



# Full wwPDB X-ray Structure Validation Report ⓘ

May 25, 2020 – 04:59 am BST

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 Full wwPDB X-ray Structure Validation 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

<https://www.wwpdb.org/validation/2017/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 : 1.8.5 (274361), CSD as541be (2020)  
Xtriage (Phenix) : 1.13  
EDS : 2.11  
buster-report : 1.1.7 (2018)  
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)  
Refmac : 5.8.0158  
CCP4 : 7.0.044 (Gargrove)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.11

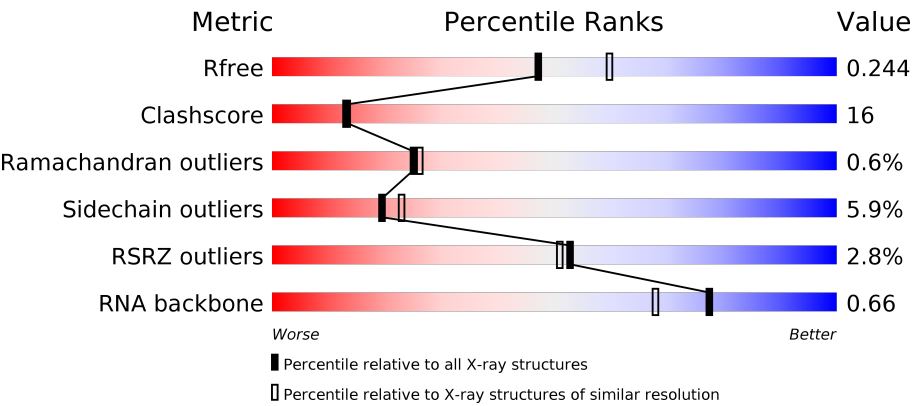
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

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 <sub>free</sub>	130704	4898 (2.20-2.20)
Clashscore	141614	5594 (2.20-2.20)
Ramachandran outliers	138981	5503 (2.20-2.20)
Sidechain outliers	138945	5504 (2.20-2.20)
RSRZ outliers	127900	4800 (2.20-2.20)
RNA backbone	3102	1032 (2.60-1.80)

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  $\geq 3$ , 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  $\leq 5\%$ . 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	E	10	<div><div>10%</div><div><div></div><div>60%</div><div>10%</div><div>30%</div></div></div>
1	F	10	<div><div>70%</div><div>30%</div></div>
1	G	10	<div><div>40%</div><div>30%</div><div>30%</div></div>
1	H	10	<div><div>10%</div><div><div></div><div>60%</div><div>40%</div></div></div>

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Mol	Chain	Length	Quality of chain
2	A	434	<div><div>5%</div><div><div></div><div>64%</div><div>29%</div><div></div><div></div></div><div><div></div><div></div></div></div>
2	B	434	<div><div>%</div><div><div></div><div>74%</div><div>20%</div><div></div><div></div></div><div><div></div><div></div></div></div>
2	C	434	<div><div></div><div><div></div><div>76%</div><div>17%</div><div></div><div></div></div><div><div></div><div></div></div></div>
2	D	434	<div><div>4%</div><div><div></div><div>63%</div><div>30%</div><div></div><div></div></div><div><div></div><div></div></div></div>

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 15119 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 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).

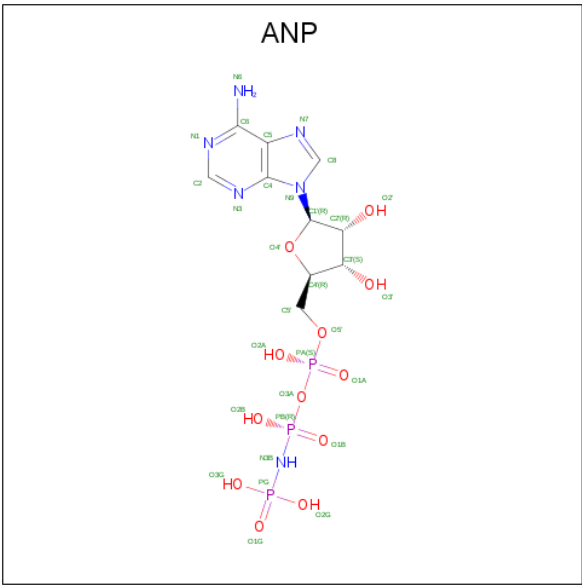
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0

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

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (three-letter code: ANP) (formula: C<sub>10</sub>H<sub>17</sub>N<sub>6</sub>O<sub>12</sub>P<sub>3</sub>).



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	E	23	Total	O	0	0
			23	23		
5	F	22	Total	O	0	0
			22	22		
5	G	29	Total	O	0	0
			29	29		
5	H	22	Total	O	0	0
			22	22		

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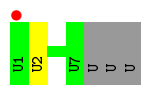
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	233	Total 233	O 233	0	0
5	B	315	Total 315	O 315	0	0
5	C	393	Total 393	O 393	0	0
5	D	282	Total 282	O 282	0	0

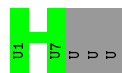
### 3 Residue-property plots [i](#)

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 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'



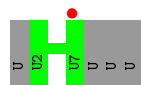
- Molecule 1: 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'



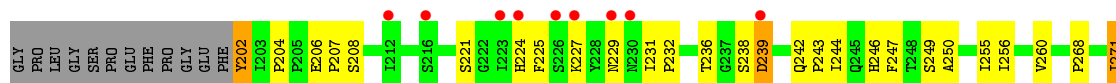
- Molecule 1: 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'

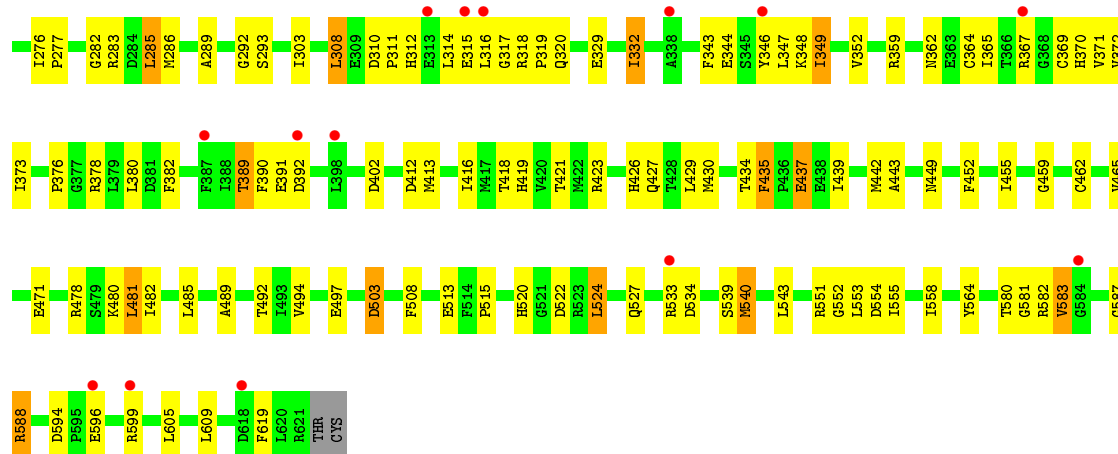


- Molecule 1: 5'-R(\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*UP\*U)-3'

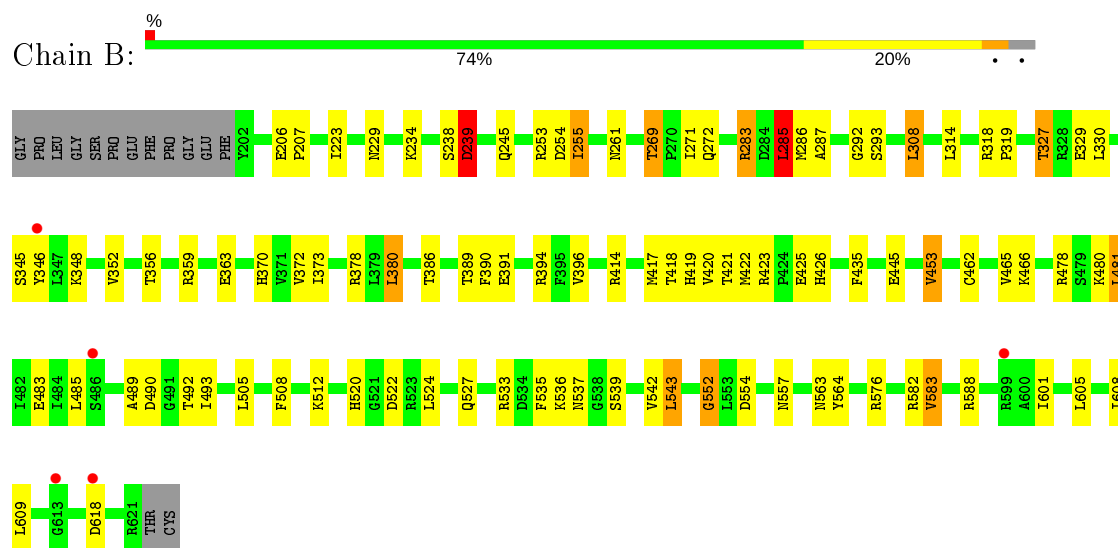


- Molecule 2: ATP-dependent RNA helicase vasa

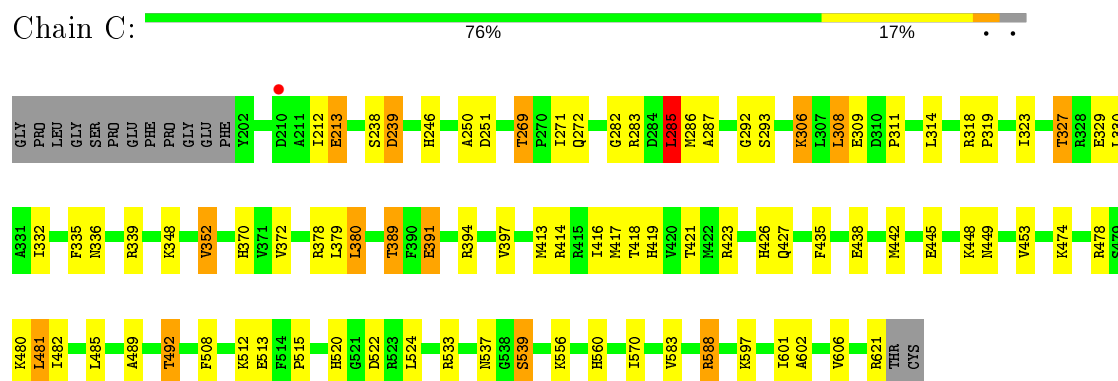




• Molecule 2: ATP-dependent RNA helicase vasa



• Molecule 2: ATP-dependent RNA helicase vasa



• Molecule 2: ATP-dependent RNA helicase vasa



GLY	PRO	LEU	GLY	SER	PRO	GLU	PHE	PRO	GLY	GLU	PHE	Y202	I203	N209	D210	A211	I212	E213	I214	I223	H224	F225	S226	N229	N230	T236	G237	S238	D239	Q242	P243	I244	Q245	H246	F247	T248	S249	A250	D251	I255	I256	I257	D258	N259	V260	T269	P270	I271	Q272	I279	
G282	I365	T366	R367	G368	C369	H370	A374	T375	P376	L300	L301	P302	I303	I308	E309	D310	P311	H312	E313	I314	E315	I316	G317	R318	F319	Q320	I323	T327	R328	E329	I330	A331	I332	F335	R339	F343	E344	S345	I346	K347	R348	V352	Y353	T356	S357	F358	R359	R360	Q361	N362	E363
C364	I365	T366	R367	G368	C369	H370	A374	T375	P376	L300	L301	P302	I303	I308	E309	D310	P311	H312	E313	I314	E315	I316	G317	R318	F319	Q320	I323	T327	R328	E329	I330	A331	I332	F335	R339	F343	E344	S345	I346	K347	R348	V352	Y353	T356	S357	F358	R359	R360	Q361	N362	E363
L447	Y450	Y451	F452	V453	C462	V465	K466	E471	Y475	L481	L485	A489	T492	V496	K499	A502	D503	S507	F508	L509	E511	K512	H520	G521	D522	S526	G527	R528	D534	F535	K536	M540	L543	R551	G552	I558	K559	H560													
V561	D571	T580	G581	R582	A589	P595	E596	K597	D598	R599	I608	P617	L620	R621	THR	CYS																																			

## 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 0.192 , 0.244	Depositor DCC
$R_{free}$ test set	11749 reflections (10.00%)	wwPDB-VP
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> )	0.35 , 51.9	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.076 for h,-k,-l	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.

