



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:09 PM UTC

PDB ID : 7PLI / pdb_00007pli
Title : DEAD-box helicase DbpA bound to single stranded RNA and ADP/BeF3
Authors : Wurm, J.P.
Deposited on : 2021-08-31
Resolution : 2.50 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:

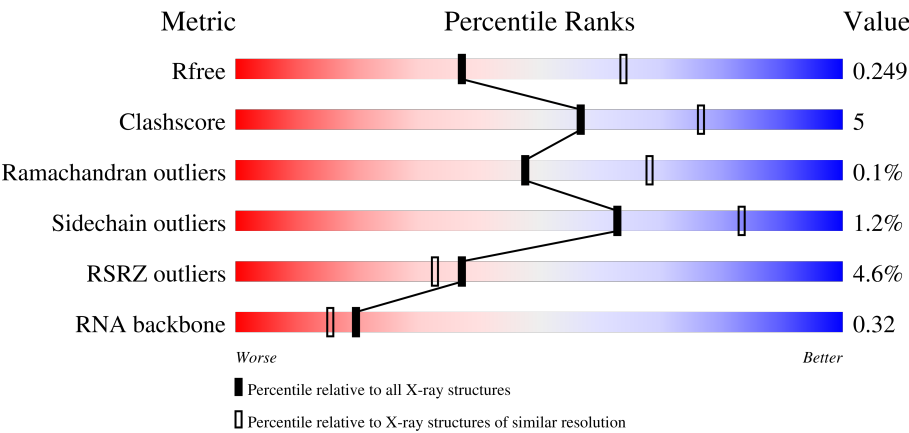
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal 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 2.50 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	5829 (2.50-2.50)
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)
RSRZ outliers	180081	5833 (2.50-2.50)
RNA backbone	3983	1003 (2.78-2.22)

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	A	459	90%9%
1	B	459	88%11%
1	E	459	89%10%
1	F	459	83%14%

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Mol	Chain	Length	Quality of chain
1	I	459	10% 84% 14%
1	J	459	3% 87% 12%
2	C	24	71% 21%
2	D	24	8% 67% 25%
2	G	24	4% 58% 29% 8%
2	H	24	71% 21%
2	K	24	58% 33%
2	L	24	63% 21% 12%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 23591 atoms, of which 0 are hydrogens and 0 are deuteriums.

In the tables below, the ZeroOcc column contains the number of atoms modelled with zero occupancy, the AltConf column contains the number of residues with at least one atom in alternate conformation and the Trace column contains the number of residues modelled with at most 2 atoms.

- Molecule 1 is a protein called ATP-dependent RNA helicase DbpA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	457	Total	C	N	O	S	0	0	0
			3451	2167	621	645	18			
1	B	456	Total	C	N	O	S	0	0	0
			3443	2163	619	643	18			
1	E	457	Total	C	N	O	S	0	0	0
			3451	2167	621	645	18			
1	J	453	Total	C	N	O	S	0	0	0
			3420	2149	615	639	17			
1	I	451	Total	C	N	O	S	0	0	0
			3406	2140	613	636	17			
1	F	451	Total	C	N	O	S	0	0	0
			3409	2142	613	637	17			

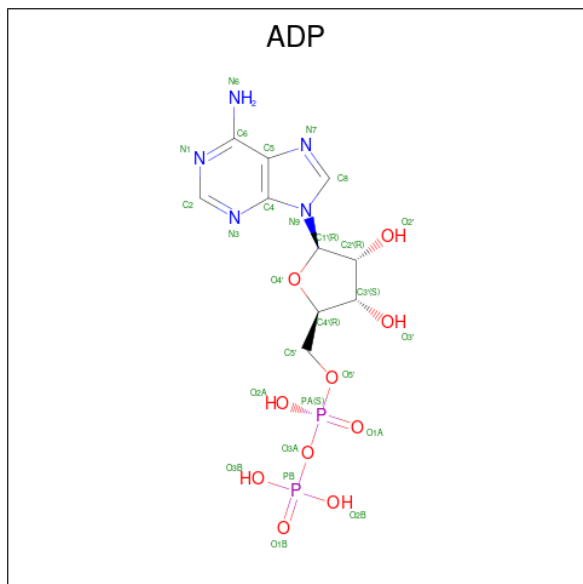
There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	GLY	-	expression tag	UNP P21693
A	0	GLY	-	expression tag	UNP P21693
B	-1	GLY	-	expression tag	UNP P21693
B	0	GLY	-	expression tag	UNP P21693
E	-1	GLY	-	expression tag	UNP P21693
E	0	GLY	-	expression tag	UNP P21693
J	-1	GLY	-	expression tag	UNP P21693
J	0	GLY	-	expression tag	UNP P21693
I	-1	GLY	-	expression tag	UNP P21693
I	0	GLY	-	expression tag	UNP P21693
F	-1	GLY	-	expression tag	UNP P21693
F	0	GLY	-	expression tag	UNP P21693

- Molecule 2 is a RNA chain called RNA (5'-D(*(POP))-R(P*GP*GP*AP*CP*AP*UP*AP*UP*GP*GP*CP*UP*GP*UP*UP*CP*GP*CP*CP*AP*UP*U)-3').

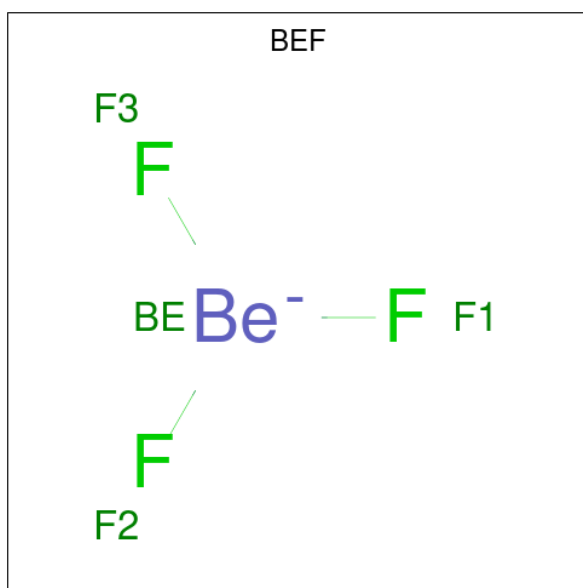
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	D	23	Total	C	N	O	P	0	2	0
			517	227	86	178	26			
2	C	23	Total	C	N	O	P	0	0	0
			467	204	77	162	24			
2	G	22	Total	C	N	O	P	0	0	0
			448	195	76	154	23			
2	L	23	Total	C	N	O	P	0	0	0
			451	195	75	157	24			
2	K	23	Total	C	N	O	P	0	0	0
			467	204	77	162	24			
2	H	23	Total	C	N	O	P	0	0	0
			445	191	75	155	24			

- Molecule 3 is ADENOSINE-5'-DIPHOSPHATE (CCD ID: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	B	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	E	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	J	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	I	1	Total	C	N	O	P	0	0
			27	10	5	10	2		
3	F	1	Total	C	N	O	P	0	0
			27	10	5	10	2		

