



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 14, 2026 – 02:22 PM UTC

PDB ID : 2DB3 / pdb_00002db3
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

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtrriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.49

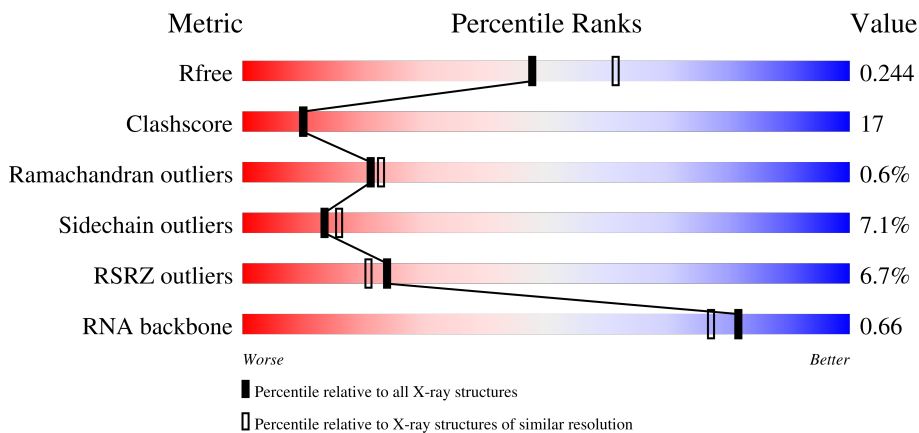
1 Overall quality at a glance i

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_{free}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)
RNA backbone	3983	1052 (2.50-1.90)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. 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	
1	F	10	
1	G	10	

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

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 (CCD ID: MG) (formula: Mg).

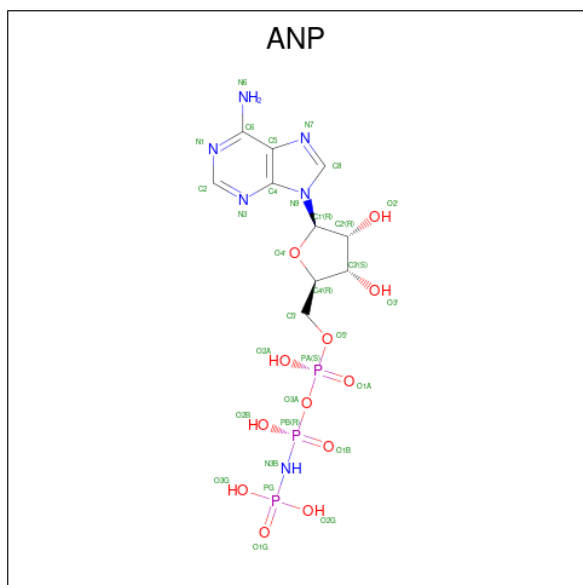
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

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

- Molecule 4 is PHOSPHOAMINOPHOSPHONIC ACID-ADENYLATE ESTER (CCD ID: ANP) (formula: C₁₀H₁₇N₆O₁₂P₃).



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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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, DNA and oligosaccharide 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.

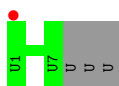
- Molecule 1: 5'-R(*UP*UP*UP*UP*UP*UP*UP*UP*U)-3'

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: 



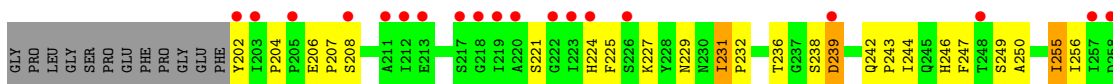
- Molecule 1: 5'-R(*UP*UP*UP*UP*UP*UP*UP*UP*U)-3'

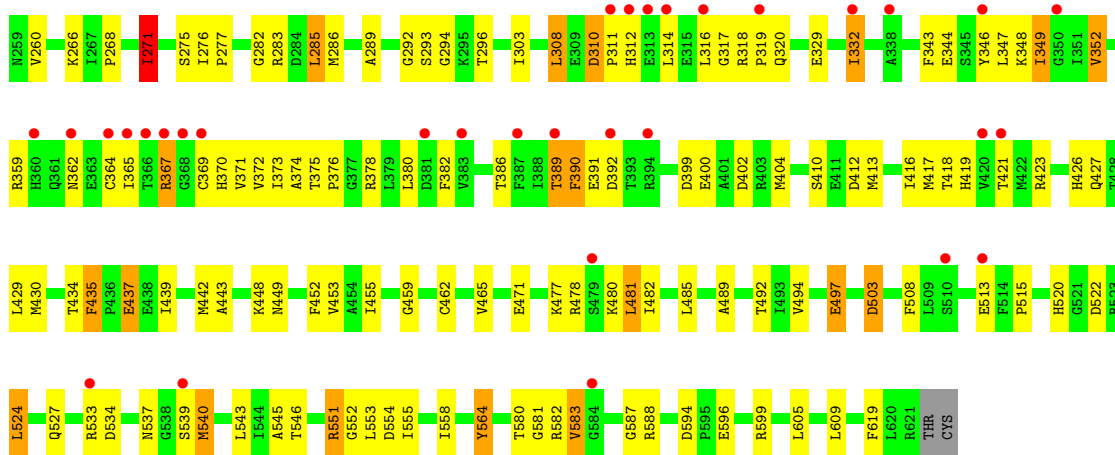
Chain H: 



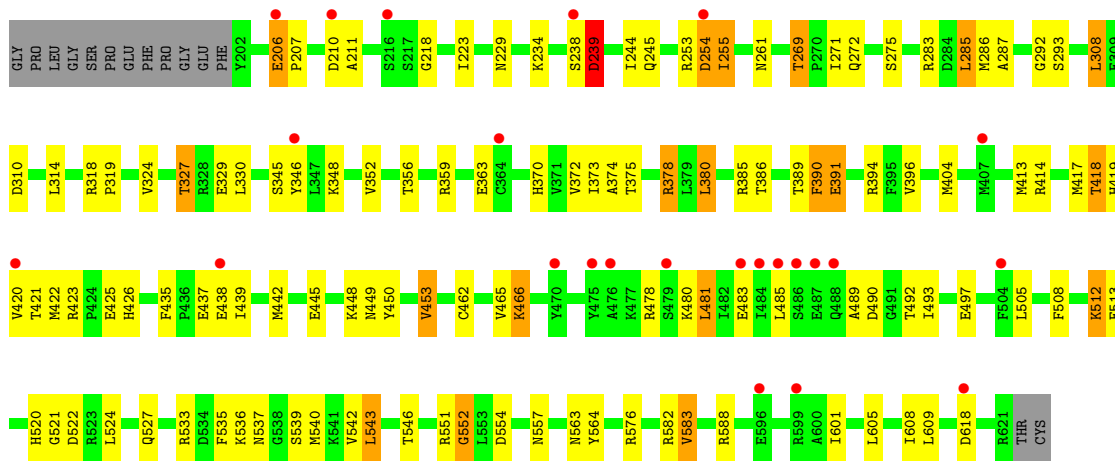
- Molecule 2: ATP-dependent RNA helicase vasa

Chain A: 

