



# wwPDB X-ray Structure Validation Summary Report

Feb 26, 2014 – 08:18 PM GMT

PDB ID : 2DB3  
Title : Structural basis for RNA unwinding by the DEAD-box protein Drosophila Vasa  
Authors : Sengoku, T.; Nureki, O.; Nakamura, A.; Kobayashi, S.; Yokoyama, S.; RIKEN Structural Genomics/Proteomics Initiative (RSGI)  
Deposited on : 2005-12-14  
Resolution : 2.20 Å(reported)

This is a wwPDB 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/ValidationPDFNotes.html>

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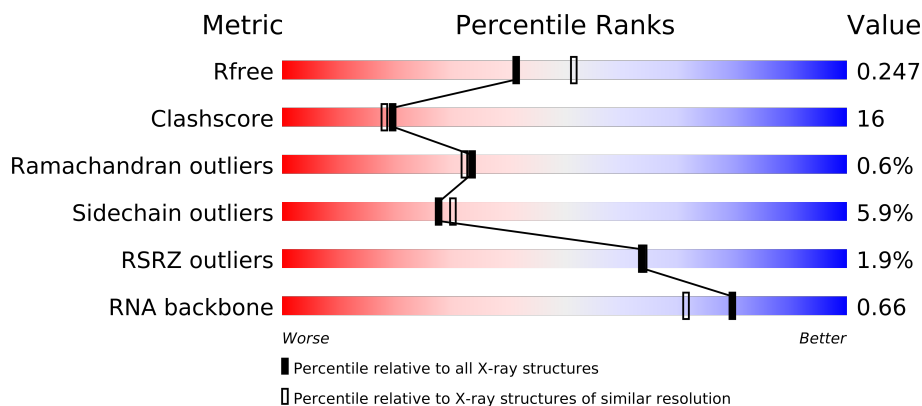
The following versions of software and data (see [references](#)) were used in the production of this report:

MolProbity : 4.02b-467  
Mogul : 1.15 2013  
Xtriage (Phenix) : dev-1323  
EDS : stable22639  
Percentile statistics : 21963  
Refmac : 5.8.0049  
CCP4 : 6.3.0 (Settle)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et. al. (1996)  
Validation Pipeline (wwPDB-VP) : stable22683

# 1 Overall quality at a glance

The reported resolution of this entry is 2.20 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))
$R_{free}$	66092	2938 (2.20-2.20)
Clashscore	79885	3751 (2.20-2.20)
Ramachandran outliers	78287	3681 (2.20-2.20)
Sidechain outliers	78261	3682 (2.20-2.20)
RSRZ outliers	66119	2939 (2.20-2.20)
RNA backbone	1838	1120 (3.00-1.40)

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. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density.

Mol	Chain	Length	Quality of chain
1	E	10	
1	F	10	
1	G	10	
1	H	10	
2	A	434	
2	B	434	
2	C	434	
2	D	434	

The following table lists non-polymeric compounds that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Geometry	Electron density
3	MG	A	2801	-	X
3	MG	B	2802	-	X
3	MG	C	2803	-	X
3	MG	D	2804	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15119 atoms, of which 0 are hydrogen and 0 are deuterium.

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 RNA chain called 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	7	Total	C	N	O	P	0	0	1
			105	45	10	44	6			
1	F	7	Total	C	N	O	P	0	0	0
			129	59	12	52	6			
1	G	7	Total	C	N	O	P	0	0	0
			137	63	14	54	6			
1	H	6	Total	C	N	O	P	0	0	0
			117	54	12	46	5			

- Molecule 2 is a protein called ATP-dependent RNA helicase vasa.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	A	420	Total	C	N	O	S	0	0	0
			3296	2089	573	619	15			
2	B	420	Total	C	N	O	S	0	0	0
			3296	2089	573	619	15			
2	C	420	Total	C	N	O	S	0	0	0
			3296	2089	573	619	15			
2	D	420	Total	C	N	O	S	0	0	0
			3296	2089	573	619	15			