- Molecule 4 is BERYLLIUM TRIFLUORIDE ION (CCD ID: BEF) (formula: BeF_3).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total 4	Be 1	F 3	0	0
4	B	1	Total 4	Be 1	F 3	0	0
4	E	1	Total 4	Be 1	F 3	0	0
4	J	1	Total 4	Be 1	F 3	0	0
4	I	1	Total 4	Be 1	F 3	0	0
4	F	1	Total 4	Be 1	F 3	0	0

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	1	Total 1	Mg 1	0	0
5	B	1	Total 1	Mg 1	0	0
5	E	1	Total 1	Mg 1	0	0
5	J	1	Total 1	Mg 1	0	0
5	I	1	Total 1	Mg 1	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	F	1	Total	Mg	0	0
			1	1		

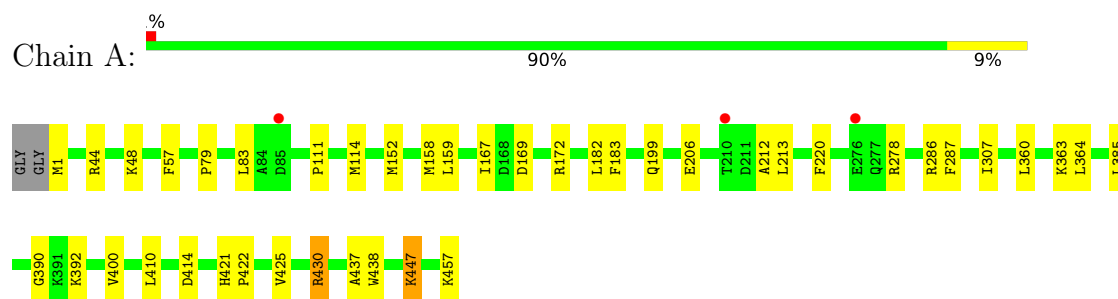
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	4	Total	O	0	0
			4	4		
6	B	4	Total	O	0	0
			4	4		
6	E	4	Total	O	0	0
			4	4		
6	J	4	Total	O	0	0
			4	4		
6	I	4	Total	O	0	0
			4	4		
6	F	4	Total	O	0	0
			4	4		

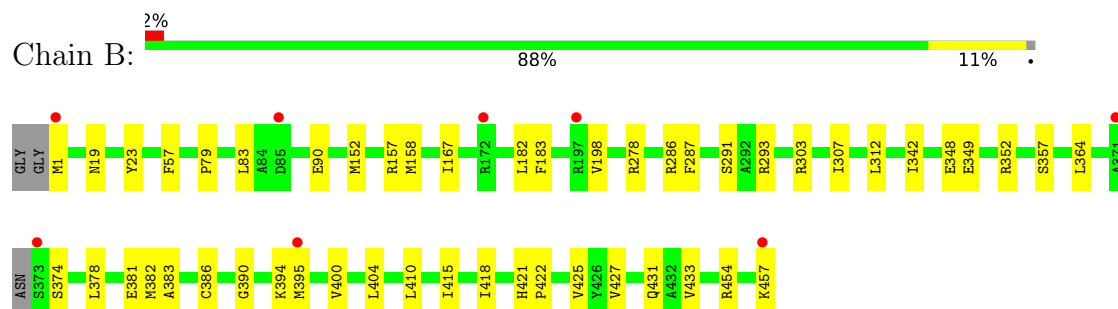
3 Residue-property plots [i](#)

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.

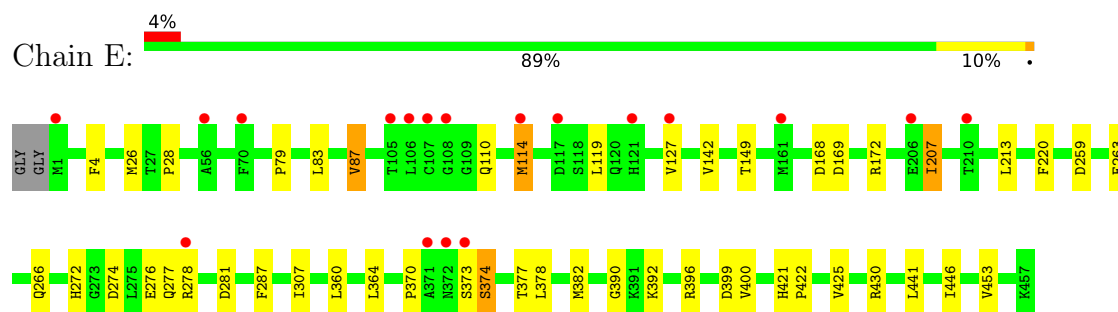
- Molecule 1: ATP-dependent RNA helicase DbpA



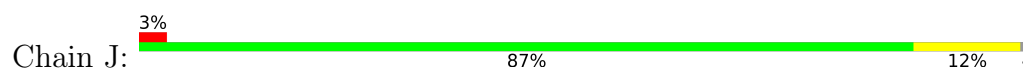
- Molecule 1: ATP-dependent RNA helicase DbpA