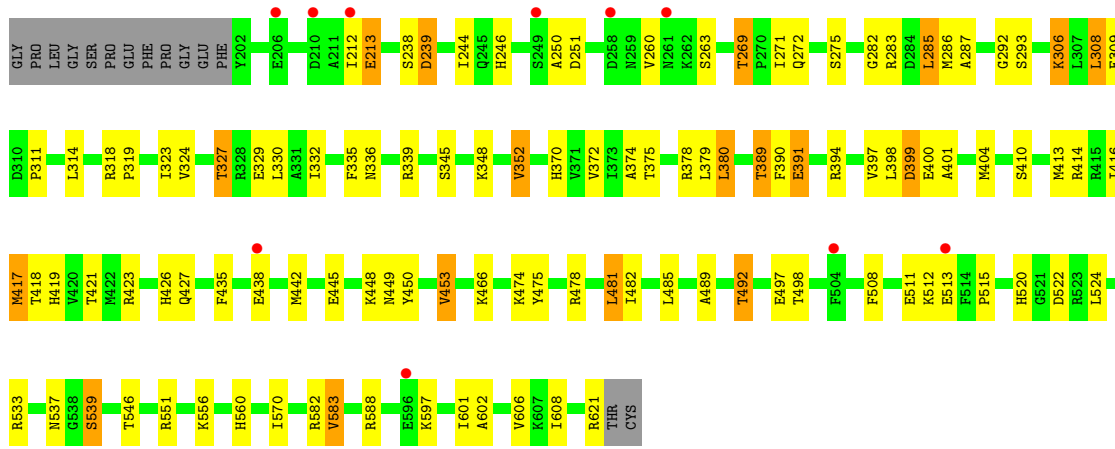




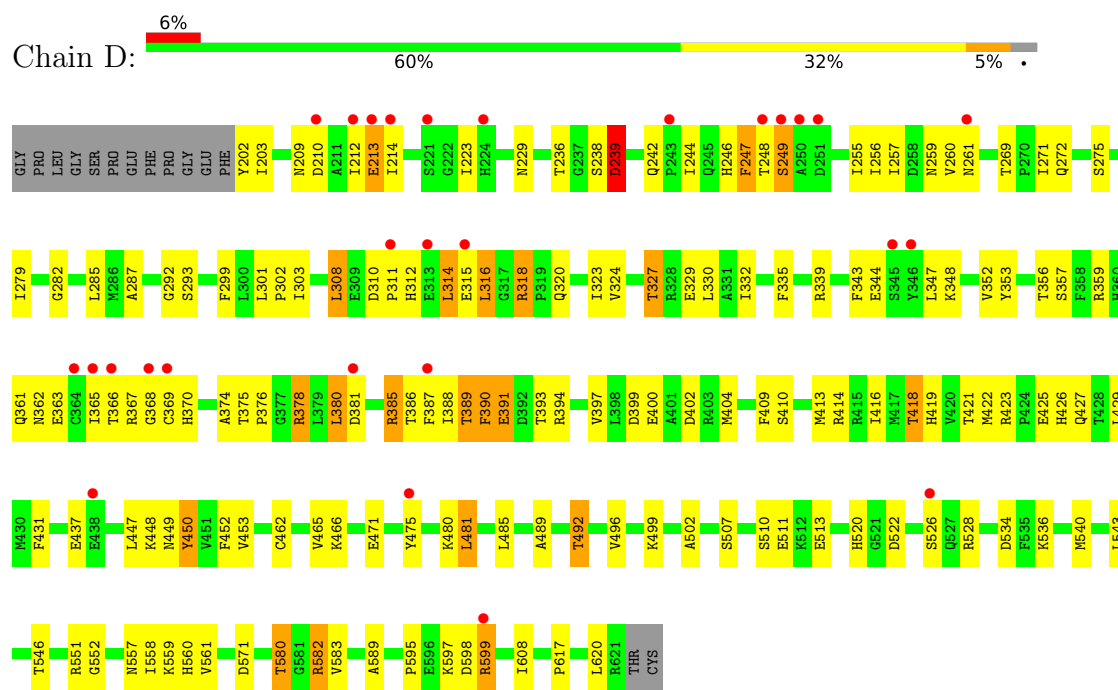
• Molecule 2: ATP-dependent RNA helicase vasa



• Molecule 2: ATP-dependent RNA helicase vasa



• Molecule 2: ATP-dependent RNA helicase vasa



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	71.05Å 142.33Å 130.47Å 90.00° 90.86° 90.00°	Depositor
Resolution (Å)	39.46 – 2.20 39.46 – 2.20	Depositor EDS
% Data completeness (in resolution range)	89.4 (39.46-2.20) 89.5 (39.46-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.88 (at 2.20Å)	Xtrriage
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 ²)	31.2	Xtrriage
Anisotropy	0.306	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 47.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.076 for h,-k,-l	Xtrriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	15119	wwPDB-VP
Average B, all atoms (Å ²)	39.0	wwPDB-VP

Xtrriage'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.*

¹Intensities estimated from amplitudes.

²Theoretical 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	0.36	0/114	0.68	0/176
1	F	0.36	0/141	0.64	0/216
1	G	0.40	0/150	0.66	0/230
1	H	0.40	0/128	0.66	0/196
2	A	0.48	0/3360	0.99	20/4539 (0.4%)
2	B	0.54	0/3360	1.01	17/4539 (0.4%)
2	C	0.57	0/3360	1.03	15/4539 (0.3%)
2	D	0.49	0/3360	1.03	14/4539 (0.3%)
All	All	0.52	0/13973	1.00	66/18974 (0.3%)

There are no bond length outliers.

All (66) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	345	SER	N-CA-C	-9.40	95.98	110.17
2	A	367	ARG	N-CA-C	-9.38	101.84	113.38
2	D	367	ARG	N-CA-C	-8.50	103.07	113.19
2	C	345	SER	N-CA-C	-8.37	97.89	109.95
2	D	390	PHE	N-CA-C	7.69	122.38	112.92
2	D	546	THR	N-CA-C	-7.47	98.89	110.17
2	D	249	SER	N-CA-C	-7.39	103.68	114.39
2	B	275	SER	N-CA-C	7.30	119.03	111.14
2	B	390	PHE	N-CA-C	7.25	121.43	112.59
2	C	375	THR	N-CA-C	-7.22	101.00	110.39
2	A	390	PHE	N-CA-C	7.17	120.68	112.57
2	B	450	TYR	N-CA-C	7.16	120.22	110.55
2	D	385	ARG	N-CA-C	-7.06	104.13	112.89
2	A	374	ALA	N-CA-C	6.66	118.98	108.79
2	C	546	THR	N-CA-C	-6.56	100.19	110.36
2	C	390	PHE	N-CA-C	6.55	120.58	112.59

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	375	THR	N-CA-C	-6.54	101.88	110.39
2	D	513	GLU	N-CA-C	6.52	120.53	112.58
2	B	254	ASP	N-CA-C	6.51	119.20	111.71
2	B	546	THR	N-CA-C	-6.49	100.30	110.36
2	D	375	THR	N-CA-C	-6.47	101.38	110.31
2	C	275	SER	N-CA-C	6.43	118.37	111.36
2	A	497	GLU	N-CA-C	6.15	118.06	111.36
2	B	513	GLU	N-CA-C	6.00	120.54	113.23
2	C	410	SER	N-CA-C	5.98	118.28	111.11
2	B	374	ALA	N-CA-C	5.97	117.93	108.79
2	B	310	ASP	CA-C-N	5.92	125.88	119.78
2	B	310	ASP	C-N-CA	5.92	125.88	119.78
2	A	410	SER	N-CA-C	5.89	118.18	111.11
2	A	275	SER	N-CA-C	5.89	117.78	111.36
2	A	375	THR	N-CA-C	-5.85	102.21	110.29
2	D	275	SER	N-CA-C	5.80	118.55	111.82
2	C	498	THR	N-CA-C	5.78	119.10	110.14
2	C	399	ASP	N-CA-C	-5.77	102.76	110.55
2	B	521	GLY	N-CA-C	5.73	120.89	113.27
2	D	598	ASP	N-CA-C	5.71	119.23	112.72
2	A	310	ASP	CA-C-N	5.69	125.62	119.76
2	A	310	ASP	C-N-CA	5.69	125.62	119.76
2	A	546	THR	N-CA-C	-5.68	101.59	110.17
2	C	401	ALA	N-CA-C	5.53	118.02	111.33
2	A	271	ILE	CB-CA-C	-5.50	103.35	112.26
2	C	374	ALA	N-CA-C	5.50	117.20	108.79
2	A	255	ILE	CB-CA-C	-5.49	104.85	111.88
2	A	477	LYS	N-CA-C	5.49	117.27	111.28
2	A	551	ARG	N-CA-C	5.48	118.41	109.59
2	D	247	PHE	N-CA-C	-5.47	103.48	110.53
2	B	552	GLY	N-CA-C	5.41	126.00	113.18
2	B	497	GLU	N-CA-C	5.40	116.97	111.14
2	A	564	TYR	N-CA-C	-5.40	105.40	111.28
2	B	512	LYS	N-CA-C	-5.38	106.30	112.92
2	B	218	GLY	N-CA-C	5.38	117.06	111.95
2	A	386	THR	N-CA-C	5.37	119.13	112.47
2	C	497	GLU	N-CA-C	5.25	116.81	111.14
2	A	231	ILE	CA-C-N	5.24	125.16	119.76
2	A	231	ILE	C-N-CA	5.24	125.16	119.76
2	C	450	TYR	N-CA-C	5.21	118.19	110.48
2	C	551	ARG	N-CA-C	5.18	117.93	109.59
2	A	545	ALA	N-CA-C	5.15	116.90	109.07

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	551	ARG	N-CA-C	5.13	117.85	109.59
2	D	450	TYR	N-CA-C	5.12	117.72	110.50
2	D	557	ASN	N-CA-C	5.10	118.60	112.38
2	D	410	SER	N-CA-C	5.09	117.48	111.33
2	C	263	SER	N-CA-C	-5.07	107.09	113.28
2	D	381	ASP	N-CA-C	-5.07	105.64	111.07
2	A	294	GLY	N-CA-C	5.06	122.81	115.32
2	C	260	VAL	N-CA-C	-5.01	105.51	110.62

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-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 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	145	0
2	B	3296	0	3312	102	0
2	C	3296	0	3312	87	0
2	D	3296	0	3312	139	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	21	0
5	C	393	0	0	21	0
5	D	282	0	0	9	0
5	E	23	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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	476	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 17.