<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: 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 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	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

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.

All (442) 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: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
2:B:271:ILE:HD11	2:B:287:ALA:HB1	1.55	0.88
2:D:318:ARG:HD2	2:D:389:THR:HG22	1.57	0.87
2:B:269:THR:HG21	2:B:293:SER:O	1.75	0.87
2:A:348:LYS:H	2:A:370:HIS:CD2	1.93	0.86
2:B:238:SER:O	2:B:283:ARG:NH2	2.08	0.86

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:582:ARG:HH11	2:D:582:ARG:HB3	1.42	0.85
2:C:556:LYS:HD3	5:C:3071:HOH:O	1.77	0.85
2:A:359:ARG:HB2	2:A:359:ARG:NH1	1.93	0.83
2:A:244:ILE:HG23	2:A:277:PRO:HG3	1.62	0.82
2:A:348:LYS:H	2:A:370:HIS:HD2	1.25	0.81
2:A:419:HIS:HD2	2:A:421:THR:HB	1.46	0.81
2:D:348:LYS:H	2:D:370:HIS:HD2	1.27	0.80
2:A:329:GLU:O	2:A:332:ILE:HD13	1.81	0.80
2:D:348:LYS:H	2:D:370:HIS:CD2	2.00	0.80
2:D:582:ARG:HH12	4:D:2904:ANP:H5'2	1.46	0.79
2:A:489:ALA:O	2:A:492:THR:HG22	1.82	0.79
2:D:462:CYS:O	2:D:465:VAL:HG12	1.84	0.78
2:A:520:HIS:CD2	2:A:522:ASP:H	2.03	0.77
2:A:582:ARG:HH21	4:A:2901:ANP:HNB1	1.30	0.77
2:C:588:ARG:HD3	5:C:3180:HOH:O	1.84	0.77
2:C:269:THR:HG21	2:C:293:SER:O	1.86	0.75
2:A:520:HIS:HD2	2:A:522:ASP:H	1.34	0.75
2:B:348:LYS:H	2:B:370:HIS:HD2	1.33	0.75
2:D:393:THR:HB	2:D:422:MET:HE3	1.69	0.75
2:B:582:ARG:NH2	4:B:2902:ANP:HNB1	1.85	0.74
2:C:442:MET:HE1	5:C:3068:HOH:O	1.88	0.73
2:A:316:LEU:HD13	5:A:3079:HOH:O	1.87	0.73
2:C:520:HIS:HD2	2:C:522:ASP:H	1.33	0.73
2:C:292:GLY:H	4:C:2903:ANP:HNB1	1.36	0.72
2:D:414:ARG:O	2:D:418:THR:HB	1.90	0.72
2:A:582:ARG:NH2	4:A:2901:ANP:HNB1	1.87	0.72
2:C:417:MET:HG3	5:C:3109:HOH:O	1.89	0.72
2:B:206:GLU:HG2	2:B:207:PRO:HD2	1.71	0.72
2:D:359:ARG:HH12	2:D:362:ASN:HD22	1.38	0.72
2:A:349:ILE:O	2:A:369:CYS:HB3	1.90	0.71
2:D:269:THR:HG22	2:D:272:GLN:CG	2.19	0.71
2:B:386:THR:HG23	5:B:3138:HOH:O	1.90	0.71
2:A:554:ASP:HA	2:A:582:ARG:HH11	1.56	0.71
2:A:580:THR:HG22	2:A:587:GLY:HA3	1.73	0.70
2:D:269:THR:HG22	2:D:272:GLN:HG3	1.72	0.70
2:A:271:ILE:HD11	2:A:293:SER:O	1.92	0.70
2:A:390:PHE:H	2:A:421:THR:CG2	2.04	0.70
2:B:389:THR:HG23	2:B:391:GLU:OE2	1.92	0.70
2:D:347:LEU:HA	2:D:370:HIS:CD2	2.26	0.70
2:A:352:VAL:CG1	2:A:378:ARG:HG3	2.21	0.69
2:C:271:ILE:HD11	2:C:287:ALA:HB1	1.72	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:327:THR:HG22	2:C:330:LEU:H	1.55	0.69
2:A:390:PHE:H	2:A:421:THR:HG22	1.58	0.68
2:A:389:THR:OG1	2:A:421:THR:HG21	1.94	0.68
2:A:206:GLU:HG3	2:A:207:PRO:HD2	1.75	0.68
2:B:582:ARG:NH2	4:B:2902:ANP:N3B	2.42	0.68
2:D:292:GLY:HA2	2:D:582:ARG:NH1	2.08	0.68
2:B:269:THR:HG23	5:B:2917:HOH:O	1.94	0.67
2:A:238:SER:O	2:A:283:ARG:NH2	2.27	0.67
2:B:462:CYS:O	2:B:465:VAL:HG12	1.95	0.67
2:D:248:THR:OG1	2:D:257:ILE:HD13	1.95	0.67
2:D:279:ILE:HD13	2:D:429:LEU:HD13	1.77	0.67
2:D:320:GLN:NE2	2:D:394:ARG:HH21	1.92	0.67
2:C:621:ARG:HD3	5:C:3032:HOH:O	1.94	0.67
2:B:292:GLY:H	4:B:2902:ANP:HNB1	1.44	0.66
2:D:315:GLU:HB3	2:D:318:ARG:HG3	1.78	0.66
2:A:554:ASP:HA	2:A:582:ARG:NH1	2.11	0.65
2:D:318:ARG:CZ	2:D:391:GLU:HG3	2.26	0.65
2:B:346:TYR:HB2	5:B:3075:HOH:O	1.94	0.65
2:D:318:ARG:HD2	2:D:389:THR:CG2	2.24	0.65
2:A:332:ILE:HD11	5:A:2936:HOH:O	1.95	0.65
2:C:348:LYS:H	2:C:370:HIS:CD2	2.07	0.64
2:A:482:ILE:HD11	2:A:508:PHE:HE2	1.63	0.64
2:C:482:ILE:HD11	2:C:508:PHE:CE2	2.31	0.64
2:A:271:ILE:HG23	2:A:455:ILE:CD1	2.28	0.64
2:C:414:ARG:NH2	2:C:445:GLU:OE2	2.31	0.64
2:A:359:ARG:HH11	2:A:359:ARG:CB	2.10	0.64
2:A:391:GLU:OE2	2:A:421:THR:HG23	1.98	0.63
2:B:445:GLU:HB3	5:B:3135:HOH:O	1.98	0.63
2:A:347:LEU:HA	2:A:370:HIS:CD2	2.33	0.63
2:A:588:ARG:HD3	5:A:3069:HOH:O	1.99	0.63
2:D:242:GLN:HG2	5:D:3145:HOH:O	1.99	0.63
2:C:418:THR:HG22	2:C:418:THR:O	1.98	0.63
2:D:617:PRO:HD2	2:D:620:LEU:HD12	1.81	0.63
2:B:207:PRO:HB3	5:B:3155:HOH:O	1.98	0.62
2:C:389:THR:CG2	2:C:391:GLU:HG2	2.29	0.62
2:B:327:THR:HG22	2:B:330:LEU:H	1.61	0.62
2:C:318:ARG:CZ	2:C:391:GLU:HG3	2.30	0.62
2:C:481:LEU:HD22	2:C:485:LEU:HG	1.81	0.62
2:B:359:ARG:O	2:B:363:GLU:HG3	2.00	0.62
2:C:513:GLU:HG3	5:C:3076:HOH:O	2.00	0.61
2:B:318:ARG:HG2	2:B:389:THR:HG23	1.82	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:462:CYS:O	2:A:465:VAL:HG22	2.00	0.61
2:D:271:ILE:HD11	2:D:287:ALA:HB1	1.81	0.61
2:D:348:LYS:N	2:D:370:HIS:HD2	1.99	0.61
2:B:386:THR:O	2:B:386:THR:HG22	2.01	0.61
2:D:492:THR:HB	2:D:560:HIS:HB3	1.81	0.61
2:A:348:LYS:N	2:A:370:HIS:HD2	1.97	0.61
2:B:420:VAL:HG23	5:B:3020:HOH:O	2.00	0.60
2:C:352:VAL:HG13	2:C:378:ARG:HG3	1.81	0.60
2:D:582:ARG:CB	2:D:582:ARG:HH11	2.11	0.60
2:D:391:GLU:OE1	2:D:421:THR:HG23	2.01	0.60
2:D:391:GLU:CD	2:D:421:THR:HG23	2.22	0.60
2:C:418:THR:CG2	2:C:418:THR:O	2.50	0.60
2:C:489:ALA:O	2:C:492:THR:CG2	2.49	0.60
2:A:314:LEU:HD22	2:A:370:HIS:CE1	2.36	0.60
2:A:271:ILE:HG23	2:A:455:ILE:HD13	1.82	0.60
2:C:533:ARG:HD2	5:C:3117:HOH:O	2.01	0.60
2:A:419:HIS:CD2	2:A:421:THR:HB	2.33	0.60
2:D:366:THR:C	2:D:368:GLY:H	2.02	0.60
2:D:582:ARG:NH1	2:D:582:ARG:HB3	2.13	0.60
2:B:389:THR:CG2	2:B:391:GLU:OE2	2.50	0.59
2:C:489:ALA:O	2:C:492:THR:HG23	2.01	0.59
2:D:269:THR:HG21	2:D:293:SER:O	2.02	0.59
2:A:580:THR:HG22	2:A:581:GLY:N	2.17	0.59
2:D:520:HIS:HD2	2:D:522:ASP:H	1.47	0.59
2:A:558:ILE:HG22	2:A:580:THR:OG1	2.01	0.59
2:B:588:ARG:HD3	5:B:2914:HOH:O	2.01	0.59
2:D:202:TYR:N	2:D:356:THR:HA	2.16	0.59
2:A:271:ILE:HG13	5:A:2963:HOH:O	2.01	0.59
2:D:327:THR:HG22	2:D:330:LEU:H	1.68	0.59
2:D:353:TYR:H	2:D:361:GLN:HE22	1.49	0.59
2:D:423:ARG:O	2:D:426:HIS:HD2	1.85	0.59
2:B:508:PHE:CE1	2:B:512:LYS:HE3	2.38	0.59
2:A:202:TYR:CE2	2:A:204:PRO:HB3	2.38	0.58
2:C:442:MET:HE2	5:C:3094:HOH:O	2.02	0.58
2:A:594:ASP:OD1	2:A:596:GLU:HB2	2.04	0.58
2:D:348:LYS:HB2	2:D:369:CYS:HA	1.86	0.58
2:A:283:ARG:NH1	2:A:449:ASN:O	2.36	0.58
2:C:269:THR:CG2	2:C:271:ILE:HG22	2.34	0.58
2:D:419:HIS:HD2	2:D:421:THR:HB	1.68	0.58
2:C:379:LEU:HD23	2:C:416:ILE:HD13	1.86	0.58
2:C:309:GLU:C	2:C:311:PRO:HD3	2.24	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:537:ASN:OD1	2:C:539:SER:OG	2.20	0.58
2:A:402:ASP:OD2	2:A:551:ARG:NH2	2.36	0.57
2:B:423:ARG:O	2:B:426:HIS:HD2	1.86	0.57
2:B:489:ALA:O	2:B:492:THR:HG22	2.04	0.57
2:C:238:SER:O	2:C:283:ARG:NH2	2.37	0.57
2:C:269:THR:HG23	5:C:3179:HOH:O	2.03	0.57
2:A:478:ARG:HD3	2:A:508:PHE:CE2	2.40	0.57
2:C:285:LEU:HD21	2:C:453:VAL:HG13	1.87	0.57
2:D:320:GLN:NE2	2:D:394:ARG:NH2	2.52	0.57
2:B:269:THR:CG2	2:B:271:ILE:HG22	2.35	0.57