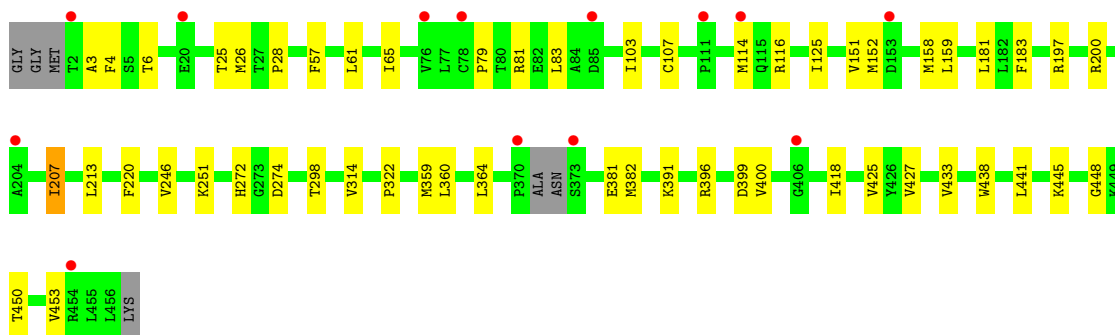


- Molecule 1: ATP-dependent RNA helicase DbpA

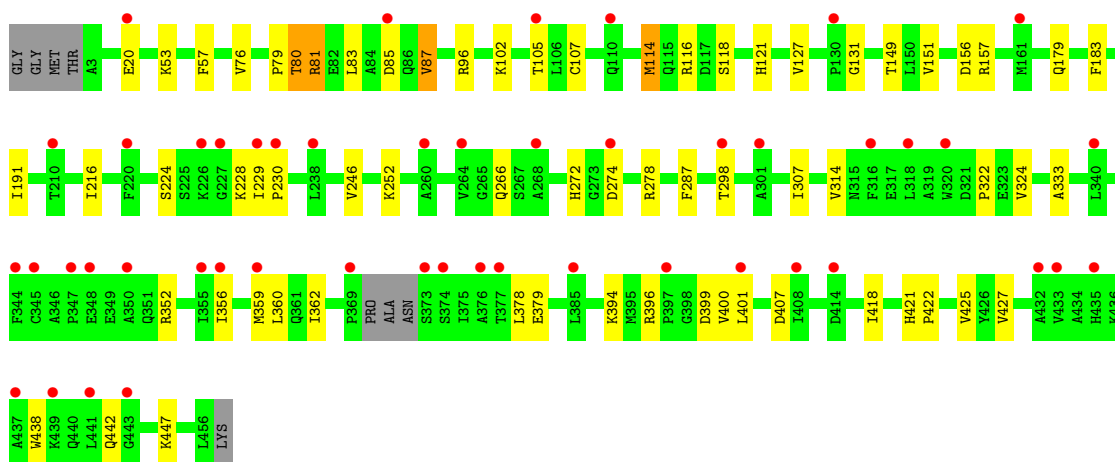
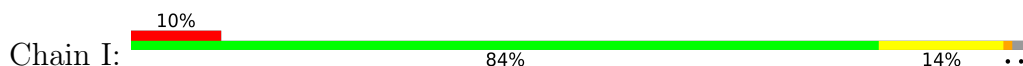


- Molecule 1: ATP-dependent RNA helicase DbpA

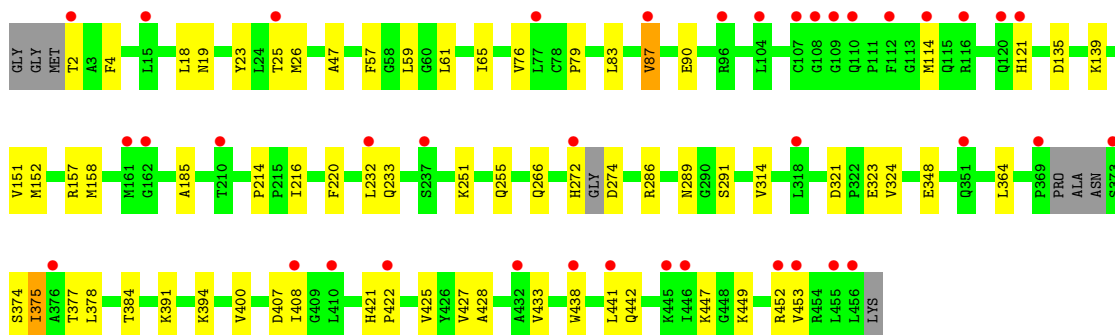
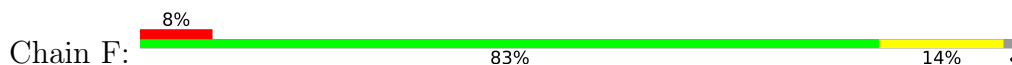




- Molecule 1: ATP-dependent RNA helicase DbpA



- Molecule 1: ATP-dependent RNA helicase DbpA



- Molecule 2: RNA (5'-D*(POP))-R(P*GP*GP*AP*CP*AP*UP*AP*UP*GP*GP*CP*UP*GP*UP*UP*CP*GP*CP*CP*AP*UP*U)-3')

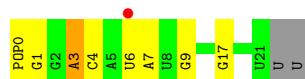




- Molecule 2: RNA (5'-D(*(POP))-R(P*GP*GP*AP*CP*AP*UP*AP*UP*GP*GP*CP*UP*GP*UP*UP*CP*GP*CP*CP*AP*UP*U)-3')



- Molecule 2: RNA (5'-D(*(POP))-R(P*GP*GP*AP*CP*AP*UP*AP*UP*GP*GP*CP*UP*GP*UP*UP*CP*GP*CP*CP*AP*UP*U)-3')



- Molecule 2: RNA (5'-D(*(POP))-R(P*GP*GP*AP*CP*AP*UP*AP*UP*GP*GP*CP*UP*GP*UP*UP*CP*GP*CP*CP*AP*UP*U)-3')



- Molecule 2: RNA (5'-D(*(POP))-R(P*GP*GP*AP*CP*AP*UP*AP*UP*GP*GP*CP*UP*GP*UP*UP*CP*GP*CP*CP*AP*UP*U)-3')



- Molecule 2: RNA (5'-D(*(POP))-R(P*GP*GP*AP*CP*AP*UP*AP*UP*GP*GP*CP*UP*GP*UP*UP*CP*GP*CP*CP*AP*UP*U)-3')



4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	58.64Å 121.60Å 122.42Å 97.16° 92.43° 103.44°	Depositor
Resolution (Å)	56.88 – 2.50 56.88 – 2.50	Depositor EDS
% Data completeness (in resolution range)	96.6 (56.88-2.50) 96.6 (56.88-2.50)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.82 (at 2.51Å)	Xtriage
Refinement program	PHENIX 1.18.2_3874+SVN	Depositor
R, R_{free}	0.213 , 0.247 0.217 , 0.249	Depositor DCC
R_{free} test set	5443 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	51.8	Xtriage
Anisotropy	0.456	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 39.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.034 for h,-h-k,-l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	23591	wwPDB-VP
Average B, all atoms (Å ²)	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.35% 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: POP, MG, ADP, BEF

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	# $ Z > 5$	RMSZ	# $ Z > 5$
1	A	0.19	0/3506	0.41	0/4756
1	B	0.18	0/3497	0.41	0/4742
1	E	0.17	0/3506	0.42	0/4756
1	F	0.24	0/3461	0.52	0/4694
1	I	0.20	0/3459	0.46	0/4692
1	J	0.16	0/3474	0.40	0/4714
2	C	0.15	0/510	0.53	0/792
2	D	0.14	0/566	0.40	0/879
2	G	0.17	0/489	0.47	0/760
2	H	0.15	0/484	0.44	0/752
2	K	0.17	0/510	0.52	0/792
2	L	0.20	0/492	0.56	0/765
All	All	0.19	0/23954	0.45	0/33094

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3451	0	3538	28	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3443	0	3531	31	0
1	E	3451	0	3538	31	0
1	F	3409	0	3490	45	0
1	I	3406	0	3487	45	0
1	J	3420	0	3501	34	0
2	C	467	0	232	1	0
2	D	517	0	257	3	0
2	G	448	0	223	3	0
2	H	445	0	215	3	0
2	K	467	0	232	3	0
2	L	451	0	221	3	0
3	A	27	0	12	0	0
3	B	27	0	12	1	0
3	E	27	0	12	0	0
3	F	27	0	12	1	0
3	I	27	0	12	1	0
3	J	27	0	12	1	0
4	A	4	0	0	0	0
4	B	4	0	0	0	0
4	E	4	0	0	0	0
4	F	4	0	0	0	0
4	I	4	0	0	0	0
4	J	4	0	0	0	0
5	A	1	0	0	0	0
5	B	1	0	0	0	0
5	E	1	0	0	0	0
5	F	1	0	0	0	0
5	I	1	0	0	0	0
5	J	1	0	0	0	0
6	A	4	0	0	0	0
6	B	4	0	0	1	0
6	E	4	0	0	0	0
6	F	4	0	0	0	0
6	I	4	0	0	0	0
6	J	4	0	0	0	0
All	All	23591	0	22537	210	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 5.