There are 40 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	190	GLY	-	CLONING ARTIFACT	UNP P09052
A	191	PRO	-	CLONING ARTIFACT	UNP P09052
A	192	LEU	-	CLONING ARTIFACT	UNP P09052
A	193	GLY	-	CLONING ARTIFACT	UNP P09052
A	194	SER	-	CLONING ARTIFACT	UNP P09052
A	195	PRO	-	CLONING ARTIFACT	UNP P09052
A	196	GLU	-	CLONING ARTIFACT	UNP P09052
A	197	PHE	-	CLONING ARTIFACT	UNP P09052

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Chain	Residue	Modelled	Actual	Comment	Reference
A	198	PRO	-	CLONING ARTIFACT	UNP P09052
A	199	GLY	-	CLONING ARTIFACT	UNP P09052
B	190	GLY	-	CLONING ARTIFACT	UNP P09052
B	191	PRO	-	CLONING ARTIFACT	UNP P09052
B	192	LEU	-	CLONING ARTIFACT	UNP P09052
B	193	GLY	-	CLONING ARTIFACT	UNP P09052
B	194	SER	-	CLONING ARTIFACT	UNP P09052
B	195	PRO	-	CLONING ARTIFACT	UNP P09052
B	196	GLU	-	CLONING ARTIFACT	UNP P09052
B	197	PHE	-	CLONING ARTIFACT	UNP P09052
B	198	PRO	-	CLONING ARTIFACT	UNP P09052
B	199	GLY	-	CLONING ARTIFACT	UNP P09052
C	190	GLY	-	CLONING ARTIFACT	UNP P09052
C	191	PRO	-	CLONING ARTIFACT	UNP P09052
C	192	LEU	-	CLONING ARTIFACT	UNP P09052
C	193	GLY	-	CLONING ARTIFACT	UNP P09052
C	194	SER	-	CLONING ARTIFACT	UNP P09052
C	195	PRO	-	CLONING ARTIFACT	UNP P09052
C	196	GLU	-	CLONING ARTIFACT	UNP P09052
C	197	PHE	-	CLONING ARTIFACT	UNP P09052
C	198	PRO	-	CLONING ARTIFACT	UNP P09052
C	199	GLY	-	CLONING ARTIFACT	UNP P09052
D	190	GLY	-	CLONING ARTIFACT	UNP P09052
D	191	PRO	-	CLONING ARTIFACT	UNP P09052
D	192	LEU	-	CLONING ARTIFACT	UNP P09052
D	193	GLY	-	CLONING ARTIFACT	UNP P09052
D	194	SER	-	CLONING ARTIFACT	UNP P09052
D	195	PRO	-	CLONING ARTIFACT	UNP P09052
D	196	GLU	-	CLONING ARTIFACT	UNP P09052
D	197	PHE	-	CLONING ARTIFACT	UNP P09052
D	198	PRO	-	CLONING ARTIFACT	UNP P09052
D	199	GLY	-	CLONING ARTIFACT	UNP P09052

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

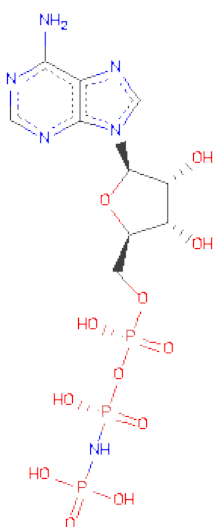
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is PHOSPHOAMINOPHOSPHONICACID-ADENYLATE ESTER (three-letter code: ANP) (formula:  $C_{10}H_{17}N_6O_{12}P_3$ ).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	B	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	C	1	Total	C	N	O	P	0	0
			31	10	6	12	3		
4	D	1	Total	C	N	O	P	0	0
			31	10	6	12	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	233	Total	O	0	0
			233	233		
5	B	315	Total	O	0	0
			315	315		
5	C	393	Total	O	0	0
			393	393		
5	D	282	Total	O	0	0
			282	282		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	E	23	Total 23	O 23	0	0
5	F	22	Total 22	O 22	0	0
5	G	29	Total 29	O 29	0	0
5	H	22	Total 22	O 22	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 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.