All (476) 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:HB2	2:A:359:ARG:HH11	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
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:B:324:VAL:CG1	2:B:404:MET:HE2	2.08	0.84
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:B:582:ARG:NH2	4:B:2902:ANP:HNB1	1.85	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:324:VAL:HG12	2:D:404:MET:HE2	1.70	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:442:MET:HE1	5:C:3068:HOH:O	1.89	0.73
2:C:292:GLY:H	4:C:2903:ANP:HNB1	1.36	0.72
2:B:324:VAL:HG12	2:B:404:MET:HE2	1.68	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:B:438:GLU:HG3	2:B:442:MET:HE2	1.73	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
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:422:MET:HE2	2:D:426:HIS:CD2	2.29	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:C:324:VAL:HG12	2:C:404:MET:HE2	1.77	0.66
2:D:315:GLU:HB3	2:D:318:ARG:HG3	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:366:THR:C	2:D:368:GLY:H	2.02	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:D:391:GLU:CD	2:D:421:THR:HG23	2.22	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:309:GLU:C	2:C:311:PRO:HD3	2.24	0.62
2:C:389:THR:CG2	2:C:391:GLU:HG2	2.29	0.62
2:C:442:MET:HE2	5:C:3094:HOH:O	1.99	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
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:A:283:ARG:HH12	2:A:449:ASN:CG	2.08	0.60
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:HH11	2:D:582:ARG:CB	2.11	0.60
2:D:391:GLU:OE1	2:D:421:THR:HG23	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:324:VAL:CG1	2:C:404:MET:HE2	2.31	0.60
2:C:418:THR:O	2:C:418:THR:CG2	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:582:ARG:HB3	2:D:582:ARG:NH1	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:324:VAL:CG1	2:D:404:MET:HE2	2.32	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:D:366:THR:C	2:D:368:GLY:N	2.59	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:C:537:ASN:OD1	2:C:539:SER:OG	2.20	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:515:PRO:C	2:A:540:MET:HE2	2.30	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:314:LEU:HG	2:D:370:HIS:ND1	2.21	0.55
2:D:347:LEU:HA	2:D:370:HIS:HD2	1.72	0.55
2:B:414:ARG:O	2:B:418:THR:HB	2.07	0.55
2:D:418:THR:CG2	2:D:418:THR:O	2.55	0.55
2:B:481:LEU:HD12	2:B:564:TYR:CE2	2.41	0.55
2:C:398:LEU:HD11	2:C:417:MET:HE1	1.88	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:H	2:D:599:ARG:HD2	1.71	0.55
2:A:390:PHE:N	2:A:421:THR:CG2	2.71	0.54
2:A:455:ILE:N	2:A:455:ILE:HD12	2.22	0.54
2:A:515:PRO:C	2:A:540:MET:CE	2.80	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:D:422:MET:HE2	2:D:426:HIS:CG	2.44	0.53
2:B:481:LEU:HD12	2:B:564:TYR:CD2	2.42	0.53
1:G:1:U:H5''	5:G:719:HOH:O	2.08	0.53
2:A:389:THR:CG2	2:A:391:GLU:OE1	2.57	0.53
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:HG23	2:A:465:VAL:O	2.09	0.53
2:C:419:HIS:HD2	2:C:421:THR:OG1	1.92	0.53
1:E:2:U:O2'	2:A:497:GLU:OE2	2.25	0.53
2:B:533:ARG:HD2	5:B:3053:HOH:O	2.08	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:C:520:HIS:CD2	2:C:522:ASP:H	2.21	0.53
2:D:238:SER:O	2:D:239:ASP:C	2.51	0.52
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:A:540:MET:HE3	2:A:540:MET:HA	1.90	0.52
2:B:540:MET:HE2	2:B:540:MET:HA	1.92	0.52
2:A:554:ASP:C	2:A:555:ILE:HD12	2.35	0.52
2:D:282:GLY:HA2	2:D:427:GLN:CD	2.35	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: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:376:PRO:HG3	2:D:413:MET:HE1	1.93	0.51
2:D:481:LEU:HD22	2:D:485:LEU:HG	1.93	0.51
2:C:512:LYS:C	2:C:513:GLU:HG2	2.35	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:404:MET:HE3	2:A:413:MET:HE3	1.91	0.50
2:D:248:THR:O	2:D:248:THR:HG22	2.10	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:D:244:ILE:HD12	2:D:244:ILE:C	2.37	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:478:ARG:HG3	2:B:564:TYR:OH	2.11	0.49
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:C:239:ASP:CG	2:C:239:ASP:O	2.54	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:221:SER:HB2	2:A:225:PHE:CD1	2.46	0.49
2:A:439:ILE:HA	2:A:442:MET:HE3	1.93	0.49
2:A:434:THR:HG22	2:A:459:GLY:HA2	1.94	0.49
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:B:478:ARG:HG3	2:B:564:TYR:HH	1.77	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: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:A:311:PRO:C	2:A:312:HIS:HD2	2.21	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:582:ARG:C	2:B:583:VAL:HG23	2.38	0.48
2:B:239:ASP:CG	2:B:239:ASP:O	2.56	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:C:285:LEU:HD22	2:C:286:MET:N	2.28	0.48
2:C:448:LYS:O	2:C:449:ASN:C	2.56	0.48
2:B:327:THR:CG2	5:B:3047:HOH:O	2.61	0.48
2:A:238:SER:O	2:A:239:ASP:C	2.56	0.48
2:A:319:PRO:HB3	2:A:372:VAL:HG23	1.96	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
4:A:2901:ANP:H8	5:A:2905:HOH:O	2.13	0.48
2:C:269:THR:HG22	2:C:272:GLN:H	1.79	0.48
2:C:282:GLY:HA2	2:C:427:GLN:CD	2.39	0.48
2:A:282:GLY:HA2	2:A:427:GLN:CD	2.38	0.48
2:A:376:PRO:HG2	2:A:404:MET:HE1	1.96	0.48
2:A:513:GLU:HA	5:A:3038:HOH:O	2.13	0.48
2:C:597:LYS:O	2:C:597:LYS:HG3	2.13	0.48
2:D:359:ARG:NH1	2:D:362:ASN:HD22	2.07	0.48
2:A:413:MET:HG3	2:A:417:MET:HE2	1.96	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: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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
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:413:MET:HA	2:C:413:MET:HE2	1.97	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
2:C:329:GLU:CD	2:C:329:GLU:H	2.23	0.47
2:C:413:MET:HE2	2:C:413:MET:CA	2.45	0.47
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:421:THR:HG22	2:A:421:THR:O	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:393:THR:HB	2:D:422:MET:HE1	1.97	0.47
2:D:465:VAL:O	2:D:465:VAL:HG13	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:B:324:VAL:HG11	2:B:404:MET:HE2	1.94	0.47
2:B:356:THR:C	2:B:378:ARG:HH22	2.21	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: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:D:413:MET:HE2	2:D:413:MET:CA	2.46	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:A:413:MET:HE2	2:A:413:MET:HA	1.97	0.46
2:C:238:SER:O	2:C:239:ASP:C	2.58	0.46
2:D:399:ASP:O	2:D:400:GLU:C	2.59	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:A:402:ASP:CG	2:A:551:ARG:HH22	2.23	0.46
2:B:413:MET:CA	2:B:413:MET:HE2	2.46	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:B:234:LYS:NZ	5:B:2982:HOH:O	2.49	0.45
2:D:402:ASP:OD2	2:D:551:ARG:NH2	2.48	0.45
2:A:413:MET:HE2	2:A:413:MET:CA	2.46	0.45
2:A:554:ASP:HB2	2:A:582:ARG:HH12	1.81	0.45
2:B:418:THR:O	2:B:418:THR:CG2	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: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:289:ALA:HB2	2:A:455:ILE:HD13	1.99	0.45
2:A:430:MET:SD	2:A:443:ALA:HB1	2.57	0.45
2:B:537:ASN:OD1	2:B:537:ASN:C	2.60	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:390:PHE:H	2:D:421:THR:CG2	2.30	0.45
2:D:419:HIS:CD2	2:D:421:THR:H	2.35	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: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: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: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:B:210:ASP:O	2:B:211:ALA:C	2.61	0.44
2:B:448:LYS:O	2:B:449:ASN:C	2.61	0.44
2:C:475:TYR:CD1	2:C:475:TYR:C	2.95	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:380:LEU:HD12	2:D:380:LEU:HA	1.79	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:B:439:ILE:HA	2:B:442:MET:HE3	2.00	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:D:212:ILE:HG23	2:D:213:GLU:N	2.33	0.43
2:A:421:THR:CG2	2:A:421:THR:O	2.66	0.43
2:B:229:ASN:ND2	5:B:3056:HOH:O	2.46	0.43
2:C:318:ARG:NH1	2:C:391:GLU:HG3	2.33	0.43
2:D:561:VAL:O	2:D:589:ALA:HA	2.18	0.43
2:D:316:LEU:HD12	2:D:366:THR:HG23	2.00	0.43
2:D:475:TYR:CD1	2:D:475:TYR:C	2.96	0.43
2:B:244:ILE:HD12	2:B:244:ILE:C	2.43	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:C:582:ARG:C	2:C:583:VAL:HG23	2.44	0.43
2:D:310:ASP:OD2	2:D:312:HIS:HE1	2.01	0.43
2:A:524:LEU:HB2	2:A:527:GLN:HG3	2.00	0.43
2:A:537:ASN:OD1	2:A:537:ASN:C	2.62	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:B:269:THR:HB	2:B:272:GLN:CD	2.43	0.43
2:C:250:ALA:O	2:C:251:ASP:HB2	2.18	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:A:582:ARG:C	2:A:583:VAL:HG23	2.43	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:D:256:ILE:O	2:D:260:VAL:HG23	2.19	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