All (210) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:278:ARG:NH2	1:F:452:ARG:HH12	1.72	0.86
1:F:272:HIS:HE1	1:F:274:ASP:HB2	1.42	0.82
1:B:410:LEU:HD21	1:B:433:VAL:HG11	1.64	0.79
1:E:278:ARG:NH2	1:F:452:ARG:NH1	2.32	0.78
1:J:381:GLU:HG3	1:J:382:MET:HG2	1.67	0.77
1:E:278:ARG:CZ	1:F:452:ARG:NH1	2.50	0.74
1:I:149:THR:HG22	1:I:179:GLN:HB3	1.73	0.70
1:I:400:VAL:HG21	1:I:425:VAL:HG11	1.75	0.68
1:F:157:ARG:HH22	1:F:324:VAL:HG22	1.59	0.68
1:F:121:HIS:ND1	2:H:8:U:O2'	2.22	0.68
1:I:266:GLN:HG2	1:I:378:LEU:HD13	1.77	0.67
1:B:381:GLU:HG3	1:B:382:MET:HG2	1.77	0.66
1:E:169:ASP:OD1	1:E:172:ARG:NH1	2.29	0.65
1:F:272:HIS:CE1	1:F:274:ASP:HB2	2.30	0.65
1:B:400:VAL:HG21	1:B:425:VAL:HG11	1.80	0.64
1:A:414:ASP:OD1	1:A:430:ARG:NH2	2.32	0.63
1:I:272:HIS:HD1	1:I:274:ASP:H	1.45	0.63
1:I:157:ARG:HH22	1:I:324:VAL:HG22	1.63	0.63
1:I:272:HIS:CE1	1:I:274:ASP:HB2	2.34	0.62
1:B:386:CYS:HB3	1:B:454:ARG:HG2	1.82	0.61
1:F:394:LYS:O	1:F:447:LYS:NZ	2.30	0.59
1:J:418:ILE:HG12	1:J:427:VAL:HG13	1.85	0.59
1:I:287:PHE:HE2	1:I:307:ILE:HD13	1.68	0.59
1:E:278:ARG:CZ	1:F:452:ARG:HH11	2.16	0.58
1:A:152:MET:HE3	1:A:158:MET:HB2	1.84	0.58
1:B:357:SER:HB2	1:B:364:LEU:HD11	1.84	0.58
1:A:111:PRO:HG2	1:A:114:MET:HG3	1.86	0.58
1:E:79:PRO:HD2	1:E:83:LEU:HD23	1.85	0.58
2:L:5:A:H5''	1:I:131:GLY:HA3	1.87	0.57
1:B:286:ARG:NH1	1:B:457:LYS:OXT	2.37	0.57
1:J:400:VAL:HG21	1:J:425:VAL:HG11	1.87	0.57
1:I:79:PRO:HD2	1:I:83:LEU:HD23	1.87	0.57
1:A:169:ASP:OD1	1:A:172:ARG:NH1	2.39	0.56
1:I:80:THR:HG22	1:I:83:LEU:H	1.70	0.56
1:F:266:GLN:HA	1:F:378:LEU:HB2	1.87	0.56
1:F:79:PRO:HD2	1:F:83:LEU:HD23	1.86	0.56
1:B:287:PHE:HE2	1:B:307:ILE:HD13	1.71	0.55
1:J:445:LYS:HD3	1:J:448:GLY:O	2.06	0.55
1:F:321:ASP:HB3	1:F:323:GLU:OE2	2.08	0.54
1:E:213:LEU:HD11	1:E:360:LEU:HD13	1.88	0.54
1:B:1:MET:HA	1:B:19:ASN:HD21	1.73	0.54
1:F:25:THR:O	3:F:500:ADP:N6	2.37	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:157:ARG:NH2	1:B:303:ARG:HE	2.05	0.54
1:J:116:ARG:HD3	1:I:116:ARG:HD3	1.90	0.54
2:G:0:POP:O2	2:G:1:G:OP1	2.25	0.53
1:I:156:ASP:HA	1:I:191:ILE:HG21	1.89	0.53
1:A:220:PHE:CE1	1:A:364:LEU:HD22	2.43	0.53
1:F:2:THR:HB	1:F:19:ASN:OD1	2.09	0.53
1:I:396:ARG:HG2	1:I:399:ASP:OD2	2.09	0.53
1:A:48:LYS:HE3	1:A:212:ALA:O	2.08	0.52
1:E:441:LEU:HD21	1:E:446:ILE:HD11	1.90	0.52
1:F:157:ARG:NH2	1:F:324:VAL:HG22	2.23	0.52
1:A:286:ARG:NH1	1:A:457:LYS:OXT	2.41	0.52
1:B:23:TYR:OH	1:B:90:GLU:OE1	2.25	0.52
1:E:396:ARG:HG2	1:E:399:ASP:OD2	2.10	0.52
1:I:272:HIS:HE1	1:I:274:ASP:HB2	1.75	0.51
1:B:404:LEU:O	1:B:410:LEU:HB2	2.11	0.51
1:F:289:ASN:HB2	1:F:428:ALA:HB2	1.92	0.51
1:J:152:MET:HE3	1:J:158:MET:HB2	1.92	0.50
1:J:322:PRO:HB2	1:J:359:MET:SD	2.51	0.50
1:I:418:ILE:HG12	1:I:427:VAL:HG13	1.93	0.50
1:I:85:ASP:OD1	1:I:105:THR:HG21	2.12	0.50
1:I:87:VAL:HG22	1:I:127:VAL:HG11	1.94	0.50
1:J:438:TRP:CH2	1:I:438:TRP:HH2	2.29	0.49
1:E:79:PRO:O	2:H:4:C:H5'	2.12	0.49
1:I:81:ARG:HG2	1:I:107:CYS:HB3	1.95	0.49
1:I:102:LYS:NZ	1:I:118:SER:O	2.46	0.49
1:E:83:LEU:O	1:E:87:VAL:HG13	2.12	0.49
1:E:266:GLN:HA	1:E:378:LEU:HB2	1.95	0.49
1:A:44:ARG:NH2	1:A:206:GLU:OE2	2.31	0.48
1:J:79:PRO:HD2	1:J:83:LEU:HD23	1.95	0.48
1:J:114:MET:HG3	1:I:114:MET:HE1	1.95	0.48
1:E:382:MET:SD	1:E:430:ARG:HD3	2.54	0.48
1:A:447:LYS:NZ	2:D:17:G:N7	2.44	0.48
1:F:220:PHE:CE1	1:F:364:LEU:HD22	2.49	0.48
1:I:83:LEU:O	1:I:87:VAL:HG13	2.13	0.47
1:I:401:LEU:HD22	2:K:13:G:H1'	1.96	0.47
1:E:287:PHE:HE2	1:E:307:ILE:HD13	1.79	0.47
1:F:233:GLN:HB3	1:F:375:ILE:HG21	1.97	0.47
1:B:394:LYS:NZ	2:C:9:G:O6	2.45	0.47
1:F:83:LEU:O	1:F:87:VAL:HG13	2.15	0.47
1:A:79:PRO:HD2	1:A:83:LEU:HD23	1.96	0.47
1:A:152:MET:HE2	1:A:182:LEU:HD22	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:390:GLY:H	1:B:395:MET:HE3	1.80	0.47
1:E:28:PRO:HB2	1:E:207:ILE:HD13	1.96	0.47
1:J:220:PHE:CE1	1:J:364:LEU:HD22	2.50	0.47
1:E:277:GLN:NE2	1:E:281:ASP:OD1	2.48	0.46
1:J:28:PRO:HB2	1:J:207:ILE:HD13	1.98	0.46
1:A:287:PHE:HE2	1:A:307:ILE:HD13	1.81	0.46
1:I:447:LYS:O	1:I:447:LYS:HG2	2.15	0.46
1:F:152:MET:HE3	1:F:158:MET:HB2	1.97	0.46
1:E:168:ASP:O	1:E:172:ARG:HG3	2.16	0.46
1:E:373:SER:OG	1:E:374:SER:N	2.48	0.46
1:B:312:LEU:HD11	1:B:342:ILE:HD12	1.98	0.46
1:B:287:PHE:CE2	1:B:307:ILE:HD13	2.49	0.46
1:I:438:TRP:O	1:I:442:GLN:HG2	2.16	0.46
1:B:158:MET:HE3	1:B:167:ILE:HD11	1.98	0.45
1:F:438:TRP:O	1:F:442:GLN:HG2	2.16	0.45
1:I:360:LEU:O	1:I:362:ILE:HG23	2.16	0.45
1:B:152:MET:HE1	1:B:198:VAL:HG21	1.98	0.45
1:J:25:THR:O	3:J:500:ADP:N6	2.48	0.45
1:E:87:VAL:HG22	1:E:127:VAL:HG11	1.99	0.45
1:F:400:VAL:HG21	1:F:425:VAL:HG11	1.97	0.45
1:J:152:MET:HE1	1:J:159:LEU:HG	1.99	0.45
1:E:276:GLU:OE2	1:F:449:LYS:NZ	2.41	0.45
1:F:391:LYS:HB2	1:F:422:PRO:HA	1.98	0.45
1:A:390:GLY:HA2	1:A:425:VAL:HG23	1.98	0.44
1:J:213:LEU:HD11	1:J:360:LEU:HD13	1.99	0.44
1:B:383:ALA:HB2	1:B:431:GLN:HG2	1.99	0.44