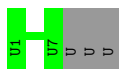
- Molecule 1: 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'

Chain E: 



- Molecule 1: 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'

Chain F: 



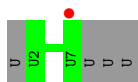
- Molecule 1: 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'

Chain G: 



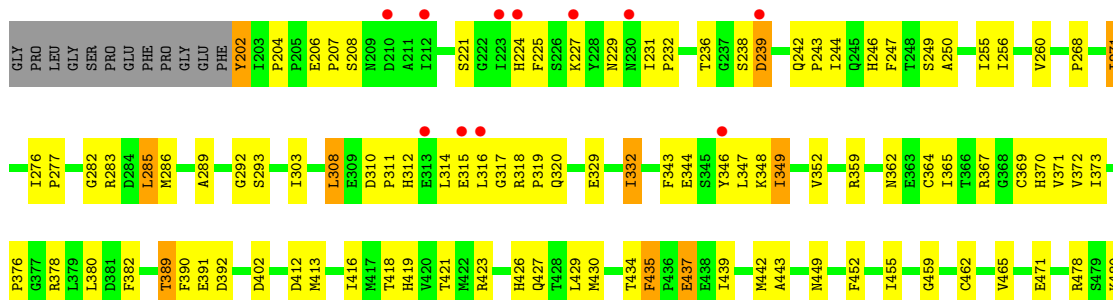
- Molecule 1: 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'

Chain H: 

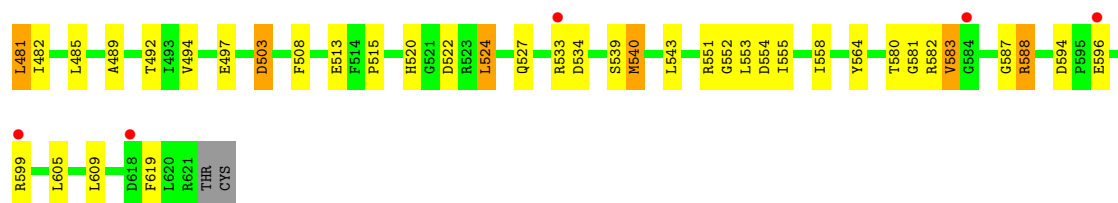


- Molecule 2: ATP-dependent RNA helicase vasa

Chain A: 