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:536:LYS:O	2:B:557:ASN:ND2	2.52	0.42
2:C:482:ILE:HD13	2:C:512:LYS:HZ2	1.83	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:A:448:LYS:O	2:A:449:ASN:C	2.62	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
2:B:319:PRO:HB3	2:B:372:VAL:HG23	2.02	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
1:G:4:U:C4	1:G:5:U:C4	3.08	0.41
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:N	2:D:387:PHE:CD2	2.88	0.41
2:A:329:GLU:HA	2:A:332:ILE:CD1	2.50	0.41
2:B:465:VAL:O	2:B:465:VAL:HG13	2.20	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:HD23	2:D:316:LEU:O	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:C:399:ASP:O	2:C:400:GLU:C	2.63	0.41
2:D:269:THR:HG22	2:D:272:GLN:CD	2.44	0.41
2:A:303:ILE:HD11	2:A:429:LEU:HD12	2.02	0.41
2:A:364:CYS:HA	2:A:367:ARG:HD2	2.03	0.41
2:B:489:ALA:O	2:B:492:THR:CG2	2.68	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:285:LEU:HD21	2:B:453:VAL:CG1	2.51	0.41
2:B:389:THR:OG1	2:B:391:GLU:OE2	2.36	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:380:LEU:HD11	2:D:416:ILE:HG12	2.03	0.41
2:D:511:GLU:H	2:D:511:GLU:HG2	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: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:287:ALA:HB3	2:D:431:PHE:CD1	2.55	0.41
2:D:352:VAL:HG23	2:D:378:ARG:HG2	2.03	0.41
2:A:391:GLU:CD	2:A:421:THR:HG23	2.44	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:D:448:LYS:O	2:D:449:ASN:C	2.64	0.41
2:A:308:LEU:HD12	2:A:346:TYR:CE1	2.56	0.41
2:C:570:ILE:HA	2:C:601:ILE:HD11	2.01	0.41
2:D:259:ASN:OD1	2:D:343:PHE:HB3	2.20	0.41
2:D:287:ALA:HA	2:D:453:VAL:CG1	2.51	0.41
2:A:276:ILE:HB	2:A:277:PRO:HD3	2.02	0.41
2:A:376:PRO:HG3	2:A:413:MET:HE1	2.01	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:D:329:GLU:CD	2:D:528:ARG:HH21	2.29	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: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:A:399:ASP:O	2:A:400:GLU:C	2.64	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%)	18	19
2	B	418/434 (96%)	398 (95%)	18 (4%)	2 (0%)	24	27
2	C	418/434 (96%)	412 (99%)	4 (1%)	2 (0%)	24	27
2	D	418/434 (96%)	400 (96%)	15 (4%)	3 (1%)	18	19
All	All	1672/1736 (96%)	1608 (96%)	54 (3%)	10 (1%)	21	23

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 [i](#)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	A	364/375 (97%)	339 (93%)	25 (7%)	14	16

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
2	B	364/375 (97%)	339 (93%)	25 (7%)	14	16
2	C	364/375 (97%)	342 (94%)	22 (6%)	17	21
2	D	364/375 (97%)	333 (92%)	31 (8%)	10	11
All	All	1456/1500 (97%)	1353 (93%)	103 (7%)	13	16

All (103) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	A	208	SER
2	A	229	ASN
2	A	255	ILE
2	A	266	LYS
2	A	271	ILE
2	A	285	LEU
2	A	296	THR
2	A	308	LEU
2	A	332	ILE
2	A	352	VAL
2	A	380	LEU
2	A	389	THR
2	A	418	THR
2	A	435	PHE
2	A	437	GLU
2	A	453	VAL
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	599	ARG
2	B	206	GLU
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

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Mol	Chain	Res	Type
2	B	352	VAL
2	B	378	ARG
2	B	380	LEU
2	B	385	ARG
2	B	391	GLU
2	B	418	THR
2	B	425	GLU
2	B	435	PHE
2	B	437	GLU
2	B	453	VAL
2	B	466	LYS
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	244	ILE
2	C	269	THR
2	C	285	LEU
2	C	306	LYS
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	417	MET
2	C	435	PHE
2	C	453	VAL
2	C	466	LYS
2	C	481	LEU
2	C	492	THR
2	C	511	GLU
2	C	524	LEU
2	C	539	SER
2	C	583	VAL
2	C	608	ILE
2	D	210	ASP
2	D	213	GLU
2	D	223	ILE

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Mol	Chain	Res	Type
2	D	229	ASN
2	D	239	ASP
2	D	261	ASN
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	418	THR
2	D	437	GLU
2	D	466	LYS
2	D	480	LYS
2	D	481	LEU
2	D	492	THR
2	D	510	SER
2	D	526	SER
2	D	543	LEU
2	D	580	THR
2	D	582	ARG
2	D	583	VAL
2	D	599	ARG
2	D	608	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (44) such sidechains are listed below:

Mol	Chain	Res	Type
2	A	224	HIS
2	A	312	HIS
2	A	362	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	A	586	ASN

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Mol	Chain	Res	Type
2	B	229	ASN
2	B	320	GLN
2	B	336	ASN
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	209	ASN
2	C	229	ASN
2	C	320	GLN
2	C	336	ASN
2	C	370	HIS
2	C	419	HIS
2	C	426	HIS
2	C	467	GLN
2	C	473	ASN
2	C	488	GLN
2	C	520	HIS
2	C	586	ASN
2	D	261	ASN
2	D	290	GLN
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	427	GLN
2	D	449	ASN
2	D	467	GLN
2	D	488	GLN
2	D	520	HIS

5.3.3 RNA [i](#)

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

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Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
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 oligosaccharides 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	B	2902	3	33,33,33	1.92	9 (27%)	45,52,52	2.53	17 (37%)
4	ANP	A	2901	3	33,33,33	1.84	9 (27%)	45,52,52	2.64	18 (40%)
4	ANP	C	2903	3	33,33,33	1.86	10 (30%)	45,52,52	2.54	18 (40%)
4	ANP	D	2904	3	33,33,33	1.81	9 (27%)	45,52,52	2.59	20 (44%)

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	B	2902	3	-	6/18/38/38	0/3/3/3
4	ANP	A	2901	3	-	5/18/38/38	0/3/3/3
4	ANP	C	2903	3	-	4/18/38/38	0/3/3/3
4	ANP	D	2904	3	-	7/18/38/38	0/3/3/3

All (37) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	2901	ANP	PG-O1G	4.17	1.52	1.46
4	B	2902	ANP	PB-O2B	-3.98	1.46	1.56
4	B	2902	ANP	PG-O1G	3.92	1.52	1.46
4	D	2904	ANP	PB-O2B	-3.79	1.46	1.56
4	C	2903	ANP	PG-O1G	3.59	1.51	1.46
4	C	2903	ANP	PB-O2B	-3.55	1.47	1.56
4	C	2903	ANP	C5-N7	-3.49	1.32	1.39
4	A	2901	ANP	C5-N7	-3.46	1.32	1.39
4	D	2904	ANP	PG-O1G	3.45	1.51	1.46
4	B	2902	ANP	PB-O3A	3.44	1.63	1.59
4	D	2904	ANP	PB-O3A	3.44	1.63	1.59
4	D	2904	ANP	C5-N7	-3.44	1.32	1.39
4	C	2903	ANP	PA-O3A	-3.34	1.55	1.59
4	A	2901	ANP	PB-O2B	-3.32	1.48	1.56
4	B	2902	ANP	PA-O3A	-3.31	1.55	1.59
4	B	2902	ANP	C5-N7	-3.22	1.33	1.39
4	B	2902	ANP	PG-O2G	-3.16	1.48	1.56
4	C	2903	ANP	PG-O2G	-3.04	1.48	1.56
4	A	2901	ANP	PB-O3A	2.95	1.62	1.59
4	A	2901	ANP	C1'-N9	2.94	1.54	1.46
4	C	2903	ANP	PB-O3A	2.93	1.62	1.59
4	D	2904	ANP	PG-O3G	-2.84	1.49	1.56
4	B	2902	ANP	PG-O3G	-2.78	1.49	1.56
4	A	2901	ANP	PG-O2G	-2.67	1.49	1.56
4	A	2901	ANP	PG-O3G	-2.64	1.49	1.56
4	D	2904	ANP	PG-O2G	-2.62	1.49	1.56
4	B	2902	ANP	C2'-C1'	-2.59	1.45	1.53
4	C	2903	ANP	PB-O1B	2.53	1.50	1.46
4	D	2904	ANP	C3'-C4'	-2.49	1.46	1.53
4	D	2904	ANP	PA-O3A	-2.44	1.56	1.59
4	B	2902	ANP	C3'-C4'	-2.42	1.46	1.53
4	C	2903	ANP	PG-O3G	-2.42	1.50	1.56
4	A	2901	ANP	C2'-C1'	-2.40	1.45	1.53
4	A	2901	ANP	C3'-C4'	-2.38	1.47	1.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	2903	ANP	C3'-C4'	-2.37	1.47	1.53
4	C	2903	ANP	C8-N9	-2.23	1.33	1.37
4	D	2904	ANP	C1'-N9	2.18	1.52	1.46