1:E:114:MET:HB3	1:E:114:MET:HE3	1.63	0.44
1:A:421:HIS:HB3	1:A:422:PRO:HD2	2.00	0.44
1:E:390:GLY:HA2	1:E:425:VAL:HG23	1.99	0.44
1:E:259:ASP:O	1:E:263:GLU:HG2	2.17	0.44
2:D:12:U:O2'	2:D:13:G:H5''	2.18	0.44
1:F:23:TYR:OH	1:F:90:GLU:OE2	2.35	0.43
1:F:61:LEU:O	1:F:65:ILE:HG12	2.18	0.43
1:F:378:LEU:HD23	1:F:378:LEU:HA	1.88	0.43
1:A:111:PRO:HG2	1:A:114:MET:CG	2.46	0.43
1:J:445:LYS:NZ	1:J:450:THR:HG23	2.33	0.43
1:F:135:ASP:OD1	1:F:139:LYS:HE3	2.18	0.43
1:F:233:GLN:HB3	1:F:375:ILE:CG2	2.49	0.43
1:I:396:ARG:HH22	1:I:447:LYS:NZ	2.16	0.43
1:F:232:LEU:HD13	1:F:314:VAL:HG11	2.01	0.43
1:A:287:PHE:CE2	1:A:307:ILE:HD13	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:433:VAL:HG12	1:B:433:VAL:O	2.18	0.43
1:B:349:GLU:HG2	1:B:352:ARG:NH1	2.34	0.43
1:F:433:VAL:HG12	1:F:433:VAL:O	2.19	0.43
1:E:272:HIS:CE1	1:E:274:ASP:HB2	2.53	0.43
1:F:57:PHE:CD1	1:F:151:VAL:HG11	2.54	0.43
1:B:348:GLU:CD	1:B:348:GLU:H	2.27	0.43
2:G:3:A:OP2	1:F:251:LYS:HD3	2.19	0.43
2:G:3:A:OP1	1:F:272:HIS:HB2	2.19	0.43
1:J:246:VAL:HG22	1:J:314:VAL:HB	2.01	0.43
1:E:421:HIS:HB3	1:E:422:PRO:HD2	2.01	0.42
1:J:103:ILE:HG12	1:J:125:ILE:HB	2.01	0.42
1:I:121:HIS:HB3	2:K:8:U:O2'	2.18	0.42
1:F:421:HIS:HB3	1:F:422:PRO:HD2	2.01	0.42
1:A:1:MET:HE3	1:A:1:MET:HB2	1.82	0.42
1:B:152:MET:HE3	1:B:182:LEU:HD21	2.01	0.42
1:B:421:HIS:HB3	1:B:422:PRO:HD2	2.00	0.42
1:J:400:VAL:HG11	1:J:427:VAL:HG21	2.00	0.42
1:I:76:VAL:HG22	1:I:151:VAL:HB	2.00	0.42
1:F:407:ASP:HB3	1:F:408:ILE:HD12	2.01	0.42
1:A:182:LEU:HG	1:A:199:GLN:NE2	2.35	0.42
1:J:3:ALA:HB3	1:J:6:THR:HG23	2.01	0.42
2:L:3:A:OP1	1:I:298:THR:OG1	2.35	0.42
1:I:20:GLU:OE1	1:I:96:ARG:NH1	2.52	0.42
1:B:286:ARG:HB3	1:B:291:SER:HB2	2.01	0.42
1:J:272:HIS:CE1	1:J:274:ASP:HB2	2.55	0.42
1:I:53:LYS:NZ	3:I:500:ADP:O3B	2.50	0.42
1:I:229:ILE:HB	1:I:230:PRO:HD3	2.00	0.42
1:A:410:LEU:HD11	1:A:437:ALA:HB2	2.02	0.42
2:D:0:POP:O	2:D:1:G:OP1	2.37	0.42
1:B:157:ARG:CZ	1:B:303:ARG:HE	2.32	0.42
1:J:61:LEU:O	1:J:65:ILE:HG12	2.20	0.42
1:J:433:VAL:HG12	1:J:433:VAL:O	2.19	0.42
1:F:47:ALA:O	1:F:185:ALA:HA	2.20	0.42
1:A:158:MET:HE3	1:A:167:ILE:HD11	2.02	0.42
1:F:441:LEU:HB3	1:F:453:VAL:HG21	2.00	0.42
1:A:392:LYS:HG2	1:A:422:PRO:O	2.20	0.42
1:A:400:VAL:HG21	1:A:425:VAL:HG11	2.01	0.42
1:E:220:PHE:CE1	1:E:364:LEU:HD22	2.55	0.42
1:J:57:PHE:HB3	1:J:183:PHE:CE1	2.55	0.42
1:J:81:ARG:HG2	1:J:107:CYS:HB3	2.01	0.42
1:I:224:SER:O	1:I:228:LYS:HG3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:213:LEU:HD11	1:A:360:LEU:HD13	2.01	0.42
1:B:418:ILE:HG12	1:B:427:VAL:HG13	2.01	0.42
1:E:4:PHE:CE1	1:E:26:MET:HG2	2.54	0.42
1:E:392:LYS:HG2	1:E:422:PRO:O	2.20	0.41
1:F:18:LEU:HD21	1:F:59:LEU:HD21	2.01	0.41
1:J:4:PHE:CE1	1:J:26:MET:HG2	2.55	0.41
1:J:220:PHE:CZ	1:J:364:LEU:HD22	2.55	0.41
1:A:114:MET:H	1:A:114:MET:HG2	1.55	0.41
1:J:441:LEU:HB3	1:J:453:VAL:HG21	2.02	0.41
1:A:385:LEU:HD21	1:A:438:TRP:HB2	2.01	0.41
1:I:57:PHE:HB3	1:I:183:PHE:CE1	2.55	0.41
1:I:278:ARG:HH21	1:I:278:ARG:HD3	1.73	0.41
1:I:421:HIS:HB3	1:I:422:PRO:HD2	2.01	0.41
1:F:286:ARG:HB3	1:F:291:SER:HB2	2.02	0.41
3:B:500:ADP:O1A	6:B:601:HOH:O	2.22	0.41
1:I:352:ARG:O	1:I:356:ILE:HG12	2.20	0.41
1:F:4:PHE:CE1	1:F:26:MET:HG2	2.56	0.41
1:J:151:VAL:HG22	1:J:181:LEU:HB2	2.01	0.41
2:L:2:G:O2'	2:L:3:A:O5'	2.21	0.41
1:I:246:VAL:HG22	1:I:314:VAL:HB	2.02	0.41
1:I:322:PRO:HB2	1:I:359:MET:CE	2.51	0.41
1:E:400:VAL:HG21	1:E:425:VAL:HG11	2.01	0.41
1:J:251:LYS:HG2	1:J:298:THR:HG21	2.02	0.41
1:J:438:TRP:HH2	1:I:438:TRP:HH2	1.67	0.41
1:I:216:ILE:HG12	1:I:333:ALA:HB3	2.03	0.41
1:I:394:LYS:O	1:I:447:LYS:HE3	2.21	0.41
1:A:363:LYS:HD2	1:A:363:LYS:N	2.36	0.41
1:B:79:PRO:HD2	1:B:83:LEU:HD23	2.02	0.41
1:J:114:MET:HG3	1:I:114:MET:CE	2.51	0.40
2:H:9:G:H2'	2:H:10:G:H8	1.85	0.40
1:A:57:PHE:HB3	1:A:183:PHE:CE1	2.57	0.40
1:A:152:MET:HE1	1:A:159:LEU:HG	2.02	0.40
1:B:57:PHE:HB3	1:B:183:PHE:CE1	2.57	0.40
1:J:4:PHE:CZ	1:J:26:MET:HG2	2.56	0.40
1:J:396:ARG:HG2	1:J:399:ASP:OD2	2.21	0.40
1:F:214:PRO:O	1:F:216:ILE:N	2.55	0.40
1:B:410:LEU:HD21	1:B:433:VAL:CG1	2.42	0.40
1:B:293:ARG:NH2	1:B:378:LEU:HD22	2.37	0.40
1:B:404:LEU:HD13	1:B:415:ILE:HG12	2.02	0.40
1:E:441:LEU:HD23	1:E:453:VAL:HG21	2.03	0.40
1:F:348:GLU:H	1:F:348:GLU:CD	2.30	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:F:384:THR:HA	1:F:427:VAL:O	2.21	0.40
1:E:119:LEU:HD22	1:E:142:VAL:HG22	2.03	0.40
1:I:407:ASP:HB2	2:K:15:U:O4	2.22	0.40
1:F:76:VAL:HG22	1:F:151:VAL:HB	2.02	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	
1	A	455/459 (99%)	448 (98%)	7 (2%)	0	100	100
1	B	452/459 (98%)	445 (98%)	7 (2%)	0	100	100
1	E	455/459 (99%)	447 (98%)	6 (1%)	2 (0%)	30	49
1	F	445/459 (97%)	437 (98%)	8 (2%)	0	100	100
1	I	447/459 (97%)	439 (98%)	8 (2%)	0	100	100
1	J	449/459 (98%)	443 (99%)	6 (1%)	0	100	100
All	All	2703/2754 (98%)	2659 (98%)	42 (2%)	2 (0%)	48	68