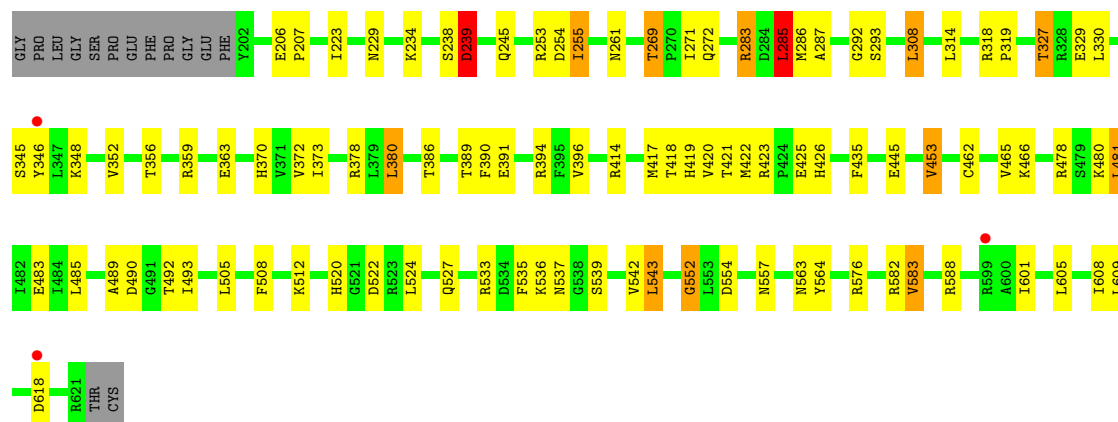






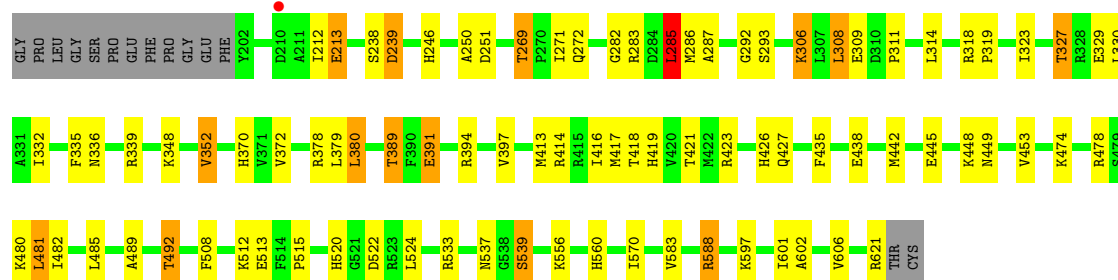
• Molecule 2: ATP-dependent RNA helicase vasa

Chain B:



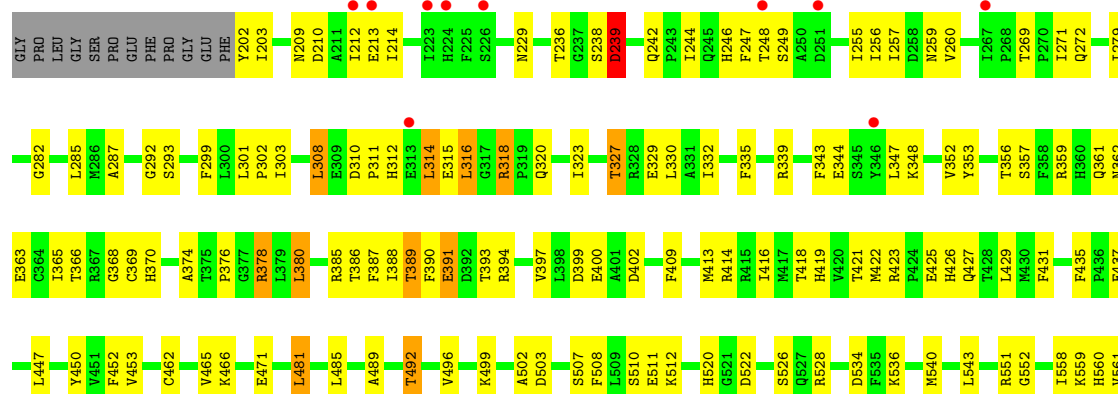
• Molecule 2: ATP-dependent RNA helicase vasa

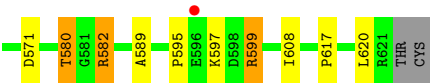
Chain C:



• Molecule 2: ATP-dependent RNA helicase vasa

Chain D:





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	71.05Å 142.33Å 130.47Å 90.00° 90.86° 90.00°	Depositor
Resolution (Å)	39.46 – 2.20 39.45 – 2.20	Depositor EDS
% Data completeness (in resolution range)	89.4 (39.46-2.20) 89.5 (39.45-2.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	0.07	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.88 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, $R_{free}$	0.197 , 0.250 0.195 , 0.247	Depositor DCC
$R_{free}$ test set	11749 reflections (11.11%)	DCC
Wilson B-factor (Å <sup>2</sup> )	31.2	Xtriage
Anisotropy	0.306	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.37 , 47.5	EDS
Estimated twinning fraction	0.076 for h,-k,-l	Xtriage
L-test for twinning	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 117457 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	15119	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	39.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.82% of the height of the origin peak. No significant pseudotranslation is detected.*