All (73) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	2904	ANP	C5-C4-N3	-7.65	116.18	126.72
4	C	2903	ANP	C5-C4-N3	-7.60	116.26	126.72
4	A	2901	ANP	C5-C4-N3	-7.53	116.35	126.72
4	B	2902	ANP	C5-C4-N3	-7.27	116.71	126.72
4	C	2903	ANP	N3-C4-N9	6.47	138.17	127.17
4	D	2904	ANP	N3-C4-N9	6.46	138.15	127.17
4	A	2901	ANP	N3-C4-N9	6.25	137.80	127.17
4	B	2902	ANP	N3-C4-N9	6.13	137.59	127.17
4	A	2901	ANP	O4'-C1'-N9	5.32	118.32	108.09
4	D	2904	ANP	C4'-O4'-C1'	5.11	120.74	109.47
4	C	2903	ANP	C4'-O4'-C1'	5.02	120.55	109.47
4	B	2902	ANP	C4'-O4'-C1'	4.96	120.42	109.47
4	A	2901	ANP	C4'-O4'-C1'	4.90	120.29	109.47
4	B	2902	ANP	O4'-C1'-N9	4.78	117.27	108.09
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	A	2901	ANP	C6-C5-C4	3.96	122.58	117.18
4	D	2904	ANP	O4'-C1'-N9	3.92	115.61	108.09
4	D	2904	ANP	C6-C5-C4	3.84	122.43	117.18
4	C	2903	ANP	C6-C5-C4	3.78	122.34	117.18
4	B	2902	ANP	C6-C5-C4	3.71	122.25	117.18
4	C	2903	ANP	C2-N3-C4	3.71	120.90	111.83
4	D	2904	ANP	C2-N3-C4	3.71	120.89	111.83
4	B	2902	ANP	O1B-PB-N3B	-3.70	106.32	111.77
4	C	2903	ANP	O4'-C1'-N9	3.70	115.19	108.09
4	A	2901	ANP	C2-N3-C4	3.68	120.82	111.83
4	B	2902	ANP	C2-N3-C4	3.62	120.66	111.83
4	B	2902	ANP	O4'-C4'-C3'	-3.23	98.74	105.15
4	D	2904	ANP	O2A-PA-O5'	3.12	121.69	107.57
4	D	2904	ANP	O4'-C4'-C3'	-3.09	99.02	105.15
4	B	2902	ANP	O3A-PB-N3B	3.08	115.14	106.59
4	A	2901	ANP	O4'-C4'-C3'	-3.03	99.13	105.15
4	C	2903	ANP	O3A-PB-N3B	3.03	115.00	106.59
4	B	2902	ANP	O2A-PA-O5'	3.01	121.22	107.57

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	2901	ANP	O3'-C3'-C2'	-2.98	102.26	111.82
4	D	2904	ANP	O3'-C3'-C2'	-2.97	102.28	111.82
4	A	2901	ANP	O2G-PG-O3G	2.97	115.57	107.59
4	A	2901	ANP	O2A-PA-O5'	2.96	120.97	107.57
4	C	2903	ANP	O2A-PA-O5'	2.94	120.89	107.57
4	C	2903	ANP	O2G-PG-O3G	2.83	115.20	107.59
4	A	2901	ANP	O3A-PB-N3B	2.82	114.42	106.59
4	B	2902	ANP	O2G-PG-O3G	2.82	115.16	107.59
4	D	2904	ANP	C6-C5-N7	-2.78	126.72	132.09
4	D	2904	ANP	O3A-PB-N3B	2.74	114.19	106.59
4	A	2901	ANP	C6-C5-N7	-2.72	126.84	132.09
4	D	2904	ANP	O4'-C1'-C2'	-2.71	100.81	106.62
4	D	2904	ANP	C2'-C3'-C4'	2.68	107.79	102.61
4	C	2903	ANP	O4'-C4'-C3'	-2.68	99.84	105.15
4	C	2903	ANP	O4'-C1'-C2'	-2.67	100.91	106.62
4	B	2902	ANP	O3'-C3'-C2'	-2.63	103.38	111.82
4	A	2901	ANP	O4'-C1'-C2'	-2.62	101.00	106.62
4	C	2903	ANP	O3'-C3'-C2'	-2.62	103.43	111.82
4	A	2901	ANP	C2'-C3'-C4'	2.61	107.65	102.61
4	C	2903	ANP	C2'-C3'-C4'	2.61	107.65	102.61
4	D	2904	ANP	O2G-PG-O3G	2.59	114.55	107.59
4	B	2902	ANP	O4'-C1'-C2'	-2.57	101.11	106.62
4	D	2904	ANP	N3-C2-N1	-2.55	124.72	128.58
4	C	2903	ANP	C3'-C2'-C1'	2.50	106.20	101.46
4	B	2902	ANP	N3-C2-N1	-2.50	124.80	128.58
4	B	2902	ANP	C2'-C3'-C4'	2.45	107.33	102.61
4	B	2902	ANP	C6-C5-N7	-2.40	127.47	132.09
4	A	2901	ANP	C3'-C2'-C1'	2.36	105.94	101.46
4	C	2903	ANP	C6-C5-N7	-2.34	127.58	132.09
4	C	2903	ANP	N3-C2-N1	-2.33	125.05	128.58
4	A	2901	ANP	N3-C2-N1	-2.33	125.06	128.58
4	D	2904	ANP	C3'-C2'-C1'	2.23	105.69	101.46
4	A	2901	ANP	O1G-PG-N3B	-2.22	108.50	111.77
4	D	2904	ANP	O1G-PG-N3B	-2.09	108.69	111.77
4	B	2902	ANP	C3'-C2'-C1'	2.09	105.42	101.46
4	D	2904	ANP	O3'-C3'-C4'	-2.05	105.19	111.08
4	D	2904	ANP	C5-C6-N6	-2.04	118.23	123.29
4	C	2903	ANP	O1G-PG-N3B	-2.02	108.80	111.77

There are no chirality outliers.

All (22) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
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	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	D	2904	ANP	C3'-C4'-C5'-O5'
4	A	2901	ANP	C3'-C4'-C5'-O5'
4	D	2904	ANP	O4'-C4'-C5'-O5'
4	B	2902	ANP	C3'-C4'-C5'-O5'
4	B	2902	ANP	PG-N3B-PB-O1B
4	D	2904	ANP	C2'-C1'-N9-C8
4	B	2902	ANP	C2'-C1'-N9-C8
4	B	2902	ANP	PA-O3A-PB-O1B
4	D	2904	ANP	PA-O3A-PB-O1B
4	C	2903	ANP	C3'-C4'-C5'-O5'
4	A	2901	ANP	C2'-C1'-N9-C8

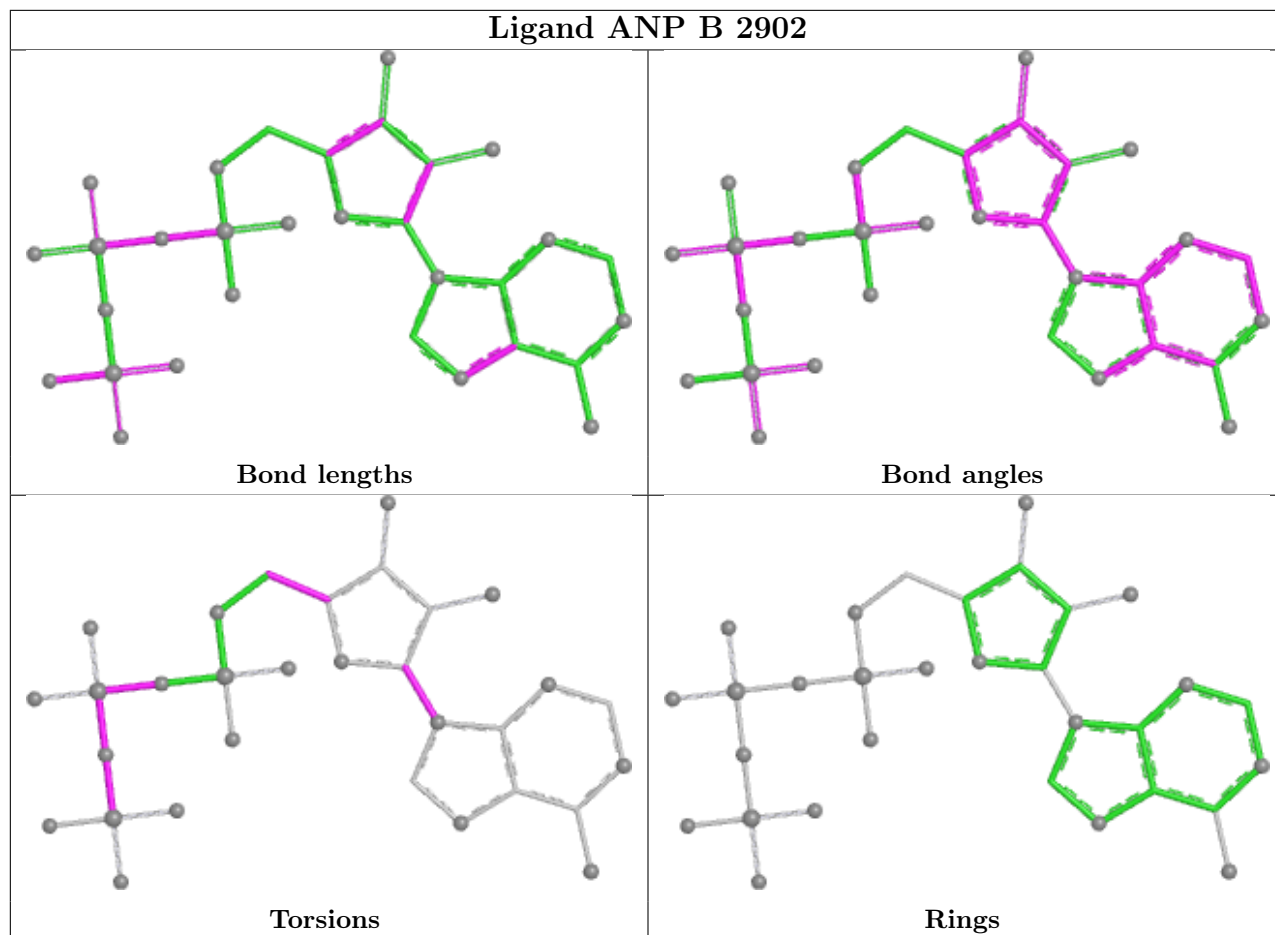
There are no ring outliers.