2:A:580:THR:CG2	2:A:587:GLY:HA3	2.35	0.56
2:A:423:ARG:O	2:A:426:HIS:HD2	1.89	0.56
2:A:520:HIS:CD2	2:A:522:ASP:HB2	2.41	0.56
2:A:580:THR:CG2	2:A:581:GLY:N	2.68	0.56
2:A:283:ARG:HH12	2:A:449:ASN:CG	2.08	0.56
2:A:390:PHE:N	2:A:421:THR:HG22	2.20	0.56
2:B:348:LYS:H	2:B:370:HIS:CD2	2.20	0.56
2:D:499:LYS:HG2	2:D:520:HIS:HB2	1.88	0.56
2:A:292:GLY:H	4:A:2901:ANP:HNB1	1.55	0.55
2:D:246:HIS:O	2:D:249:SER:HB3	2.06	0.55
2:D:489:ALA:O	2:D:492:THR:CG2	2.54	0.55
2:A:389:THR:HG21	2:A:391:GLU:OE1	2.06	0.55
2:D:347:LEU:HA	2:D:370:HIS:HD2	1.72	0.55
2:D:314:LEU:HG	2:D:370:HIS:ND1	2.21	0.55
2:B:414:ARG:O	2:B:418:THR:HB	2.07	0.55
2:D:418:THR:O	2:D:418:THR:CG2	2.55	0.55
2:B:481:LEU:HD12	2:B:564:TYR:CE2	2.41	0.55
2:C:442:MET:HB3	5:C:3094:HOH:O	2.07	0.55
2:D:389:THR:HG21	2:D:391:GLU:OE2	2.07	0.55
2:D:599:ARG:HD2	2:D:599:ARG:H	1.71	0.55
2:A:390:PHE:N	2:A:421:THR:CG2	2.71	0.54
2:D:366:THR:C	2:D:368:GLY:N	2.59	0.54
2:A:455:ILE:HD12	2:A:455:ILE:N	2.22	0.54
2:B:480:LYS:HA	2:B:483:GLU:OE2	2.08	0.54
2:C:283:ARG:NH1	2:C:449:ASN:O	2.41	0.54
2:D:292:GLY:HA2	2:D:582:ARG:HH12	1.71	0.54
2:C:336:ASN:ND2	5:C:3099:HOH:O	2.41	0.53
2:D:385:ARG:HB3	2:D:387:PHE:CE2	2.43	0.53
2:B:481:LEU:HD12	2:B:564:TYR:CD2	2.42	0.53
2:A:389:THR:CG2	2:A:391:GLU:OE1	2.57	0.53
1:G:1:U:H5"	5:G:719:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:555:ILE:N	2:A:555:ILE:HD12	2.22	0.53
2:C:389:THR:HG21	2:C:391:GLU:OE2	2.09	0.53
2:A:582:ARG:NH2	4:A:2901:ANP:N3B	2.55	0.53
2:D:489:ALA:O	2:D:492:THR:HG23	2.08	0.53
2:D:308:LEU:O	2:D:311:PRO:HD3	2.09	0.53
2:A:465:VAL:O	2:A:465:VAL:HG23	2.09	0.53
2:C:419:HIS:HD2	2:C:421:THR:OG1	1.92	0.53
2:B:533:ARG:HD2	5:B:3053:HOH:O	2.08	0.53
2:C:520:HIS:CD2	2:C:522:ASP:H	2.21	0.53
2:D:314:LEU:HG	2:D:370:HIS:CE1	2.43	0.52
2:D:582:ARG:CZ	5:D:3155:HOH:O	2.56	0.52
2:C:482:ILE:HD13	2:C:512:LYS:NZ	2.23	0.52
2:D:386:THR:O	2:D:386:THR:HG22	2.09	0.52
2:A:362:ASN:HA	2:A:382:PHE:HE1	1.75	0.51
2:A:503:ASP:OD1	2:A:520:HIS:HE1	1.93	0.51
2:B:554:ASP:OD1	2:B:582:ARG:NH1	2.41	0.51
2:D:209:ASN:HA	2:D:214:ILE:HD11	1.92	0.51
2:D:248:THR:HG22	2:D:248:THR:O	2.10	0.51
2:A:534:ASP:HB3	2:A:539:SER:HB2	1.92	0.51
2:D:255:ILE:HD11	2:D:344:GLU:O	2.10	0.51
2:D:481:LEU:HD22	2:D:485:LEU:HG	1.93	0.51
2:D:534:ASP:HB3	2:D:540:MET:HG2	1.93	0.51
2:D:335:PHE:O	2:D:339:ARG:HG3	2.10	0.51
2:B:356:THR:O	2:B:378:ARG:NH2	2.33	0.51
2:C:423:ARG:O	2:C:426:HIS:HD2	1.94	0.51
2:D:292:GLY:H	4:D:2904:ANP:HNB1	1.57	0.51
2:B:419:HIS:HD2	2:B:421:THR:OG1	1.93	0.51
2:A:364:CYS:HA	2:A:367:ARG:CZ	2.41	0.50
2:A:373:ILE:N	2:A:373:ILE:HD12	2.26	0.50
2:A:349:ILE:O	2:A:371:VAL:O	2.28	0.50
2:D:559:LYS:HE2	5:D:3097:HOH:O	2.10	0.50
2:C:389:THR:HG22	2:C:391:GLU:HG2	1.92	0.50
2:C:246:HIS:HD2	5:C:3175:HOH:O	1.94	0.50
2:B:261:ASN:HB2	5:B:3145:HOH:O	2.12	0.50
2:B:520:HIS:HD2	2:B:522:ASP:H	1.60	0.50
2:C:318:ARG:HG2	2:C:389:THR:HG22	1.94	0.50
2:B:480:LYS:HD3	2:B:483:GLU:OE2	2.11	0.49
2:B:505:LEU:HD12	2:B:508:PHE:HD2	1.76	0.49
2:B:478:ARG:HG3	2:B:564:TYR:OH	2.11	0.49
2:A:221:SER:HB2	2:A:225:PHE:CD1	2.46	0.49
2:A:434:THR:HG22	2:A:459:GLY:HA2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:299:PHE:HB3	2:D:431:PHE:CE2	2.47	0.49
2:A:310:ASP:N	2:A:311:PRO:HD3	2.27	0.49
2:D:582:ARG:NH1	4:D:2904:ANP:H5'2	2.22	0.49
2:A:352:VAL:HG13	2:A:378:ARG:CG	2.31	0.49
2:A:515:PRO:C	2:A:540:MET:CE	2.80	0.49
2:C:339:ARG:NH1	5:C:3099:HOH:O	2.36	0.49
2:B:394:ARG:NE	5:B:3137:HOH:O	2.46	0.49
2:B:537:ASN:OD1	2:B:539:SER:HB2	2.12	0.49
2:D:323:ILE:HG12	2:D:397:VAL:HB	1.95	0.49
2:D:418:THR:O	2:D:418:THR:HG22	2.12	0.49
2:A:435:PHE:HE1	2:A:439:ILE:HG22	1.78	0.48
2:B:327:THR:HG21	5:B:3047:HOH:O	2.12	0.48
2:A:224:HIS:O	2:A:227:LYS:HB2	2.14	0.48
2:A:515:PRO:C	2:A:540:MET:HE2	2.33	0.48
2:C:285:LEU:HD22	2:C:286:MET:N	2.28	0.48
2:D:376:PRO:HG3	2:D:413:MET:HE1	1.95	0.48
2:B:327:THR:CG2	5:B:3047:HOH:O	2.61	0.48
2:A:319:PRO:HB3	2:A:372:VAL:HG23	1.96	0.48
4:A:2901:ANP:H8	5:A:2905:HOH:O	2.13	0.48
2:A:320:GLN:HA	2:A:392:ASP:O	2.14	0.48
2:A:534:ASP:HB3	2:A:540:MET:HG2	1.94	0.48
2:A:554:ASP:CA	2:A:582:ARG:NH1	2.76	0.48
2:C:269:THR:HG22	2:C:272:GLN:H	1.79	0.48
2:A:513:GLU:HA	5:A:3038:HOH:O	2.13	0.48
2:C:597:LYS:HG3	2:C:597:LYS:O	2.13	0.48
2:D:359:ARG:NH1	2:D:362:ASN:HD22	2.07	0.48
2:A:437:GLU:HG2	5:A:3019:HOH:O	2.14	0.48
2:A:605:LEU:O	2:A:609:LEU:HG	2.14	0.48
2:D:238:SER:O	2:D:239:ASP:C	2.51	0.48
2:D:282:GLY:HA2	2:D:427:GLN:NE2	2.28	0.48
2:A:520:HIS:NE2	2:A:522:ASP:HB2	2.29	0.47
2:C:438:GLU:OE2	2:C:442:MET:HG3	2.13	0.47
2:D:316:LEU:CD1	2:D:366:THR:HG23	2.43	0.47
2:B:563:ASN:OD1	2:B:576:ARG:HD3	2.14	0.47
2:A:390:PHE:H	2:A:421:THR:HG21	1.78	0.47
2:C:327:THR:HG21	5:C:2921:HOH:O	2.13	0.47
2:D:365:ILE:HD13	2:D:388:ILE:HD11	1.96	0.47
2:D:421:THR:HG22	2:D:421:THR:O	2.14	0.47
2:A:308:LEU:HD11	2:A:347:LEU:HG	1.95	0.47
2:A:362:ASN:HA	2:A:382:PHE:CE1	2.50	0.47
2:B:329:GLU:HB2	5:B:3047:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:474:LYS:HE3	5:C:2949:HOH:O	2.15	0.47
2:C:482:ILE:HD11	2:C:508:PHE:HE2	1.74	0.47
2:A:554:ASP:C	2:A:555:ILE:HD12	2.35	0.47
2:D:282:GLY:HA2	2:D:427:GLN:CD	2.35	0.47
2:A:421:THR:O	2:A:421:THR:HG22	2.14	0.47
2:B:285:LEU:HD22	2:B:286:MET:N	2.29	0.47
2:D:380:LEU:HD11	2:D:416:ILE:CG1	2.45	0.47
2:D:391:GLU:O	2:D:423:ARG:HD2	2.14	0.47
2:D:465:VAL:HG13	2:D:465:VAL:O	2.15	0.47
2:B:269:THR:CG2	2:B:293:SER:O	2.54	0.47
2:C:314:LEU:HD21	2:C:370:HIS:HA	1.97	0.47
2:C:512:LYS:C	2:C:513:GLU:HG2	2.35	0.47
2:D:352:VAL:CG2	2:D:378:ARG:HG2	2.45	0.47
2:D:582:ARG:NE	5:D:3155:HOH:O	2.48	0.47
2:D:423:ARG:NH1	2:D:425:GLU:O	2.48	0.46
2:A:478:ARG:HD3	2:A:508:PHE:CD2	2.50	0.46
2:A:551:ARG:HD2	5:A:3032:HOH:O	2.14	0.46
2:B:255:ILE:HD11	2:B:308:LEU:CD2	2.44	0.46
2:B:417:MET:HE2	5:B:2962:HOH:O	2.14	0.46
2:B:582:ARG:NH2	4:B:2902:ANP:O2G	2.48	0.46
2:C:306:LYS:NZ	5:C:3226:HOH:O	2.49	0.46
2:C:426:HIS:HE1	5:C:3109:HOH:O	1.98	0.46
2:D:303:ILE:HD11	2:D:429:LEU:HD12	1.98	0.46
2:C:414:ARG:NH1	5:C:3058:HOH:O	2.47	0.46
2:A:316:LEU:HD22	5:A:3079:HOH:O	2.14	0.46
2:D:597:LYS:HD3	5:D:3151:HOH:O	2.14	0.46
2:B:253:ARG:HD3	5:B:2954:HOH:O	2.16	0.46
2:B:318:ARG:NH1	2:B:391:GLU:HG3	2.31	0.46
2:C:478:ARG:HD3	5:C:2936:HOH:O	2.16	0.46
2:B:223:ILE:HD13	5:B:2967:HOH:O	2.16	0.46
2:D:402:ASP:OD2	2:D:551:ARG:NH2	2.48	0.45
2:A:554:ASP:HB2	2:A:582:ARG:HH12	1.81	0.45
2:B:418:THR:CG2	2:B:418:THR:O	2.63	0.45
2:C:394:ARG:HD2	5:C:3211:HOH:O	2.17	0.45
2:A:271:ILE:HG23	2:A:455:ILE:HD11	1.97	0.45
2:B:601:ILE:HG12	2:B:601:ILE:O	2.17	0.45
2:D:244:ILE:HD12	2:D:244:ILE:C	2.37	0.45