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	374	SER
1	E	370	PRO

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	
1	A	368/368 (100%)	365 (99%)	3 (1%)	73	88
1	B	367/368 (100%)	365 (100%)	2 (0%)	81	92
1	E	368/368 (100%)	362 (98%)	6 (2%)	55	79
1	F	364/368 (99%)	358 (98%)	6 (2%)	55	79
1	I	363/368 (99%)	357 (98%)	6 (2%)	53	78
1	J	365/368 (99%)	361 (99%)	4 (1%)	65	84
All	All	2195/2208 (99%)	2168 (99%)	27 (1%)	63	83

All (27) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	278	ARG
1	A	430	ARG
1	A	447	LYS
1	B	278	ARG
1	B	374	SER
1	E	87	VAL
1	E	110	GLN
1	E	114	MET
1	E	149	THR
1	E	207	ILE
1	E	377	THR
1	J	197	ARG
1	J	200	ARG
1	J	207	ILE
1	J	391	LYS
1	I	80	THR
1	I	81	ARG
1	I	87	VAL
1	I	114	MET
1	I	252	LYS
1	I	379	GLU
1	F	87	VAL
1	F	114	MET
1	F	255	GLN
1	F	374	SER
1	F	375	ILE
1	F	377	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (20) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	239	HIS
1	A	240	GLN
1	B	19	ASN
1	B	71	GLN
1	B	199	GLN
1	B	351	GLN
1	E	199	GLN
1	E	239	HIS
1	E	361	GLN
1	J	351	GLN
1	J	354	ASN
1	J	431	GLN
1	J	442	GLN
1	I	120	GLN
1	I	255	GLN
1	I	367	GLN
1	I	442	GLN
1	F	365	ASN
1	F	421	HIS
1	F	431	GLN

5.3.3 RNA ⓘ

Mol	Chain	Analysed	Backbone Outliers	Pucker Outliers
2	C	21/24 (87%)	6 (28%)	0
2	D	19/24 (79%)	3 (15%)	0
2	G	20/24 (83%)	5 (25%)	1 (5%)
2	H	18/24 (75%)	3 (16%)	0
2	K	21/24 (87%)	7 (33%)	0
2	L	20/24 (83%)	7 (35%)	1 (5%)
All	All	119/144 (82%)	31 (26%)	2 (1%)