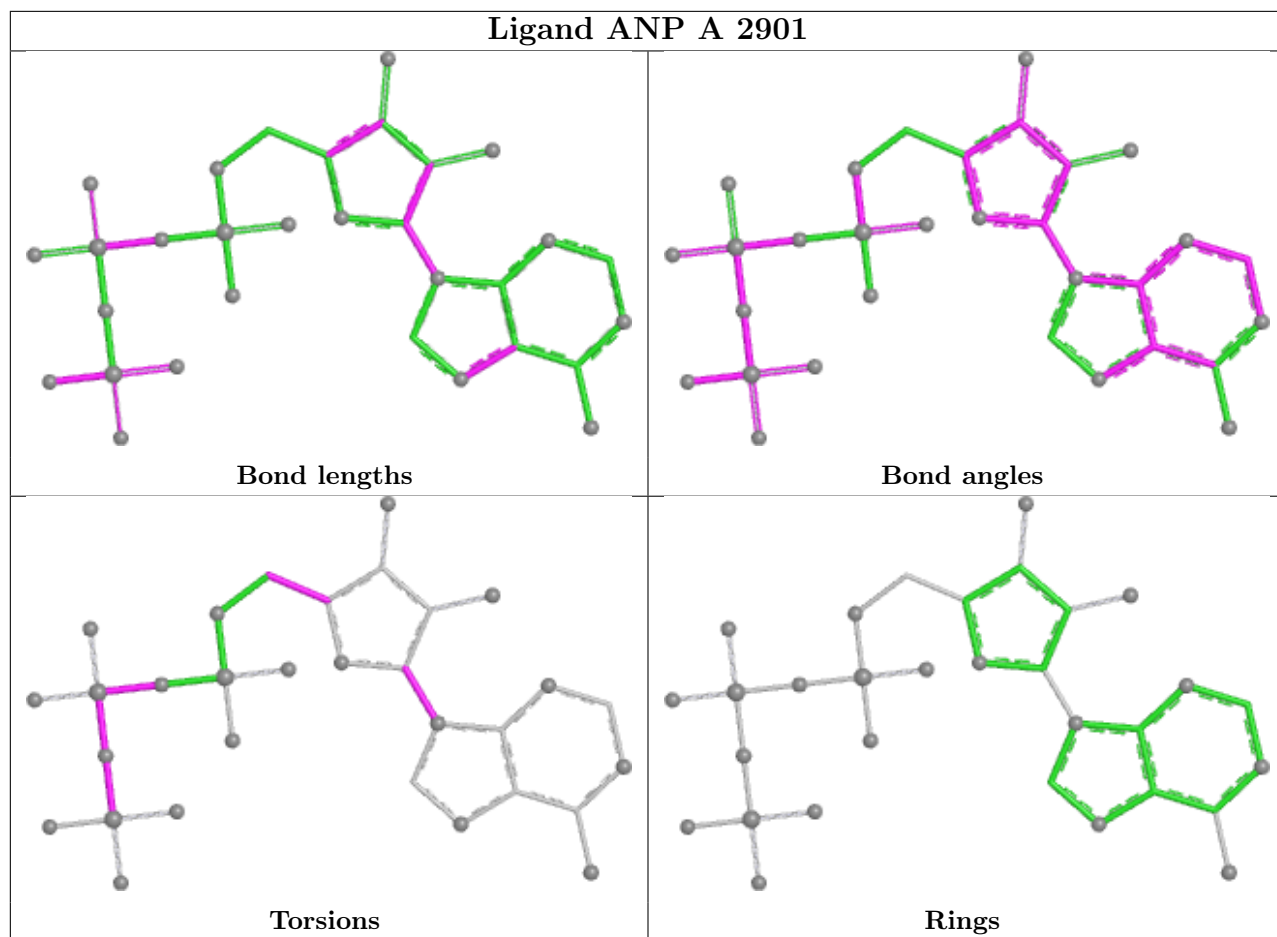
4 monomers are involved in 13 short contacts:

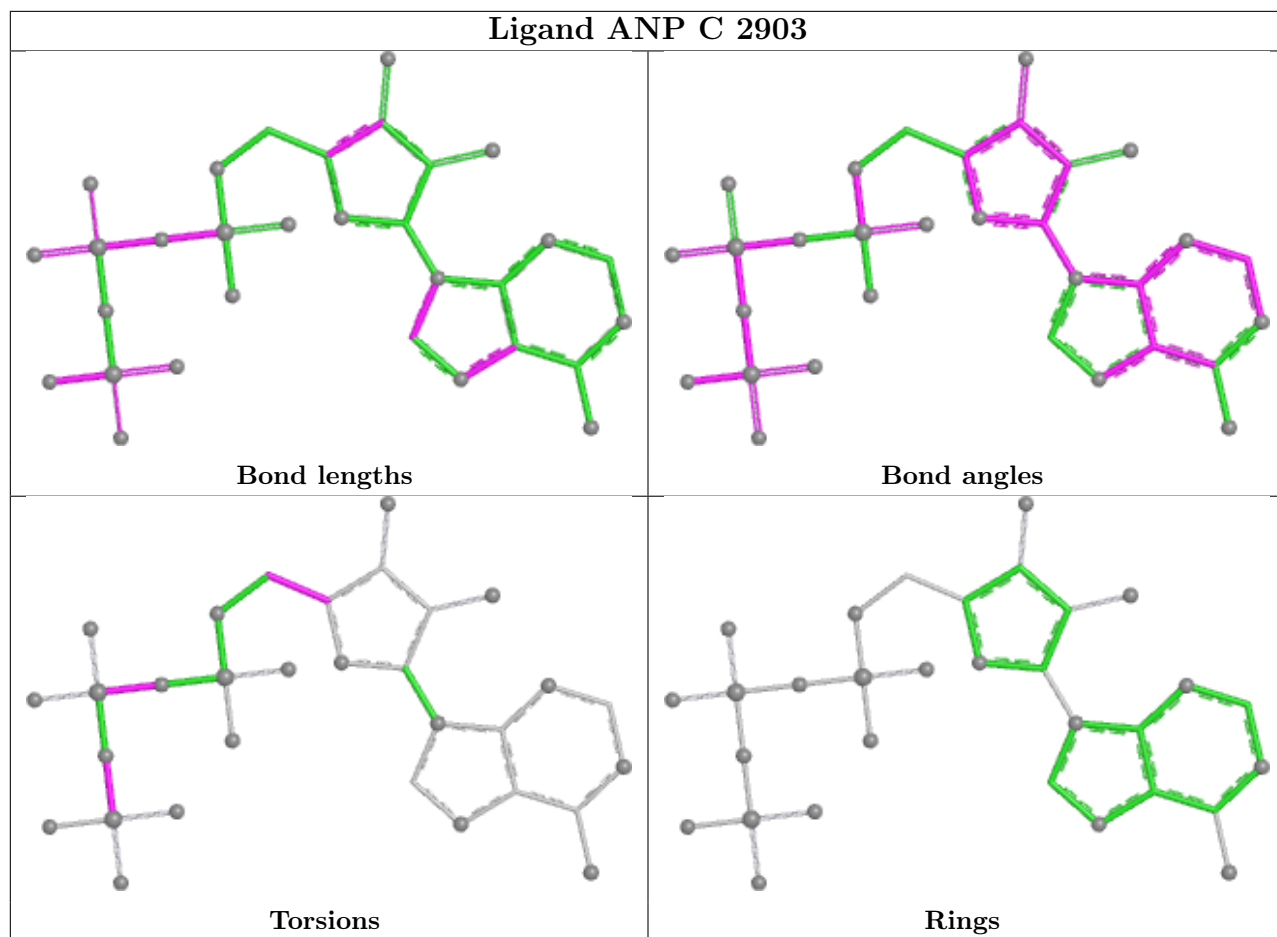
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	2902	ANP	4	0
4	A	2901	ANP	5	0
4	C	2903	ANP	1	0
4	D	2904	ANP	3	0