2:D:287:ALA:HA	2:D:453:VAL:HG13	1.98	0.45
2:A:365:ILE:HA	2:A:369:CYS:SG	2.56	0.45
2:A:430:MET:SD	2:A:443:ALA:HB1	2.57	0.45
2:A:289:ALA:HB2	2:A:455:ILE:HD13	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:239:ASP:O	2:C:239:ASP:CG	2.54	0.45
2:D:329:GLU:OE2	2:D:528:ARG:NE	2.48	0.45
2:A:435:PHE:CE1	2:A:439:ILE:HG22	2.52	0.45
2:D:419:HIS:CD2	2:D:421:THR:H	2.35	0.45
2:D:390:PHE:H	2:D:421:THR:CG2	2.30	0.45
2:A:256:ILE:O	2:A:260:VAL:HG23	2.17	0.45
2:A:283:ARG:NH1	2:A:449:ASN:OD1	2.50	0.45
2:C:480:LYS:NZ	5:C:3147:HOH:O	2.50	0.45
2:C:602:ALA:O	2:C:606:VAL:HG23	2.16	0.45
2:D:558:ILE:HG22	2:D:580:THR:HG23	1.98	0.45
2:A:439:ILE:HG12	2:A:442:MET:HE3	2.00	0.44
2:A:471:GLU:OE2	2:A:619:PHE:HB2	2.17	0.44
2:A:246:HIS:HB2	2:A:249:SER:OG	2.17	0.44
2:C:308:LEU:O	2:C:311:PRO:HG3	2.17	0.44
2:D:389:THR:CG2	2:D:391:GLU:HG2	2.47	0.44
2:A:247:PHE:CZ	2:A:268:PRO:HA	2.52	0.44
2:B:419:HIS:CD2	2:B:421:THR:H	2.36	0.44
2:C:348:LYS:N	2:C:370:HIS:HD2	1.98	0.44
2:D:318:ARG:NH2	2:D:391:GLU:HG3	2.33	0.44
2:A:285:LEU:HD22	2:A:286:MET:N	2.33	0.44
2:B:239:ASP:CG	2:B:239:ASP:O	2.56	0.44
2:C:327:THR:CG2	5:C:2921:HOH:O	2.65	0.44
2:A:244:ILE:HG23	2:A:277:PRO:CG	2.41	0.44
2:D:380:LEU:HD12	2:D:380:LEU:HA	1.79	0.44
2:A:311:PRO:C	2:A:312:HIS:HD2	2.21	0.44
2:B:234:LYS:NZ	5:B:2982:HOH:O	2.49	0.44
2:B:582:ARG:C	2:B:583:VAL:HG23	2.38	0.44
2:A:231:ILE:HA	2:A:232:PRO:HD3	1.86	0.44
2:B:356:THR:OG1	2:B:378:ARG:NH2	2.51	0.44
2:C:212:ILE:HG23	2:C:213:GLU:OE2	2.18	0.44
2:D:236:THR:HB	2:D:452:PHE:HB3	2.00	0.44
2:C:448:LYS:O	2:C:449:ASN:C	2.56	0.44
2:B:396:VAL:HG11	2:B:417:MET:SD	2.58	0.43
2:C:492:THR:HB	2:C:560:HIS:HB3	2.00	0.43
2:D:599:ARG:NH2	5:D:3054:HOH:O	2.51	0.43
2:A:238:SER:O	2:A:239:ASP:C	2.56	0.43
2:D:212:ILE:HG23	2:D:213:GLU:N	2.33	0.43
2:A:421:THR:O	2:A:421:THR:CG2	2.66	0.43
2:B:229:ASN:ND2	5:B:3056:HOH:O	2.46	0.43
2:C:250:ALA:O	2:C:251:ASP:HB2	2.18	0.43
2:C:318:ARG:NH1	2:C:391:GLU:HG3	2.33	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:282:GLY:HA2	2:C:427:GLN:CD	2.39	0.43
2:D:561:VAL:O	2:D:589:ALA:HA	2.18	0.43
2:A:282:GLY:HA2	2:A:427:GLN:CD	2.38	0.43
2:A:540:MET:HA	2:A:540:MET:HE3	1.99	0.43
2:D:316:LEU:HD12	2:D:366:THR:HG23	2.00	0.43
2:D:508:PHE:HZ	2:D:512:LYS:HZ2	1.65	0.43
2:B:245:GLN:HG3	5:B:3028:HOH:O	2.18	0.43
2:B:255:ILE:HD11	2:B:308:LEU:HG	2.00	0.43
2:D:310:ASP:OD2	2:D:312:HIS:HE1	2.01	0.43
1:E:2:U:O2'	2:A:497:GLU:OE2	2.25	0.43
2:A:524:LEU:HB2	2:A:527:GLN:HG3	2.00	0.43
2:B:285:LEU:HD21	2:B:453:VAL:HG12	2.01	0.43
2:D:335:PHE:CE2	2:D:339:ARG:HD2	2.53	0.43
2:C:413:MET:HE2	2:C:413:MET:HA	2.01	0.43
2:A:236:THR:HB	2:A:452:PHE:HB3	2.01	0.42
2:A:554:ASP:CB	2:A:582:ARG:NH1	2.82	0.42
2:B:314:LEU:HD21	2:B:370:HIS:HA	2.01	0.42
2:B:605:LEU:O	2:B:609:LEU:HG	2.18	0.42
2:D:279:ILE:CD1	2:D:429:LEU:HD13	2.47	0.42
2:B:269:THR:HG22	2:B:272:GLN:H	1.84	0.42
2:B:493:ILE:HD12	2:B:543:LEU:CD1	2.49	0.42
2:D:327:THR:HG22	2:D:330:LEU:HB3	2.01	0.42
2:D:419:HIS:HE1	5:D:3045:HOH:O	2.02	0.42
2:C:329:GLU:H	2:C:329:GLU:CD	2.23	0.42
2:D:256:ILE:O	2:D:260:VAL:HG23	2.19	0.42
2:A:376:PRO:HG3	2:A:413:MET:HE1	2.02	0.42
2:A:553:LEU:HB3	2:A:555:ILE:CD1	2.49	0.42
2:B:485:LEU:HD21	2:B:492:THR:HG21	2.01	0.42
2:B:492:THR:HG23	2:B:542:VAL:HG13	2.01	0.42
2:B:536:LYS:O	2:B:557:ASN:ND2	2.52	0.42
2:D:247:PHE:O	2:D:248:THR:HB	2.20	0.42
2:D:310:ASP:OD2	2:D:312:HIS:CE1	2.73	0.42
2:B:390:PHE:HB2	2:B:422:MET:HA	2.00	0.42
2:D:389:THR:HG23	2:D:421:THR:HG21	2.01	0.42
2:D:447:LEU:HB3	2:D:450:TYR:HB3	2.01	0.42
2:D:536:LYS:HE2	5:D:3009:HOH:O	2.19	0.42
2:B:373:ILE:HD12	2:B:373:ILE:N	2.34	0.42
2:B:493:ILE:HD12	2:B:543:LEU:HD13	2.02	0.42
2:A:316:LEU:HD12	2:A:317:GLY:N	2.34	0.42
2:B:524:LEU:HB2	2:B:527:GLN:HG3	2.01	0.42
2:A:494:VAL:CG1	2:A:564:TYR:HB2	2.49	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:319:PRO:HB3	2:B:372:VAL:HG23	2.02	0.42
2:B:356:THR:C	2:B:378:ARG:HH22	2.21	0.42
2:C:319:PRO:HB3	2:C:372:VAL:HG23	2.02	0.42
2:D:471:GLU:HG3	2:D:595:PRO:HG3	2.01	0.42
2:C:323:ILE:HG12	2:C:397:VAL:HB	2.02	0.42
2:A:221:SER:HA	2:A:583:VAL:CG1	2.50	0.42
2:A:412:ASP:O	2:A:416:ILE:HG13	2.20	0.41
2:B:466:LYS:HE3	5:B:3151:HOH:O	2.20	0.41
2:D:202:TYR:N	2:D:357:SER:N	2.67	0.41
2:D:387:PHE:CD2	2:D:387:PHE:N	2.88	0.41
1:G:4:U:C4	1:G:5:U:C4	3.08	0.41
2:A:329:GLU:HA	2:A:332:ILE:CD1	2.50	0.41
2:B:465:VAL:HG13	2:B:465:VAL:O	2.20	0.41
2:C:238:SER:O	2:C:239:ASP:C	2.58	0.41
2:C:332:ILE:O	2:C:335:PHE:HB3	2.20	0.41
2:D:301:LEU:HB2	2:D:302:PRO:CD	2.51	0.41
2:D:316:LEU:O	2:D:316:LEU:HD23	2.20	0.41
2:A:481:LEU:CD2	2:A:485:LEU:HG	2.51	0.41
2:B:253:ARG:NH2	5:B:2958:HOH:O	2.53	0.41
2:B:537:ASN:OD1	2:B:539:SER:CB	2.69	0.41
2:A:364:CYS:HA	2:A:367:ARG:HD2	2.03	0.41
2:A:413:MET:HE2	2:A:413:MET:HA	2.02	0.41
2:A:303:ILE:HD11	2:A:429:LEU:HD12	2.02	0.41
2:B:489:ALA:O	2:B:492:THR:CG2	2.68	0.41
2:C:482:ILE:HD13	2:C:512:LYS:HZ2	1.84	0.41
2:D:399:ASP:O	2:D:400:GLU:C	2.59	0.41
2:A:242:GLN:HA	2:A:243:PRO:HD3	1.87	0.41
2:A:329:GLU:HB2	5:A:3057:HOH:O	2.20	0.41
2:B:389:THR:OG1	2:B:391:GLU:OE2	2.36	0.41
2:B:285:LEU:HD21	2:B:453:VAL:CG1	2.51	0.41
2:D:380:LEU:HD11	2:D:416:ILE:HG12	2.03	0.41
2:D:511:GLU:HG2	2:D:511:GLU:H	1.66	0.41
2:A:271:ILE:HG13	2:A:271:ILE:H	1.66	0.41
2:A:343:PHE:CE2	2:A:344:GLU:HG3	2.56	0.41
2:A:402:ASP:CG	2:A:551:ARG:HH22	2.23	0.41
2:B:417:MET:CE	5:B:2962:HOH:O	2.69	0.41
2:C:212:ILE:HG23	2:C:213:GLU:N	2.35	0.41
2:C:380:LEU:HD12	2:C:380:LEU:HA	1.90	0.41
2:D:352:VAL:CG2	2:D:378:ARG:CG	2.98	0.41
2:A:485:LEU:CD2	2:A:492:THR:HG21	2.50	0.41
2:D:352:VAL:HG23	2:D:378:ARG:HG2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:287:ALA:HB3	2:D:431:PHE:CD1	2.55	0.41
2:B:380:LEU:HD12	2:B:380:LEU:HA	1.96	0.41
2:D:389:THR:OG1	2:D:421:THR:HG21	2.21	0.41
2:C:570:ILE:HA	2:C:601:ILE:HD11	2.01	0.41
2:D:287:ALA:HA	2:D:453:VAL:CG1	2.51	0.41
2:A:308:LEU:HD12	2:A:346:TYR:CE1	2.56	0.41
2:D:259:ASN:OD1	2:D:343:PHE:HB3	2.20	0.41
2:A:276:ILE:HB	2:A:277:PRO:HD3	2.02	0.41
2:D:332:ILE:O	2:D:335:PHE:HB3	2.21	0.41
2:A:308:LEU:HD12	2:A:346:TYR:CZ	2.55	0.40
2:B:481:LEU:CD1	2:B:505:LEU:HD21	2.50	0.40
2:D:327:THR:CG2	2:D:330:LEU:H	2.32	0.40
2:B:535:PHE:CD2	2:B:543:LEU:HB2	2.57	0.40
2:C:520:HIS:CD2	2:C:522:ASP:HB2	2.56	0.40
2:D:391:GLU:N	2:D:421:THR:HG22	2.37	0.40
2:D:507:SER:O	2:D:511:GLU:HG2	2.22	0.40
2:D:571:ASP:HB2	5:D:3143:HOH:O	2.20	0.40
2:A:244:ILE:HG21	2:A:250:ALA:HA	2.03	0.40
2:B:537:ASN:OD1	2:B:537:ASN:C	2.60	0.40
2:D:352:VAL:HG13	2:D:374:ALA:CB	2.52	0.40
2:D:376:PRO:HG2	2:D:409:PHE:CD2	2.56	0.40
2:D:496:VAL:HG21	2:D:502:ALA:CA	2.52	0.40

