F242 T243 T244 A247 K252 D253 R254 L255 G259 V260 N261 T262 F263 T264 L265 E266 T267 E268 R269 L270 Q271 T272 P273 D274 K277 L278 F279 A280 E281 T284 R285 S286 V287 Y288 V289 E290 G291 G292 V295 H296 C297



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	86.13Å 107.95Å 186.84Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.97 46.74 – 2.97	Depositor EDS
% Data completeness (in resolution range)	97.5 (30.00-2.97) 97.2 (46.74-2.97)	Depositor EDS
$R_{merge}$	0.07	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	3.59 (at 2.96Å)	Xtriage
Refinement program	CNS 1.0	Depositor
R, $R_{free}$	0.224 , 0.270 0.214 , 0.264	Depositor DCC
$R_{free}$ test set	3566 reflections (9.97%)	DCC
Wilson B-factor (Å <sup>2</sup> )	71.8	Xtriage
Anisotropy	0.442	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.29 , 48.2	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.93	EDS
Total number of atoms	11257	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	67.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.79% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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: NDP, ZN

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	0.39	0/2792	0.67	1/3778 (0.0%)
1	B	0.38	0/2792	0.64	0/3778
1	C	0.37	0/2792	0.63	0/3778
1	D	0.37	0/2798	0.64	1/3786 (0.0%)
All	All	0.38	0/11174	0.65	2/15120 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	74	CYS	CA-CB-SG	6.18	125.13	114.00
1	D	83	CYS	CA-CB-SG	-5.45	104.19	114.00

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	2741	0	2782	156	0
1	B	2741	0	2782	232	0
1	C	2741	0	2782	217	0
1	D	2747	0	2787	174	0
2	A	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	1	0	0	0	0
2	C	1	0	0	0	0
2	D	1	0	0	0	0
3	B	48	0	26	10	0
4	A	66	0	0	17	2
4	B	64	0	0	4	1
4	C	54	0	0	3	0
4	D	51	0	0	5	0
All	All	11257	0	11159	744	2

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 34.

The worst 5 of 744 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:309:ILE:HG12	1:B:355:THR:HG22	1.33	1.06
1:A:94:ARG:HA	4:A:1377:HOH:O	1.55	1.06
1:A:355:THR:HG22	4:A:1415:HOH:O	1.58	1.01
1:C:21:GLU:HG3	1:C:22:SER:H	1.26	1.00
1:D:270:ILE:H	1:D:270:ILE:HD13	1.24	0.98

All (2) 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)
4:A:1398:HOH:O	4:B:1422:HOH:O[3_645]	1.93	0.27
4:A:1410:HOH:O	4:A:1419:HOH:O[3_645]	2.19	0.01

## 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	357/373 (96%)	310 (87%)	41 (12%)	6 (2%)	11	42
1	B	357/373 (96%)	303 (85%)	44 (12%)	10 (3%)	6	27
1	C	357/373 (96%)	303 (85%)	43 (12%)	11 (3%)	5	24
1	D	358/373 (96%)	309 (86%)	33 (9%)	16 (4%)	3	15
All	All	1429/1492 (96%)	1225 (86%)	161 (11%)	43 (3%)	5	25

5 of 43 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	208	PRO
1	A	329	GLU
1	B	168	LYS
1	B	208	PRO
1	B	211	THR

### 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	293/305 (96%)	276 (94%)	17 (6%)	23	60
1	B	293/305 (96%)	277 (94%)	16 (6%)	25	62
1	C	293/305 (96%)	272 (93%)	21 (7%)	17	49
1	D	294/305 (96%)	268 (91%)	26 (9%)	12	39
All	All	1173/1220 (96%)	1093 (93%)	80 (7%)	18	52

5 of 80 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	74	CYS
1	C	181	GLN
1	D	266	GLU
1	C	76	HIS
1	C	125	ILE



Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 48 such sidechains are listed below:

Mol	Chain	Res	Type
1	B	341	GLN
1	C	89	ASN
1	D	186	HIS
1	B	347	GLN
1	C	23	ASN

### 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 5 ligands modelled in this entry, 4 are monoatomic - leaving 1 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	$\# Z  > 2$
3	NDP	B	381	-	43,52,52	1.26	3 (6%)	49,80,80	1.08	3 (6%)

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	NDP	B	381	-	-	0/30/77/77	0/5/5/5

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	381	NDP	C4N-C5N	-3.54	1.41	1.49
3	B	381	NDP	C2A-N3A	2.57	1.36	1.32
3	B	381	NDP	C6N-C5N	4.07	1.40	1.33

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	381	NDP	N3A-C2A-N1A	-3.18	126.09	128.86
3	B	381	NDP	C1D-N1N-C2N	-2.72	116.47	121.09
3	B	381	NDP	C4A-C5A-N7A	2.43	111.76	109.41

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	381	NDP	10	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](#)

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	359/373 (96%)	0.00	0 100 100	37, 58, 78, 99	0
1	B	359/373 (96%)	0.27	8 (2%) 62 41	45, 66, 98, 128	0
1	C	359/373 (96%)	0.32	17 (4%) 32 18	41, 70, 99, 122	0
1	D	360/373 (96%)	0.19	10 (2%) 53 33	44, 66, 110, 123	0
All	All	1437/1492 (96%)	0.20	35 (2%) 59 38	37, 64, 99, 128	0

The worst 5 of 35 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	209	ASN	7.6
1	C	86	LEU	5.2
1	B	209	ASN	5.0
1	C	208	PRO	5.0
1	D	209	ASN	4.6

### 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95<sup>th</sup> 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
3	NDP	B	381	48/48	0.92	0.22	0.38	76,85,88,91	0
2	ZN	D	1360	1/1	0.97	0.15	-	78,78,78,78	0
2	ZN	B	1360	1/1	1.00	0.10	-	63,63,63,63	0
2	ZN	A	1360	1/1	0.99	0.18	-	73,73,73,73	0
2	ZN	C	1360	1/1	0.98	0.12	-	92,92,92,92	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.