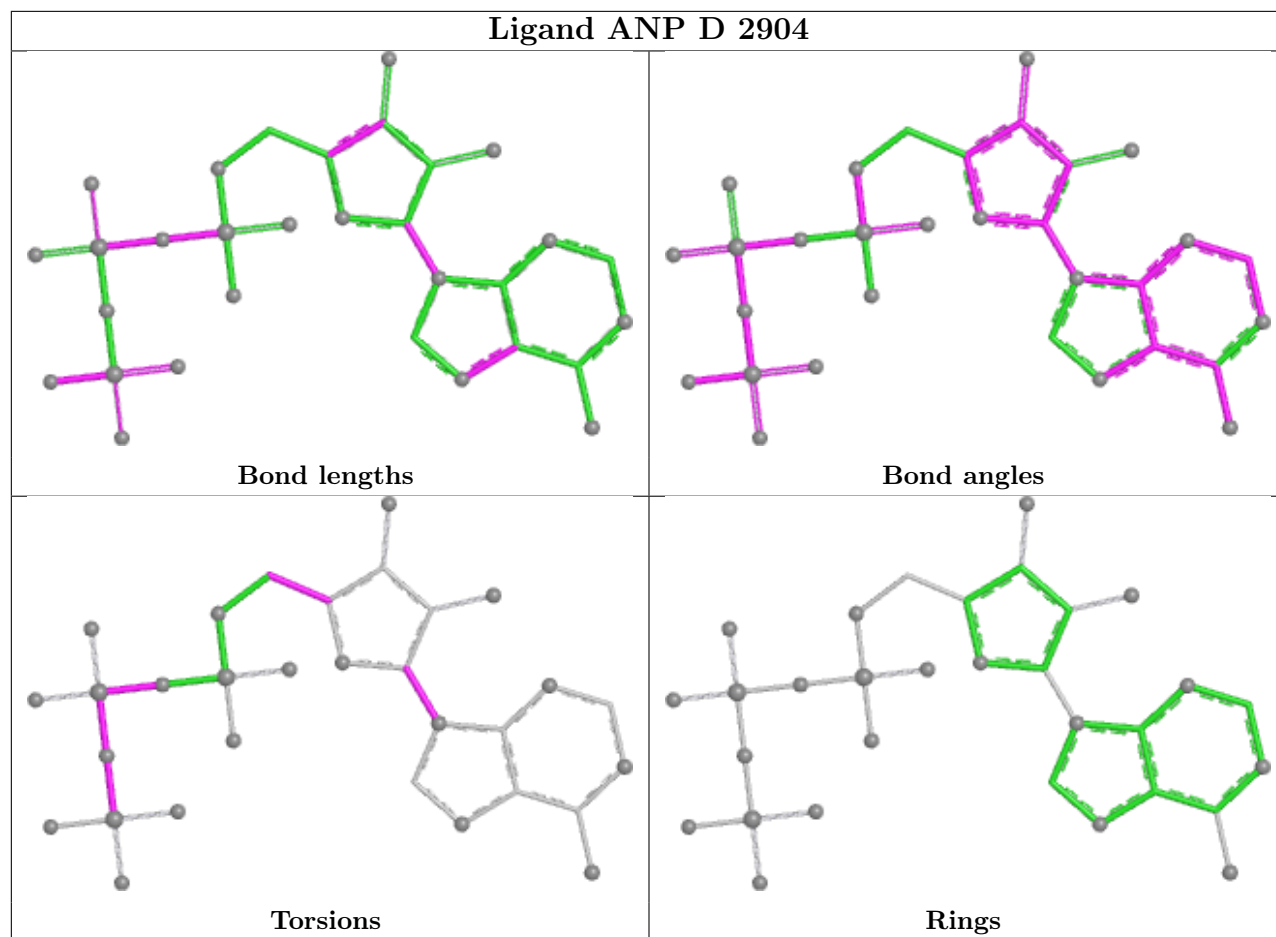
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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, 95th 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 ²)	Q<0.9
1	E	7/10 (70%)	-0.12	0 100 100	28, 31, 48, 59	0
1	F	7/10 (70%)	-0.07	1 (14%) 6 4	25, 30, 56, 64	0
1	G	7/10 (70%)	-0.22	0 100 100	24, 27, 53, 68	0
1	H	6/10 (60%)	-0.31	0 100 100	29, 30, 43, 70	0
2	A	420/434 (96%)	0.68	51 (12%) 8 6	23, 43, 77, 85	0
2	B	420/434 (96%)	0.28	24 (5%) 29 26	18, 36, 59, 66	0
2	C	420/434 (96%)	-0.05	10 (2%) 59 56	18, 31, 47, 59	0
2	D	420/434 (96%)	0.43	28 (6%) 24 21	20, 39, 66, 77	0
All	All	1707/1776 (96%)	0.33	114 (6%) 24 21	18, 37, 63, 85	0

All (114) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	248	THR	4.7
2	A	421	THR	4.1
2	A	584	GLY	3.9
2	C	438	GLU	3.8
2	A	366	THR	3.7
2	B	484	ILE	3.6
2	D	249	SER	3.6
2	D	366	THR	3.5
2	B	438	GLU	3.5
2	A	239	ASP	3.5
2	D	475	TYR	3.4
2	A	223	ILE	3.4
2	A	219	ILE	3.4
2	C	212	ILE	3.3
2	A	533	ARG	3.3
2	B	486	SER	3.2

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Mol	Chain	Res	Type	RSRZ
2	D	365	ILE	3.1
2	C	210	ASP	3.1
2	A	311	PRO	3.1
2	B	470	TYR	3.1
2	D	212	ILE	3.1
2	A	338	ALA	3.1
2	B	487	GLU	3.0
2	B	479	SER	3.0
2	B	407	MET	3.0
2	D	250	ALA	3.0
2	D	345	SER	3.0
2	B	475	TYR	2.9
2	D	311	PRO	2.9
2	A	364	CYS	2.9
2	A	360	HIS	2.9
2	A	420	VAL	2.8
2	D	213	GLU	2.8
2	D	369	CYS	2.8
2	B	346	TYR	2.8
2	A	220	ALA	2.8
2	A	365	ILE	2.7
2	A	392	ASP	2.7
2	A	218	GLY	2.7
2	B	599	ARG	2.7
2	B	483	GLU	2.7
2	A	368	GLY	2.7
2	A	316	LEU	2.7
2	A	248	THR	2.6
2	A	313	GLU	2.6
2	A	258	ASP	2.6
2	D	438	GLU	2.5
2	A	369	CYS	2.5
2	D	368	GLY	2.5
2	A	312	HIS	2.5
2	D	221	SER	2.5
2	C	513	GLU	2.5
2	B	254	ASP	2.5
2	B	485	LEU	2.5
2	A	203	ILE	2.4
2	A	332	ILE	2.4
2	C	258	ASP	2.4
2	A	314	LEU	2.4

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Mol	Chain	Res	Type	RSRZ
2	D	346	TYR	2.4
2	C	206	GLU	2.4
2	A	350	GLY	2.4
2	B	504	PHE	2.4
2	B	206	GLU	2.4
2	C	261	ASN	2.4
2	A	212	ILE	2.4
2	B	488	GLN	2.4
2	A	213	GLU	2.4
2	D	261	ASN	2.3
2	A	389	THR	2.3
2	A	226	SER	2.3
2	A	367	ARG	2.3
2	B	364	CYS	2.3
2	D	364	CYS	2.3
2	B	618	ASP	2.3
2	A	222	GLY	2.3
2	A	217	SER	2.3
2	A	510	SER	2.3
2	C	504	PHE	2.3
2	A	362	ASN	2.3
2	A	381	ASP	2.3
2	D	251	ASP	2.3
2	A	387	PHE	2.2
2	D	381	ASP	2.2
2	A	211	ALA	2.2
2	A	224	HIS	2.2
2	A	208	SER	2.2
2	B	420	VAL	2.2
2	B	596	GLU	2.2
2	D	526	SER	2.2
2	A	346	TYR	2.1
2	D	599	ARG	2.1
2	A	319	PRO	2.1
2	A	479	SER	2.1
2	A	539	SER	2.1
2	B	216	SER	2.1
2	C	249	SER	2.1
2	C	596	GLU	2.1
2	D	313	GLU	2.1
2	D	315	GLU	2.1
2	A	383	VAL	2.1

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Mol	Chain	Res	Type	RSRZ
2	B	476	ALA	2.1
2	A	513	GLU	2.1
2	B	210	ASP	2.1
2	D	214	ILE	2.1
2	B	238	SER	2.1
2	D	243	PRO	2.1
2	D	224	HIS	2.0
2	A	257	ILE	2.0
2	A	202	TYR	2.0
1	F	1	U	2.0
2	D	387	PHE	2.0
2	D	210	ASP	2.0
2	A	205	PRO	2.0
2	A	394	ARG	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](#)