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	
2	A	418/434 (96%)	398 (95%)	17 (4%)	3 (1%)	22	22
2	B	418/434 (96%)	398 (95%)	18 (4%)	2 (0%)	29	31
2	C	418/434 (96%)	412 (99%)	4 (1%)	2 (0%)	29	31

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	D	418/434 (96%)	400 (96%)	15 (4%)	3 (1%)	22	22
All	All	1672/1736 (96%)	1608 (96%)	54 (3%)	10 (1%)	25	26

All (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
2	A	239	ASP
2	D	203	ILE
2	C	515	PRO
2	D	552	GLY
2	A	552	GLY

### 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%)	16	19
2	B	364/375 (97%)	346 (95%)	18 (5%)	25	31
2	C	364/375 (97%)	347 (95%)	17 (5%)	26	33
2	D	364/375 (97%)	337 (93%)	27 (7%)	13	14
All	All	1456/1500 (97%)	1370 (94%)	86 (6%)	19	23

All (86) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	202	TYR
2	A	208	SER
2	A	229	ASN
2	A	255	ILE

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Mol	Chain	Res	Type
2	A	271	ILE
2	A	285	LEU
2	A	308	LEU
2	A	315	GLU
2	A	332	ILE
2	A	380	LEU
2	A	389	THR
2	A	418	THR
2	A	435	PHE
2	A	437	GLU
2	A	480	LYS
2	A	481	LEU
2	A	503	ASP
2	A	524	LEU
2	A	533	ARG
2	A	540	MET
2	A	543	LEU
2	A	583	VAL
2	A	588	ARG
2	A	599	ARG
2	B	239	ASP
2	B	254	ASP
2	B	255	ILE
2	B	269	THR
2	B	285	LEU
2	B	308	LEU
2	B	327	THR
2	B	352	VAL
2	B	380	LEU
2	B	425	GLU
2	B	435	PHE
2	B	453	VAL
2	B	481	LEU
2	B	490	ASP
2	B	543	LEU
2	B	583	VAL
2	B	608	ILE
2	B	618	ASP
2	C	213	GLU
2	C	269	THR
2	C	285	LEU
2	C	306	LYS

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Mol	Chain	Res	Type
2	C	308	LEU
2	C	327	THR
2	C	352	VAL
2	C	380	LEU
2	C	389	THR
2	C	391	GLU
2	C	435	PHE
2	C	481	LEU
2	C	492	THR
2	C	524	LEU
2	C	539	SER
2	C	583	VAL
2	C	588	ARG
2	D	210	ASP
2	D	229	ASN
2	D	239	ASP
2	D	285	LEU
2	D	308	LEU
2	D	314	LEU
2	D	316	LEU
2	D	318	ARG
2	D	327	THR
2	D	363	GLU
2	D	378	ARG
2	D	380	LEU
2	D	389	THR
2	D	391	GLU
2	D	435	PHE
2	D	437	GLU
2	D	466	LYS
2	D	481	LEU
2	D	492	THR
2	D	503	ASP
2	D	510	SER
2	D	526	SER
2	D	543	LEU
2	D	580	THR
2	D	582	ARG
2	D	599	ARG
2	D	608	ILE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (32) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	312	HIS
2	A	336	ASN
2	A	370	HIS
2	A	419	HIS
2	A	426	HIS
2	A	427	GLN
2	A	449	ASN
2	A	520	HIS
2	B	229	ASN
2	B	320	GLN
2	B	370	HIS
2	B	419	HIS
2	B	426	HIS
2	B	427	GLN
2	B	449	ASN
2	B	520	HIS
2	C	224	HIS
2	C	320	GLN
2	C	370	HIS
2	C	419	HIS
2	C	426	HIS
2	C	473	ASN
2	C	520	HIS
2	D	320	GLN
2	D	361	GLN
2	D	362	ASN
2	D	370	HIS
2	D	419	HIS
2	D	426	HIS
2	D	449	ASN
2	D	488	GLN
2	D	520	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 [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 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	D	2904	3	29,33,33	1.88	8 (27%)	31,52,52	2.08	13 (41%)
4	ANP	B	2902	3	29,33,33	2.01	7 (24%)	31,52,52	1.99	10 (32%)
4	ANP	C	2903	3	29,33,33	1.81	8 (27%)	31,52,52	2.01	11 (35%)
4	ANP	A	2901	3	29,33,33	1.94	8 (27%)	31,52,52	2.10	11 (35%)

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	D	2904	3	-	5/14/38/38	0/3/3/3
4	ANP	B	2902	3	-	4/14/38/38	0/3/3/3
4	ANP	C	2903	3	-	3/14/38/38	0/3/3/3
4	ANP	A	2901	3	-	4/14/38/38	0/3/3/3

All (31) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	2902	ANP	C2'-C1'	-5.55	1.45	1.53
4	A	2901	ANP	C2'-C1'	-5.16	1.45	1.53
4	D	2904	ANP	C2'-C1'	-4.24	1.47	1.53
4	A	2901	ANP	PG-O1G	3.99	1.52	1.46
4	B	2902	ANP	PB-O2B	-3.91	1.46	1.56
4	C	2903	ANP	C2'-C1'	-3.84	1.47	1.53
4	B	2902	ANP	PG-O1G	3.76	1.52	1.46
4	D	2904	ANP	PB-O2B	-3.72	1.46	1.56
4	C	2903	ANP	PB-O2B	-3.49	1.47	1.56
4	C	2903	ANP	PG-O1G	3.45	1.51	1.46
4	B	2902	ANP	PB-O3A	3.40	1.63	1.59
4	D	2904	ANP	PB-O3A	3.40	1.63	1.59
4	D	2904	ANP	PG-O1G	3.31	1.51	1.46
4	A	2901	ANP	PB-O2B	-3.26	1.48	1.56
4	B	2902	ANP	PG-O2G	-3.10	1.48	1.56
4	C	2903	ANP	PG-O2G	-2.98	1.48	1.56
4	A	2901	ANP	PB-O3A	2.92	1.62	1.59
4	C	2903	ANP	PB-O3A	2.90	1.62	1.59
4	A	2901	ANP	C2-N3	2.79	1.36	1.32
4	D	2904	ANP	PG-O3G	-2.78	1.49	1.56
4	B	2902	ANP	PG-O3G	-2.73	1.49	1.56
4	A	2901	ANP	PG-O2G	-2.62	1.49	1.56
4	D	2904	ANP	C2-N3	2.60	1.36	1.32
4	A	2901	ANP	PG-O3G	-2.59	1.49	1.56
4	D	2904	ANP	PG-O2G	-2.56	1.49	1.56
4	D	2904	ANP	C3'-C4'	-2.47	1.46	1.53
4	C	2903	ANP	PB-O1B	2.44	1.50	1.46
4	B	2902	ANP	C3'-C4'	-2.40	1.46	1.53
4	C	2903	ANP	PG-O3G	-2.36	1.50	1.56
4	A	2901	ANP	C3'-C4'	-2.36	1.47	1.53
4	C	2903	ANP	C3'-C4'	-2.36	1.47	1.53