All (31) RNA backbone outliers are listed below:

Mol	Chain	Res	Type
2	D	9	G
2	D	17	G
2	D	22	U
2	C	5	A
2	C	9	G

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Mol	Chain	Res	Type
2	C	12	U
2	C	13	G
2	C	17	G
2	C	22	U
2	G	4	C
2	G	6	U
2	G	7	A
2	G	9	G
2	G	17	G
2	L	3	A
2	L	4	C
2	L	5	A
2	L	9	G
2	L	12	U
2	L	13	G
2	L	17	G
2	K	4	C
2	K	5	A
2	K	9	G
2	K	12	U
2	K	13	G
2	K	17	G
2	K	22	U
2	H	7	A
2	H	9	G
2	H	17	G

All (2) RNA pucker outliers are listed below:

Mol	Chain	Res	Type
2	G	3	A
2	L	2	G

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

Of 18 ligands modelled in this entry, 6 are monoatomic - leaving 12 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	ADP	B	500	5,4	28,29,29	1.42	4 (14%)	43,45,45	1.76	8 (18%)
3	ADP	A	500	5,4	28,29,29	1.41	4 (14%)	43,45,45	1.77	8 (18%)
3	ADP	I	500	5	28,29,29	1.41	4 (14%)	43,45,45	1.78	8 (18%)
4	BEF	F	501	3	0,3,3	-	-	-	-	-
3	ADP	J	500	5	28,29,29	1.40	4 (14%)	43,45,45	1.77	9 (20%)
3	ADP	F	500	5,4	28,29,29	1.41	4 (14%)	43,45,45	1.78	8 (18%)
4	BEF	E	501	3	0,3,3	-	-	-	-	-
4	BEF	A	501	3	0,3,3	-	-	-	-	-
4	BEF	B	501	3	0,3,3	-	-	-	-	-
4	BEF	J	501	-	0,3,3	-	-	-	-	-
3	ADP	E	500	5,4	28,29,29	1.41	4 (14%)	43,45,45	1.81	8 (18%)
4	BEF	I	501	-	0,3,3	-	-	-	-	-

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ADP	B	500	5,4	-	6/16/32/32	0/3/3/3
3	ADP	A	500	5,4	-	4/16/32/32	0/3/3/3
3	ADP	I	500	5	-	3/16/32/32	0/3/3/3
3	ADP	J	500	5	-	5/16/32/32	0/3/3/3
3	ADP	F	500	5,4	-	5/16/32/32	0/3/3/3
3	ADP	E	500	5,4	-	5/16/32/32	0/3/3/3

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	I	500	ADP	C5-C4	4.73	1.47	1.39
3	E	500	ADP	C5-C4	4.70	1.47	1.39
3	B	500	ADP	C5-C4	4.69	1.47	1.39
3	F	500	ADP	C5-C4	4.67	1.47	1.39
3	A	500	ADP	C5-C4	4.64	1.47	1.39
3	J	500	ADP	C5-C4	4.64	1.47	1.39
3	J	500	ADP	C5-C6	2.74	1.48	1.41
3	I	500	ADP	C5-C6	2.74	1.48	1.41
3	E	500	ADP	C5-C6	2.73	1.48	1.41
3	F	500	ADP	C5-C6	2.72	1.48	1.41
3	A	500	ADP	C5-C6	2.71	1.48	1.41
3	B	500	ADP	C5-C6	2.70	1.48	1.41
3	F	500	ADP	C8-N7	2.35	1.36	1.31
3	J	500	ADP	C8-N7	2.35	1.36	1.31
3	I	500	ADP	C8-N7	2.29	1.36	1.31
3	B	500	ADP	C8-N7	2.29	1.36	1.31
3	I	500	ADP	C5-N7	-2.26	1.35	1.39
3	A	500	ADP	C8-N7	2.26	1.36	1.31
3	E	500	ADP	C8-N7	2.26	1.36	1.31
3	B	500	ADP	C5-N7	-2.23	1.35	1.39
3	A	500	ADP	C5-N7	-2.22	1.35	1.39
3	E	500	ADP	C5-N7	-2.20	1.35	1.39
3	J	500	ADP	C5-N7	-2.18	1.35	1.39
3	F	500	ADP	C5-N7	-2.16	1.35	1.39

All (49) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	E	500	ADP	C5-C4-N3	-5.83	118.69	126.72
3	I	500	ADP	C5-C4-N3	-5.77	118.78	126.72
3	B	500	ADP	C5-C4-N3	-5.75	118.79	126.72
3	F	500	ADP	C5-C4-N3	-5.69	118.88	126.72
3	A	500	ADP	C5-C4-N3	-5.68	118.89	126.72
3	J	500	ADP	C5-C4-N3	-5.59	119.02	126.72
3	E	500	ADP	N3-C4-N9	4.70	135.16	127.17
3	I	500	ADP	N3-C4-N9	4.67	135.11	127.17
3	A	500	ADP	N3-C4-N9	4.64	135.06	127.17
3	B	500	ADP	N3-C4-N9	4.62	135.03	127.17
3	F	500	ADP	N3-C4-N9	4.47	134.78	127.17
3	J	500	ADP	N3-C4-N9	4.43	134.69	127.17
3	E	500	ADP	C2-N3-C4	3.72	120.92	111.83
3	I	500	ADP	C2-N3-C4	3.71	120.90	111.83
3	F	500	ADP	C2-N3-C4	3.71	120.89	111.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	J	500	ADP	C2-N3-C4	3.66	120.78	111.83
3	B	500	ADP	C2-N3-C4	3.66	120.78	111.83
3	A	500	ADP	C2-N3-C4	3.66	120.78	111.83
3	F	500	ADP	C4-C5-N7	-3.48	106.60	110.58
3	J	500	ADP	C4-C5-N7	-3.44	106.65	110.58
3	E	500	ADP	C4-C5-N7	-3.42	106.68	110.58
3	B	500	ADP	C4-C5-N7	-3.40	106.70	110.58
3	F	500	ADP	N3-C2-N1	-3.32	123.56	128.58
3	J	500	ADP	N3-C2-N1	-3.31	123.58	128.58
3	I	500	ADP	N3-C2-N1	-3.30	123.58	128.58
3	A	500	ADP	N3-C2-N1	-3.30	123.59	128.58
3	A	500	ADP	C4-C5-N7	-3.28	106.83	110.58
3	E	500	ADP	N3-C2-N1	-3.28	123.61	128.58
3	I	500	ADP	C4-C5-N7	-3.26	106.85	110.58
3	B	500	ADP	N3-C2-N1	-3.25	123.66	128.58
3	A	500	ADP	C4-N9-C8	2.86	108.74	105.74
3	J	500	ADP	C4-N9-C8	2.81	108.69	105.74
3	E	500	ADP	C4-N9-C8	2.79	108.67	105.74
3	B	500	ADP	C4-N9-C8	2.74	108.62	105.74
3	F	500	ADP	C4-N9-C8	2.71	108.58	105.74
3	I	500	ADP	C4-N9-C8	2.68	108.55	105.74
3	F	500	ADP	C5-N7-C8	2.50	107.38	103.45
3	E	500	ADP	C5-N7-C8	2.50	107.37	103.45
3	J	500	ADP	C5-N7-C8	2.50	107.37	103.45
3	B	500	ADP	C5-N7-C8	2.49	107.36	103.45
3	A	500	ADP	C5-N7-C8	2.41	107.23	103.45
3	I	500	ADP	C5-N7-C8	2.39	107.21	103.45
3	J	500	ADP	C6-C5-N7	2.20	136.32	132.09
3	F	500	ADP	C6-C5-N7	2.17	136.27	132.09
3	J	500	ADP	N9-C8-N7	-2.06	111.01	113.94
3	E	500	ADP	C6-C5-N7	2.06	136.06	132.09
3	B	500	ADP	C6-C5-N7	2.04	136.02	132.09
3	I	500	ADP	C6-C5-N7	2.01	135.96	132.09
3	A	500	ADP	C6-C5-N7	2.00	135.95	132.09