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

## 5 Model quality

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, ANP

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	E	0.48	0/114	0.70	0/176
1	F	0.42	0/141	0.63	0/216
1	G	0.49	0/150	0.64	0/230
1	H	0.46	0/128	0.64	0/196
2	A	0.39	0/3360	0.65	0/4539
2	B	0.45	0/3360	0.69	4/4539 (0.1%)
2	C	0.46	0/3360	0.70	1/4539 (0.0%)
2	D	0.42	0/3360	0.68	0/4539
All	All	0.43	0/13973	0.68	5/18974 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	283	ARG	NE-CZ-NH2	-5.70	117.45	120.30
2	C	285	LEU	CA-CB-CG	5.66	128.32	115.30
2	B	345	SER	N-CA-C	-5.56	95.98	111.00
2	B	285	LEU	CA-CB-CG	5.24	127.36	115.30
2	B	552	GLY	N-CA-C	5.16	126.00	113.10

There are no chirality outliers.

There are no planarity outliers.

### 5.2 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 hydrogens added by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, and the number in parentheses is this value normalized per 1000 atoms of the molecule in the

chain. The Symm-Clashes column gives symmetry related clashes, in the same way as for the Clashes column.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	E	105	0	50	1	0
1	F	129	0	68	0	0
1	G	137	0	72	2	0
1	H	117	0	62	0	0
2	A	3296	0	3312	136	0
2	B	3296	0	3312	91	0
2	C	3296	0	3312	81	0
2	D	3296	0	3312	131	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	31	0	13	5	0
4	B	31	0	13	4	0
4	C	31	0	13	1	0
4	D	31	0	13	3	0
5	A	233	0	0	11	0
5	B	315	0	0	22	0
5	C	393	0	0	22	0
5	D	282	0	0	9	0
5	E	23	0	0	0	0
5	F	22	0	0	0	0
5	G	29	0	0	1	0
5	H	22	0	0	0	0
All	All	15119	0	13552	442	0

Clashscore is defined as the number of clashes calculated for the entry per 1000 atoms (including hydrogens) of the entry. The overall clashscore for this entry is 16.

The worst 5 of 442 close contacts within the same asymmetric unit are listed below.

Atom-1	Atom-2	Distance(Å)	Clash(Å)
2:A:352:VAL:HG13	2:A:378:ARG:HG3	1.46	0.95
2:C:348:LYS:H	2:C:370:HIS:HD2	1.17	0.92
2:A:318:ARG:HG2	2:A:389:THR:HG22	1.50	0.91
2:A:359:ARG:HH11	2:A:359:ARG:HB2	1.33	0.91
2:A:423:ARG:HD3	5:A:3067:HOH:O	1.70	0.89

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	
2	A	418/434 (96%)	398 (95%)	17 (4%)	3 (1%)	30	28
2	B	418/434 (96%)	398 (95%)	18 (4%)	2 (0%)	38	38
2	C	418/434 (96%)	412 (99%)	4 (1%)	2 (0%)	38	38
2	D	418/434 (96%)	400 (96%)	15 (4%)	3 (1%)	30	28
All	All	1672/1736 (96%)	1608 (96%)	54 (3%)	10 (1%)	33	32

5 of 10 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	A	349	ILE
2	B	552	GLY
2	C	239	ASP
2	B	239	ASP
2	D	239	ASP

### 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	
2	A	364/375 (97%)	340 (93%)	24 (7%)	24	25
2	B	364/375 (97%)	346 (95%)	18 (5%)	35	40
2	C	364/375 (97%)	347 (95%)	17 (5%)	36	42
2	D	364/375 (97%)	337 (93%)	27 (7%)	20	19
All	All	1456/1500 (97%)	1370 (94%)	86 (6%)	28	30

5 of 86 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	543	LEU
2	C	352	VAL
2	D	510	SER
2	B	608	ILE
2	C	269	THR

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 32 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	449	ASN
2	C	320	GLN
2	D	449	ASN
2	C	224	HIS
2	C	370	HIS

### 5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
1	E	4/10 (40%)	0	0
1	F	6/10 (60%)	0	0
1	G	6/10 (60%)	0	0
1	H	5/10 (50%)	0	0
All	All	21/40 (52%)	0	0

There are no RNA backbone outliers to report.