All (45) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2901	ANP	O1B-PB-N3B	-4.68	104.87	111.77
4	C	2903	ANP	O1B-PB-N3B	-4.59	105.02	111.77
4	D	2904	ANP	O1B-PB-N3B	-4.22	105.56	111.77
4	D	2904	ANP	O4'-C1'-C2'	-4.19	100.81	106.93
4	C	2903	ANP	O4'-C1'-C2'	-4.12	100.91	106.93
4	A	2901	ANP	O4'-C1'-C2'	-4.05	101.00	106.93
4	B	2902	ANP	O4'-C1'-C2'	-3.98	101.11	106.93
4	B	2902	ANP	O1B-PB-N3B	-3.70	106.32	111.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	C	2903	ANP	C3'-C2'-C1'	3.47	106.20	100.98
4	A	2901	ANP	C3'-C2'-C1'	3.29	105.94	100.98
4	B	2902	ANP	O4'-C4'-C3'	-3.22	98.74	105.11
4	D	2904	ANP	C3'-C2'-C1'	3.13	105.69	100.98
4	B	2902	ANP	O3A-PB-N3B	3.08	115.14	106.59
4	D	2904	ANP	O4'-C4'-C3'	-3.08	99.02	105.11
4	C	2903	ANP	O3A-PB-N3B	3.03	115.00	106.59
4	A	2901	ANP	O4'-C4'-C3'	-3.02	99.13	105.11
4	D	2904	ANP	O2A-PA-O5'	3.00	121.69	107.75
4	A	2901	ANP	O3G-PG-O2G	2.98	115.57	107.64
4	A	2901	ANP	O3'-C3'-C2'	-2.96	102.26	111.82
4	B	2902	ANP	C3'-C2'-C1'	2.95	105.42	100.98
4	D	2904	ANP	O3'-C3'-C2'	-2.95	102.28	111.82
4	B	2902	ANP	O2A-PA-O5'	2.90	121.22	107.75
4	A	2901	ANP	O2A-PA-O5'	2.85	120.97	107.75
4	C	2903	ANP	O3G-PG-O2G	2.84	115.20	107.64
4	C	2903	ANP	O2A-PA-O5'	2.83	120.89	107.75
4	B	2902	ANP	O3G-PG-O2G	2.82	115.16	107.64
4	A	2901	ANP	O3A-PB-N3B	2.82	114.42	106.59
4	D	2904	ANP	O3A-PB-N3B	2.74	114.19	106.59
4	C	2903	ANP	O4'-C4'-C3'	-2.67	99.84	105.11
4	D	2904	ANP	C2'-C3'-C4'	2.65	107.79	102.64
4	B	2902	ANP	O3'-C3'-C2'	-2.61	103.38	111.82
4	D	2904	ANP	O3G-PG-O2G	2.60	114.55	107.64
4	C	2903	ANP	O3'-C3'-C2'	-2.59	103.43	111.82
4	A	2901	ANP	C2'-C3'-C4'	2.58	107.65	102.64
4	C	2903	ANP	C2'-C3'-C4'	2.58	107.65	102.64
4	D	2904	ANP	N3-C2-N1	-2.53	124.72	128.68
4	B	2902	ANP	N3-C2-N1	-2.48	124.80	128.68
4	B	2902	ANP	C2'-C3'-C4'	2.41	107.33	102.64
4	C	2903	ANP	N3-C2-N1	-2.32	125.05	128.68
4	A	2901	ANP	N3-C2-N1	-2.31	125.06	128.68
4	A	2901	ANP	O1G-PG-N3B	-2.22	108.50	111.77
4	D	2904	ANP	PA-O3A-PB	2.22	140.42	132.62
4	D	2904	ANP	O1G-PG-N3B	-2.09	108.69	111.77
4	D	2904	ANP	O3'-C3'-C4'	-2.03	105.19	111.05
4	C	2903	ANP	O1G-PG-N3B	-2.02	108.80	111.77

There are no chirality outliers.

All (16) torsion outliers are listed below:

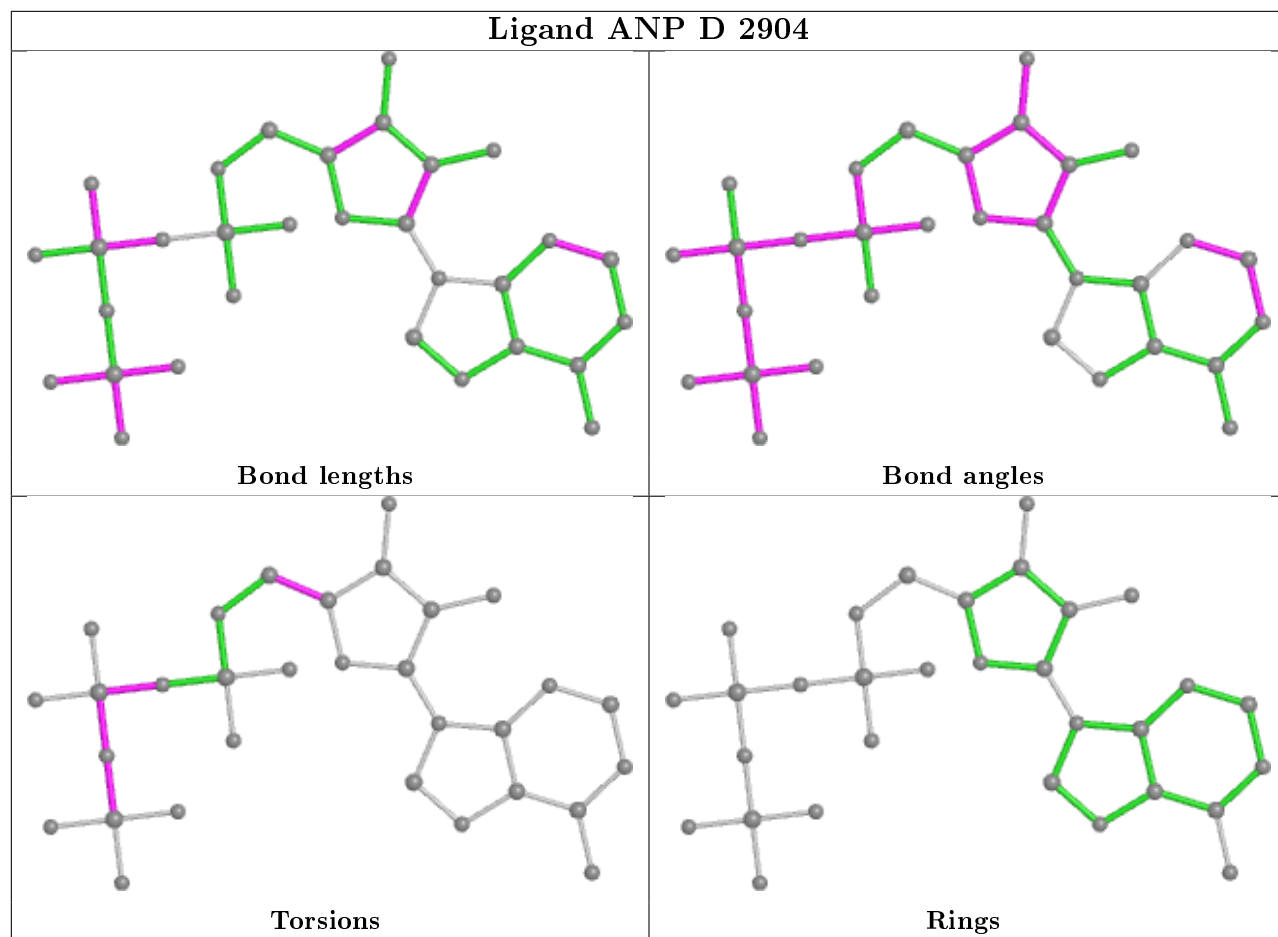
Mol	Chain	Res	Type	Atoms
4	C	2903	ANP	PB-N3B-PG-O1G
4	C	2903	ANP	PA-O3A-PB-O1B
4	C	2903	ANP	PA-O3A-PB-O2B
4	D	2904	ANP	PB-N3B-PG-O1G
4	D	2904	ANP	PG-N3B-PB-O1B
4	D	2904	ANP	PA-O3A-PB-O2B
4	A	2901	ANP	PB-N3B-PG-O1G
4	A	2901	ANP	PG-N3B-PB-O1B
4	A	2901	ANP	PA-O3A-PB-O2B
4	B	2902	ANP	PB-N3B-PG-O1G
4	B	2902	ANP	PA-O3A-PB-O2B
4	D	2904	ANP	C3'-C4'-C5'-O5'
4	D	2904	ANP	O4'-C4'-C5'-O5'
4	A	2901	ANP	C3'-C4'-C5'-O5'
4	B	2902	ANP	C3'-C4'-C5'-O5'
4	B	2902	ANP	PG-N3B-PB-O1B