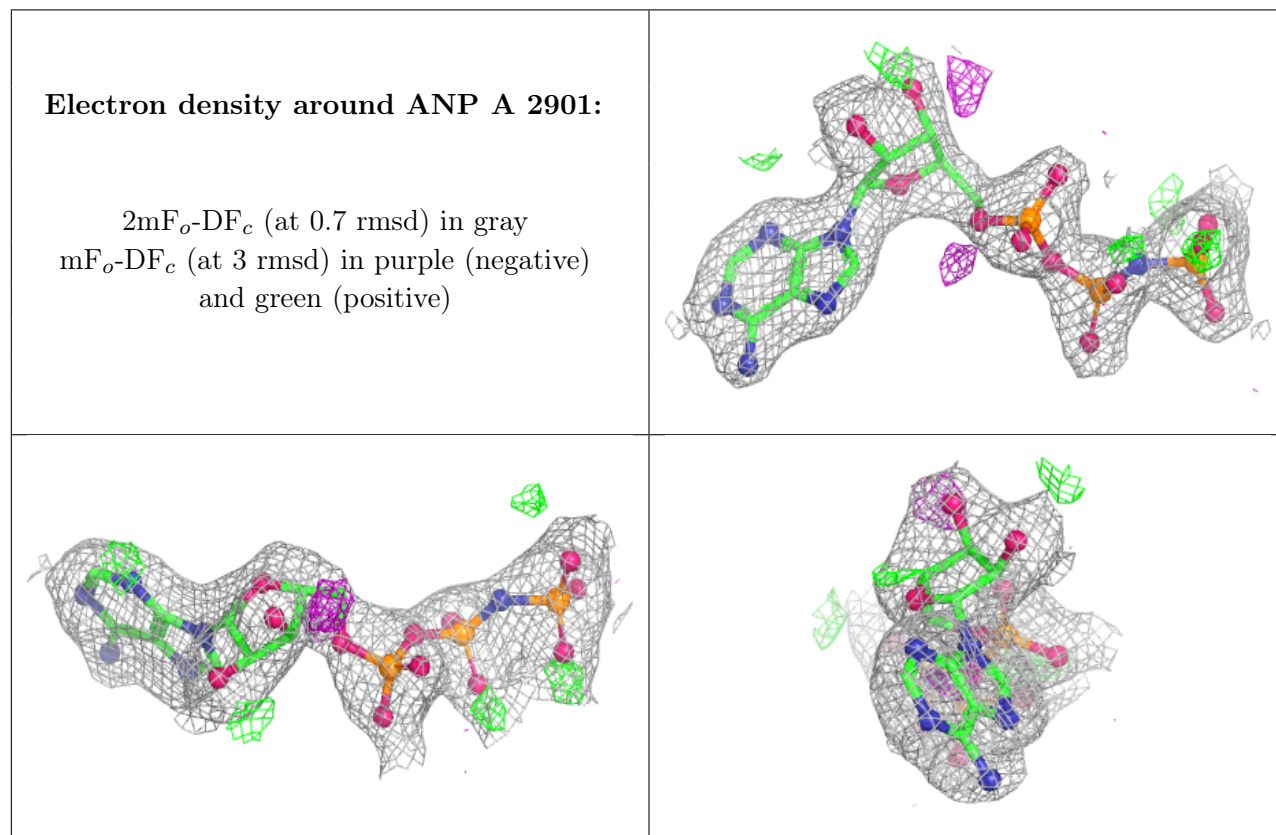
There are no oligosaccharides in this entry.

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. The B-factors column lists the minimum, median, 95th 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.

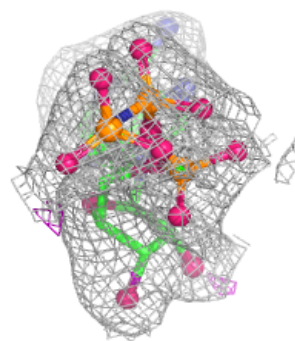
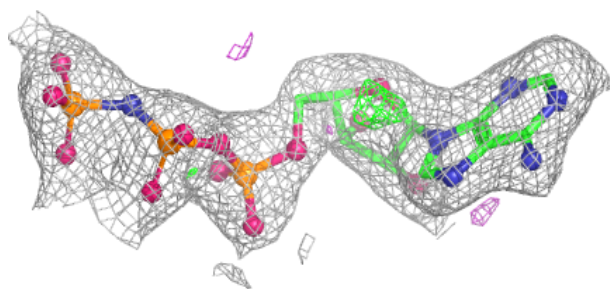
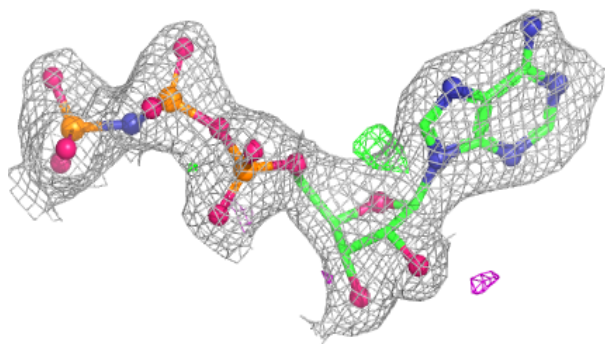
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	A	2801	1/1	0.90	0.13	37,37,37,37	0
3	MG	C	2803	1/1	0.94	0.14	22,22,22,22	0
3	MG	B	2802	1/1	0.97	0.09	21,21,21,21	0
3	MG	D	2804	1/1	0.97	0.07	25,25,25,25	0
4	ANP	A	2901	31/31	0.97	0.07	24,36,39,39	0
4	ANP	D	2904	31/31	0.97	0.07	22,33,34,36	0
4	ANP	C	2903	31/31	0.98	0.06	17,22,25,26	0
4	ANP	B	2902	31/31	0.98	0.06	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.

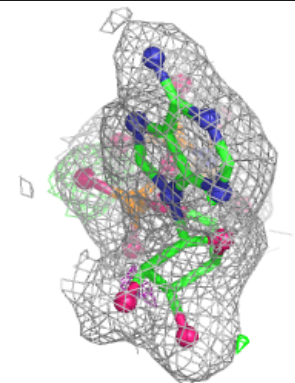
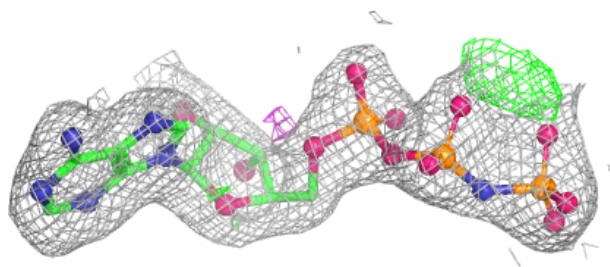
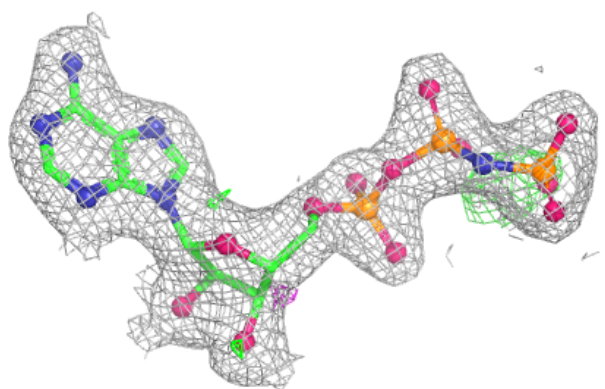


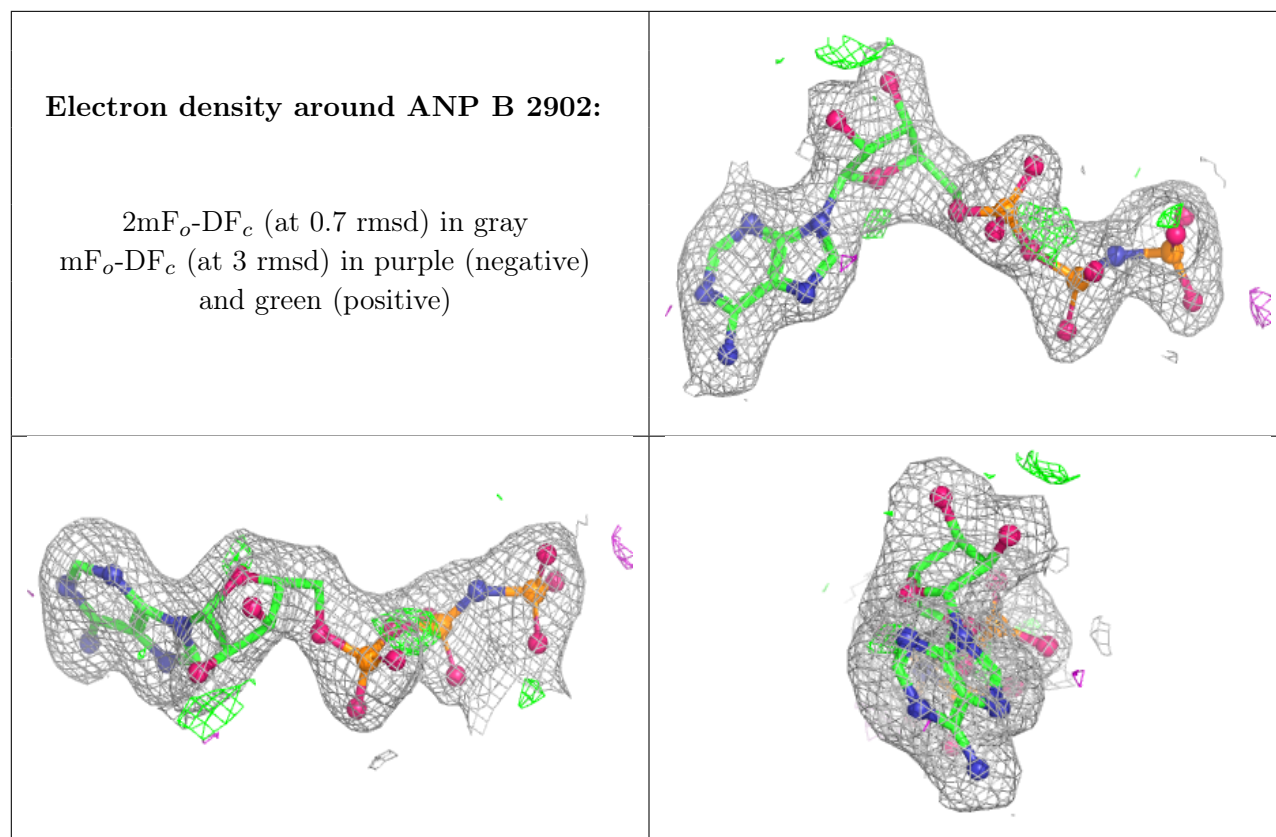
Electron density around ANP D 2904:

$2mF_o-DF_c$ (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)





6.5 Other polymers [i](#)

There are no such residues in this entry.