There are no RNA pucker outliers to report.

## 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 ⓘ

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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	ANP	A	2901	3	33,33,33	2.05	11 (33%)	51,52,52	3.06	21 (41%)
4	ANP	B	2902	3	33,33,33	2.09	10 (30%)	51,52,52	2.94	22 (43%)
4	ANP	C	2903	3	33,33,33	2.04	11 (33%)	51,52,52	2.84	21 (41%)
4	ANP	D	2904	3	33,33,33	1.94	12 (36%)	51,52,52	2.93	22 (43%)

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	ANP	A	2901	3	-	0/18/38/38	0/1/3/3
4	ANP	B	2902	3	-	0/18/38/38	0/1/3/3
4	ANP	C	2903	3	-	0/18/38/38	0/1/3/3
4	ANP	D	2904	3	-	0/18/38/38	0/1/3/3

The worst 5 of 44 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2902	ANP	C2'-C1'	-5.71	1.45	1.53
4	C	2903	ANP	PB-N3B	-5.66	1.59	1.64
4	A	2901	ANP	C2'-C1'	-5.29	1.45	1.53
4	A	2901	ANP	PG-O1G	5.12	1.52	1.46
4	B	2902	ANP	PG-O1G	4.82	1.52	1.46

The worst 5 of 86 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2901	ANP	O4'-C1'-N9	10.62	118.32	108.44
4	D	2904	ANP	C4'-O4'-C1'	10.12	120.74	109.75
4	C	2903	ANP	C4'-O4'-C1'	9.95	120.55	109.75
4	B	2902	ANP	C4'-O4'-C1'	9.83	120.42	109.75
4	A	2901	ANP	C4'-O4'-C1'	9.71	120.29	109.75



There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

## 5.7 Other polymers ⓘ

There are no such residues in this entry.

## 5.8 Polymer linkage issues

There are no chain breaks in this entry.

## 6 Fit of model and data ⓘ

### 6.1 Protein, DNA and RNA chains ⓘ

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	E	7/10 (70%)	-0.19	1 (14%) 3 3	28, 31, 48, 59	0
1	F	7/10 (70%)	0.04	0 100 100	25, 30, 56, 64	0
1	G	7/10 (70%)	-0.12	0 100 100	24, 27, 53, 68	0
1	H	6/10 (60%)	-0.08	1 (16%) 2 2	29, 30, 43, 70	0
2	A	420/434 (96%)	0.10	16 (3%) 38 39	23, 43, 77, 85	0
2	B	420/434 (96%)	-0.21	3 (0%) 84 86	18, 36, 59, 66	0
2	C	420/434 (96%)	-0.38	1 (0%) 93 94	18, 31, 47, 59	0
2	D	420/434 (96%)	-0.03	11 (2%) 53 53	20, 39, 66, 77	0
All	All	1707/1776 (96%)	-0.13	33 (1%) 64 64	18, 37, 63, 85	0

The worst 5 of 33 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	223	ILE	5.3
2	A	316	LEU	4.3
2	D	248	THR	3.6
2	B	599	ARG	3.4
2	D	346	TYR	3.3

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

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

### 6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 6.4 Ligands

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	RSR	LLDF	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	C	2803	1/1	0.26	6.43	22,22,22,22	0
3	MG	A	2801	1/1	0.25	3.43	37,37,37,37	0
3	MG	B	2802	1/1	0.18	3.17	21,21,21,21	0
3	MG	D	2804	1/1	0.21	2.21	25,25,25,25	0
4	ANP	B	2902	31/31	0.11	0.21	19,26,30,31	0
4	ANP	C	2903	31/31	0.10	-0.72	17,22,25,26	0
4	ANP	A	2901	31/31	0.10	-0.97	24,36,39,39	0
4	ANP	D	2904	31/31	0.10	-1.19	22,33,34,36	0

## 6.5 Other polymers

There are no such residues in this entry.