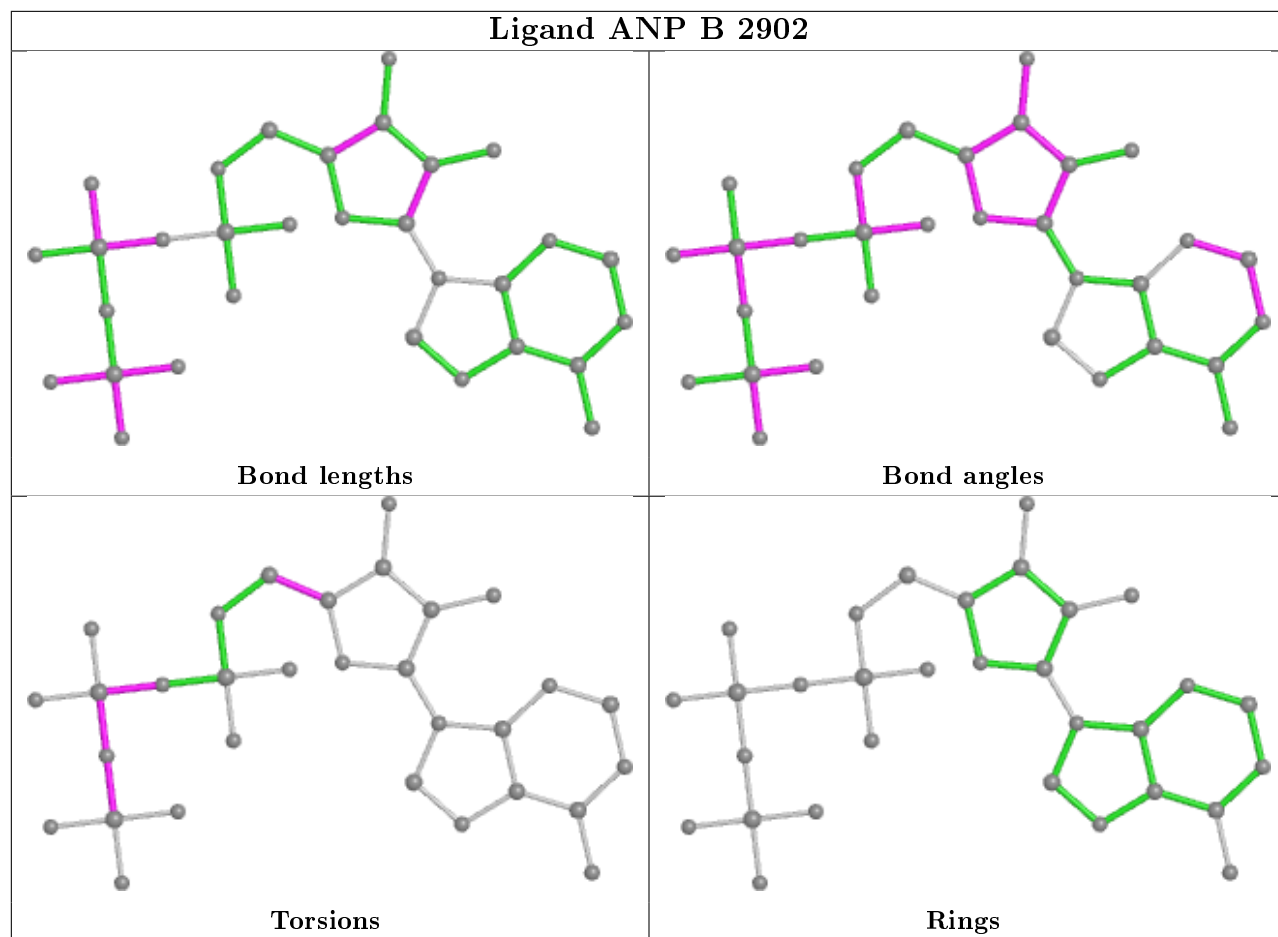
There are no ring outliers.

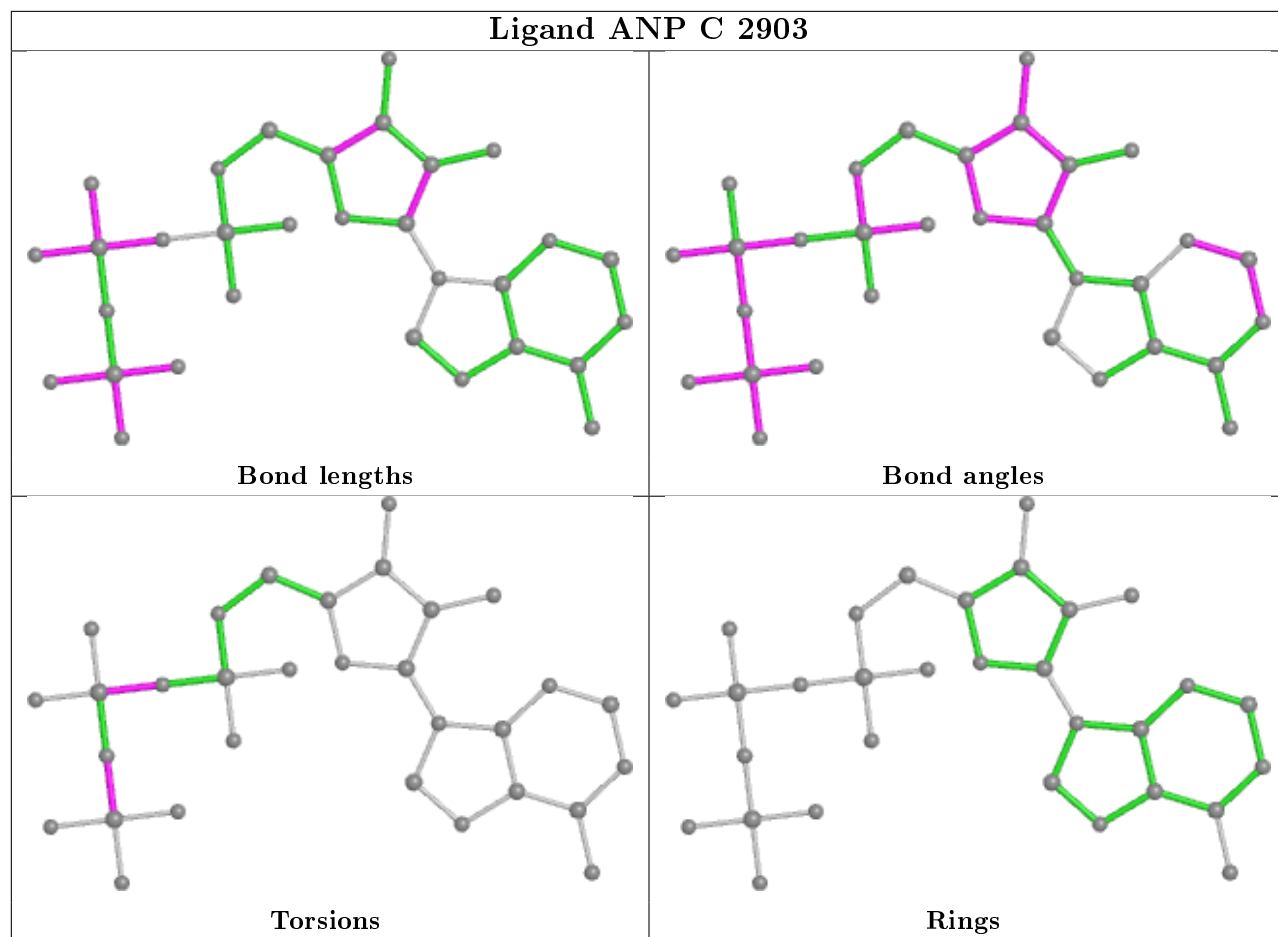
4 monomers are involved in 13 short contacts:

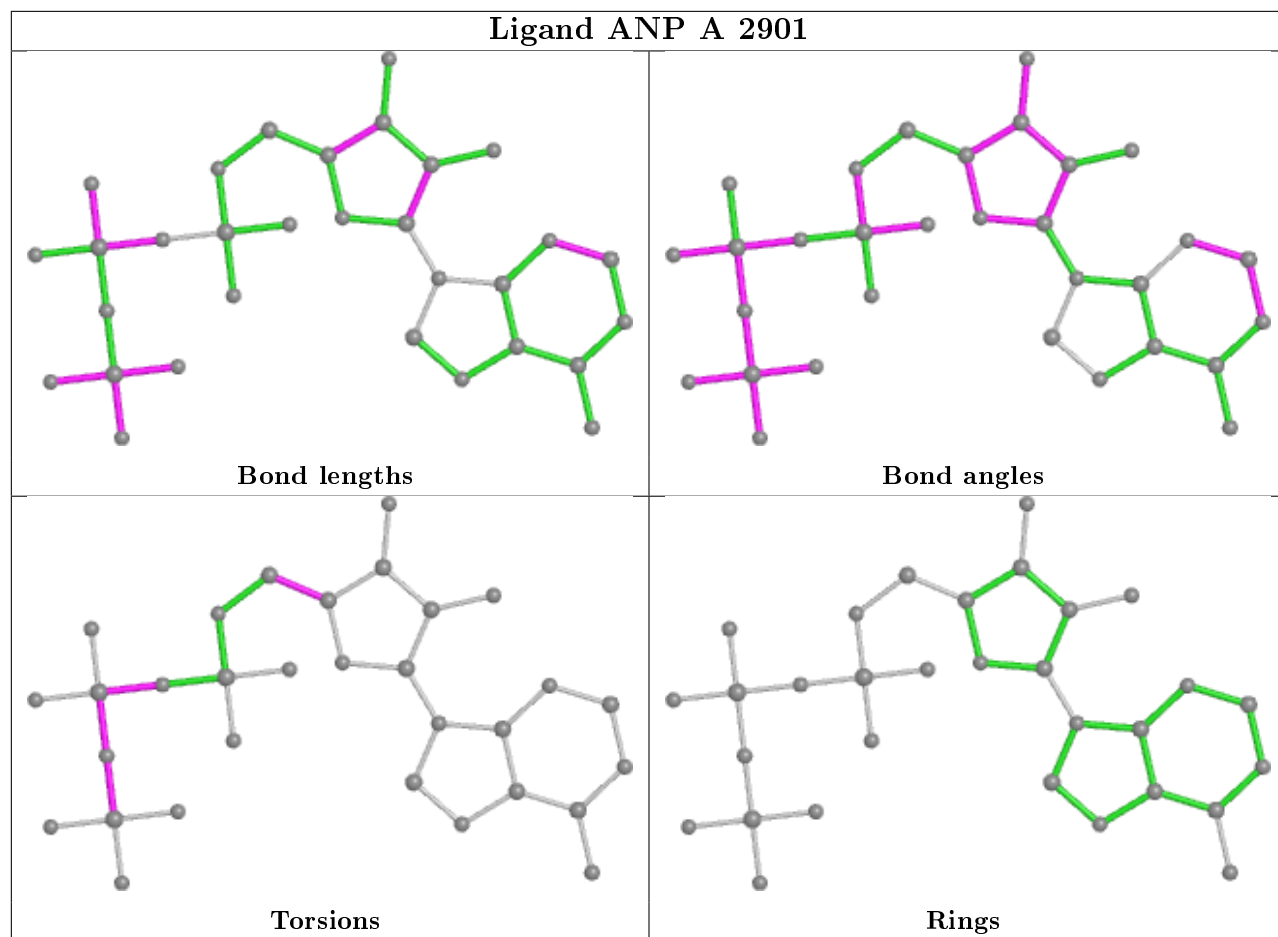
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	2904	ANP	3	0
4	B	2902	ANP	4	0
4	C	2903	ANP	1	0
4	A	2901	ANP	5	0

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 than 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.









## 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 ⓘ

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%)	-0.11	1 (14%) 2 2	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%)	-0.15	0 100 100	24, 27, 53, 68	0
1	H	6/10 (60%)	-0.08	1 (16%) 1 1	29, 30, 43, 70	0
2	A	420/434 (96%)	0.12	23 (5%) 25 24	23, 43, 77, 85	0
2	B	420/434 (96%)	-0.22	5 (1%) 79 77	18, 36, 59, 66	0
2	C	420/434 (96%)	-0.39	1 (0%) 95 94	18, 31, 47, 59	0
2	D	420/434 (96%)	-0.01	16 (3%) 40 38	20, 39, 66, 77	0
All	All	1707/1776 (96%)	-0.12	47 (2%) 53 51	18, 37, 63, 85	0

All (47) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	A	223	ILE	5.5
2	A	316	LEU	4.2
2	A	212	ILE	3.7
2	B	599	ARG	3.6
2	D	313	GLU	3.4
2	A	313	GLU	3.4
2	A	224	HIS	3.4
2	D	223	ILE	3.3
2	C	210	ASP	3.2
2	D	248	THR	3.1
2	D	346	TYR	2.9
2	A	618	ASP	2.8
2	A	230	ASN	2.8
2	D	251	ASP	2.8
1	E	1	U	2.8
2	D	212	ILE	2.8

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Mol	Chain	Res	Type	RSRZ
2	A	596	GLU	2.7
2	D	596	GLU	2.7
2	D	224	HIS	2.7
2	D	226	SER	2.6
2	B	346	TYR	2.6
2	A	239	ASP	2.6
2	A	229	ASN	2.6
2	A	584	GLY	2.5
2	A	599	ARG	2.5
2	A	346	TYR	2.5
2	A	533	ARG	2.5
2	D	599	ARG	2.5
2	D	475	TYR	2.4
2	A	315	GLU	2.4
1	H	7	U	2.4
2	A	227	LYS	2.4
2	A	226	SER	2.4
2	D	230	ASN	2.4
2	A	387	PHE	2.2
2	D	213	GLU	2.2
2	A	367	ARG	2.2
2	D	250	ALA	2.2
2	D	229	ASN	2.2
2	B	486	SER	2.1
2	B	618	ASP	2.1
2	D	239	ASP	2.1
2	A	216	SER	2.1
2	A	338	ALA	2.1
2	B	613	GLY	2.0
2	A	392	ASP	2.0
2	A	398	LEU	2.0

## 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](#)

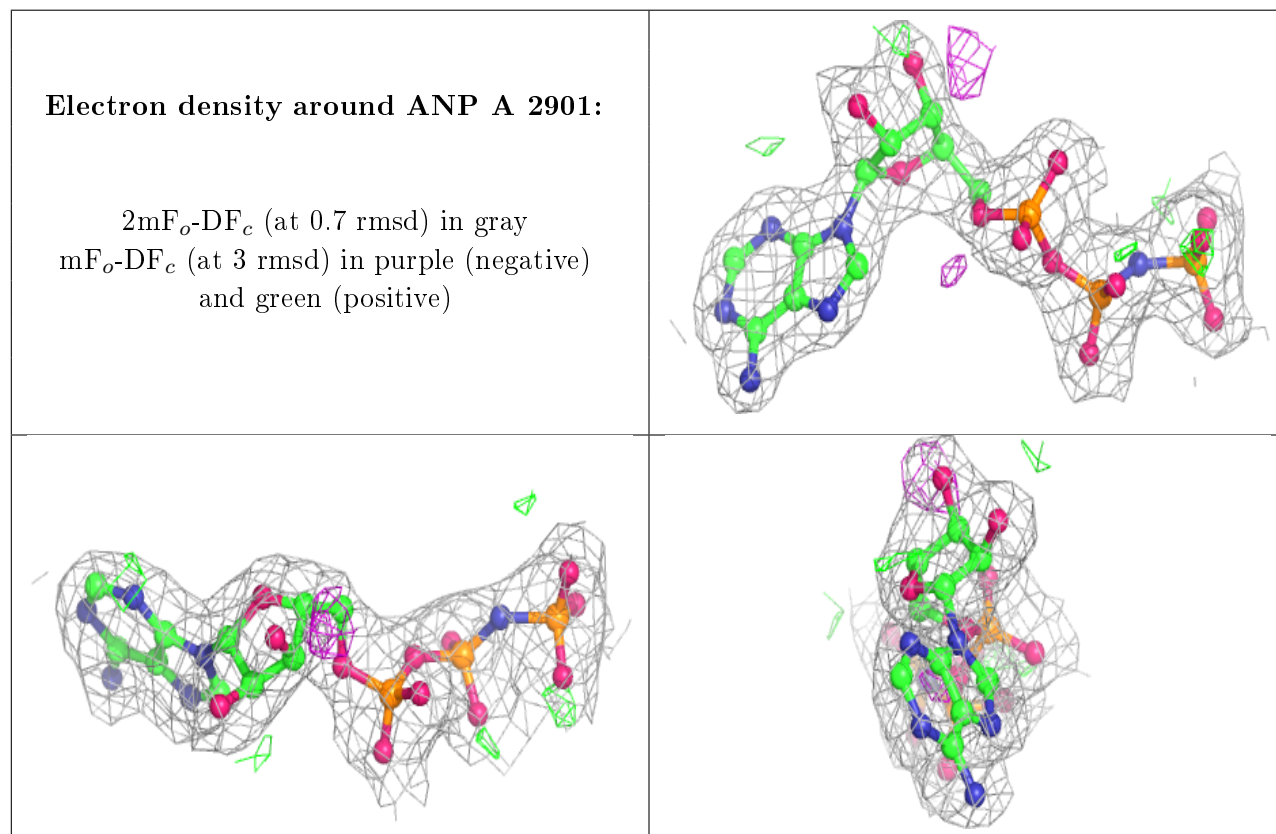
There are no carbohydrates in this entry.

## 6.4 Ligands ⓘ

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. 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.

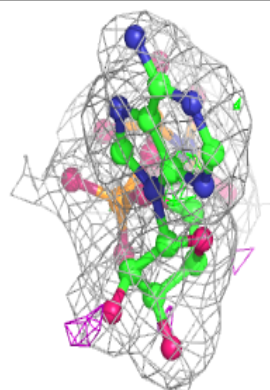
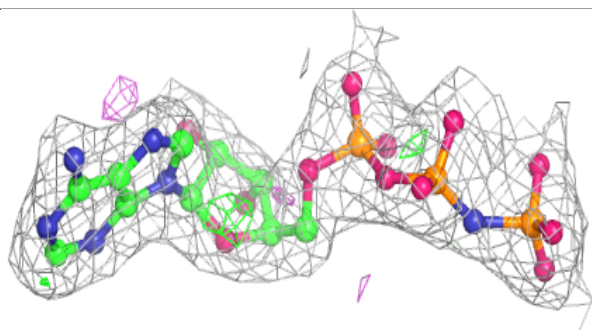
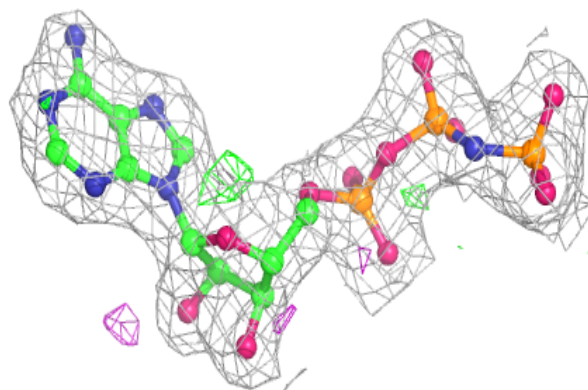
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å <sup>2</sup> )	Q<0.9
3	MG	A	2801	1/1	0.94	0.25	37,37,37,37	0
3	MG	D	2804	1/1	0.97	0.21	25,25,25,25	0
3	MG	C	2803	1/1	0.97	0.26	22,22,22,22	0
4	ANP	A	2901	31/31	0.98	0.10	24,36,39,39	0
4	ANP	D	2904	31/31	0.98	0.10	22,33,34,36	0
4	ANP	C	2903	31/31	0.99	0.10	17,22,25,26	0
3	MG	B	2802	1/1	0.99	0.20	21,21,21,21	0
4	ANP	B	2902	31/31	0.99	0.12	19,26,30,31	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

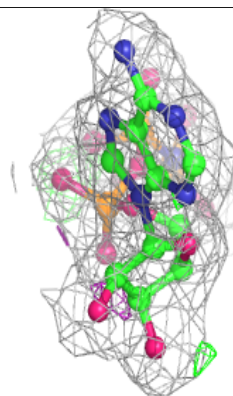
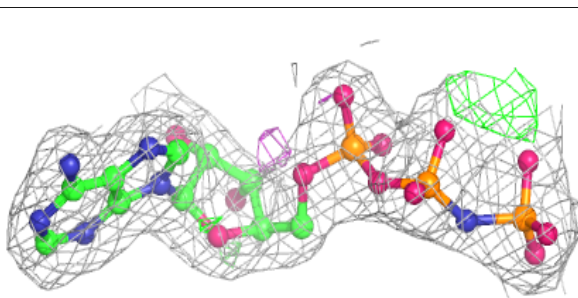
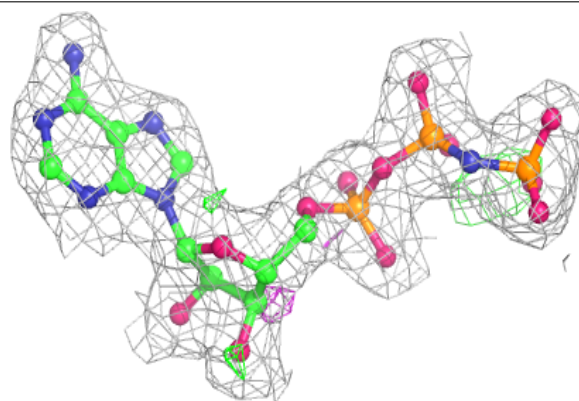


**Electron density around ANP D 2904:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)

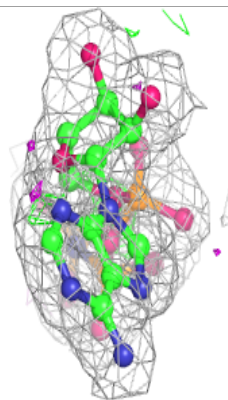
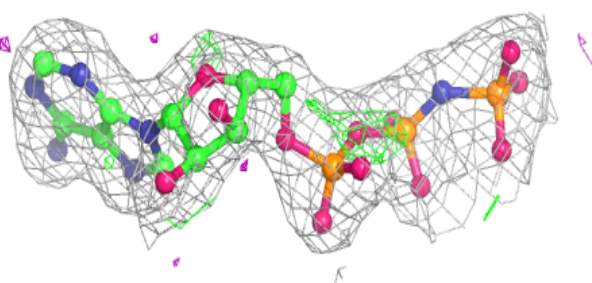
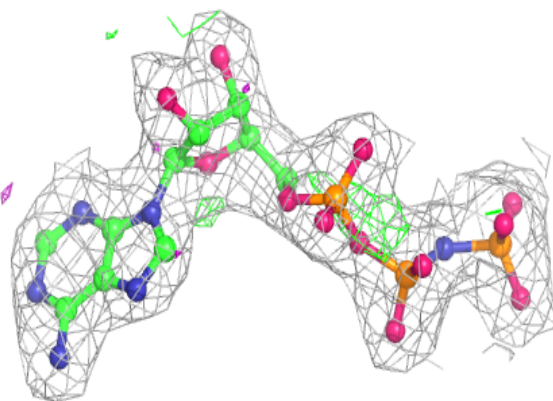
**Electron density around ANP C 2903:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



**Electron density around ANP B 2902:**

$2mF_o-DF_c$  (at 0.7 rmsd) in gray  
 $mF_o-DF_c$  (at 3 rmsd) in purple (negative)  
and green (positive)



## 6.5 Other polymers [i](#)

There are no such residues in this entry.