There are no chirality outliers.

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	500	ADP	C5'-O5'-PA-O1A
3	B	500	ADP	PA-O3A-PB-O3B
3	E	500	ADP	PA-O3A-PB-O3B

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Mol	Chain	Res	Type	Atoms
3	J	500	ADP	PA-O3A-PB-O3B
3	J	500	ADP	C5'-O5'-PA-O1A
3	F	500	ADP	PA-O3A-PB-O3B
3	F	500	ADP	C5'-O5'-PA-O1A
3	E	500	ADP	O4'-C4'-C5'-O5'
3	I	500	ADP	O4'-C4'-C5'-O5'
3	F	500	ADP	O4'-C4'-C5'-O5'
3	A	500	ADP	O4'-C4'-C5'-O5'
3	B	500	ADP	O4'-C4'-C5'-O5'
3	J	500	ADP	O4'-C4'-C5'-O5'
3	A	500	ADP	PA-O3A-PB-O3B
3	B	500	ADP	PA-O3A-PB-O2B
3	E	500	ADP	PA-O3A-PB-O2B
3	I	500	ADP	PA-O3A-PB-O3B
3	F	500	ADP	C3'-C4'-C5'-O5'
3	E	500	ADP	C3'-C4'-C5'-O5'
3	I	500	ADP	C3'-C4'-C5'-O5'
3	A	500	ADP	C3'-C4'-C5'-O5'
3	B	500	ADP	C3'-C4'-C5'-O5'
3	J	500	ADP	C3'-C4'-C5'-O5'
3	B	500	ADP	PA-O3A-PB-O1B
3	E	500	ADP	PA-O3A-PB-O1B
3	J	500	ADP	PA-O3A-PB-O1B
3	F	500	ADP	PA-O3A-PB-O1B
3	B	500	ADP	C2'-C1'-N9-C8

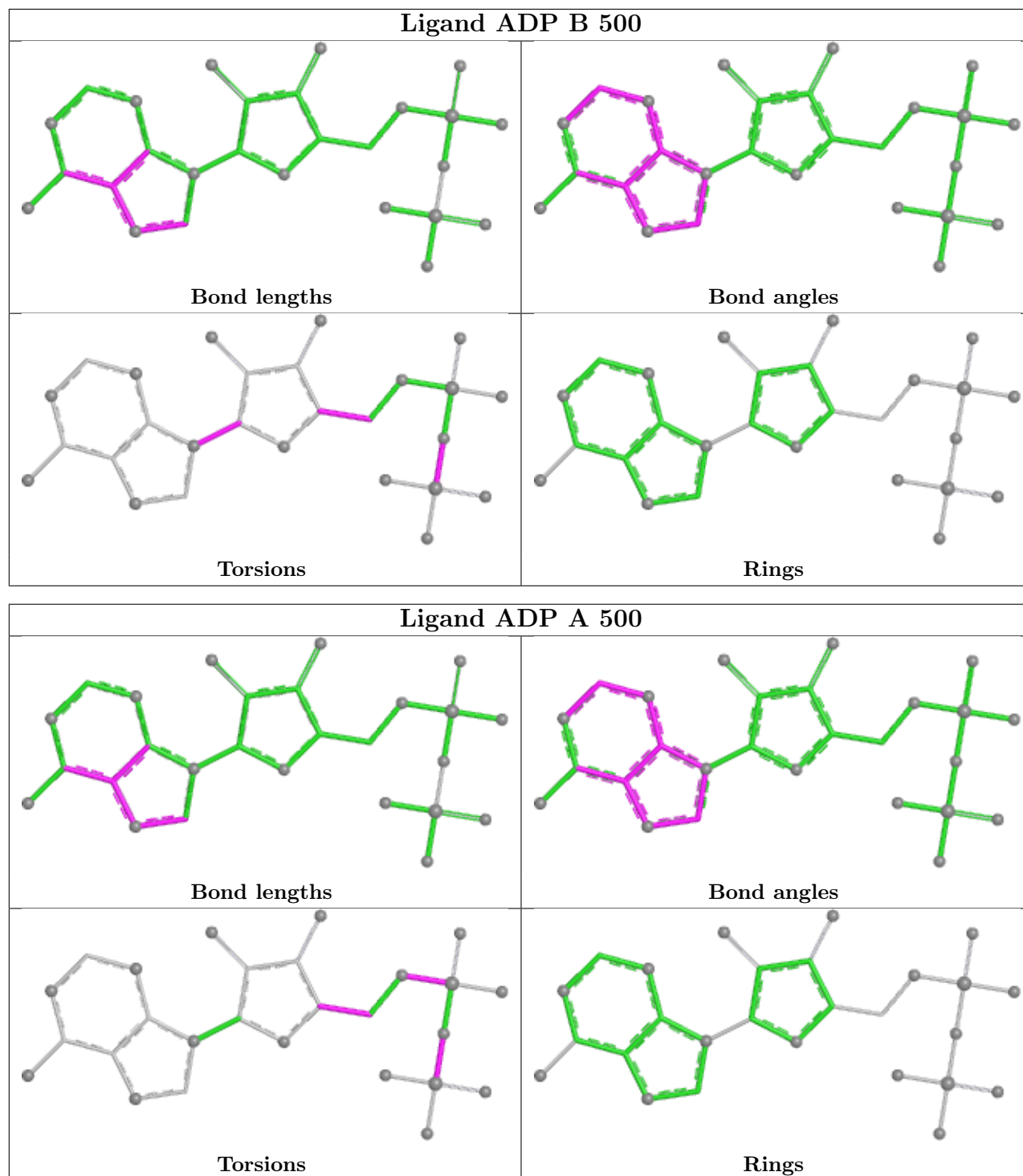
There are no ring outliers.

4 monomers are involved in 4 short contacts:

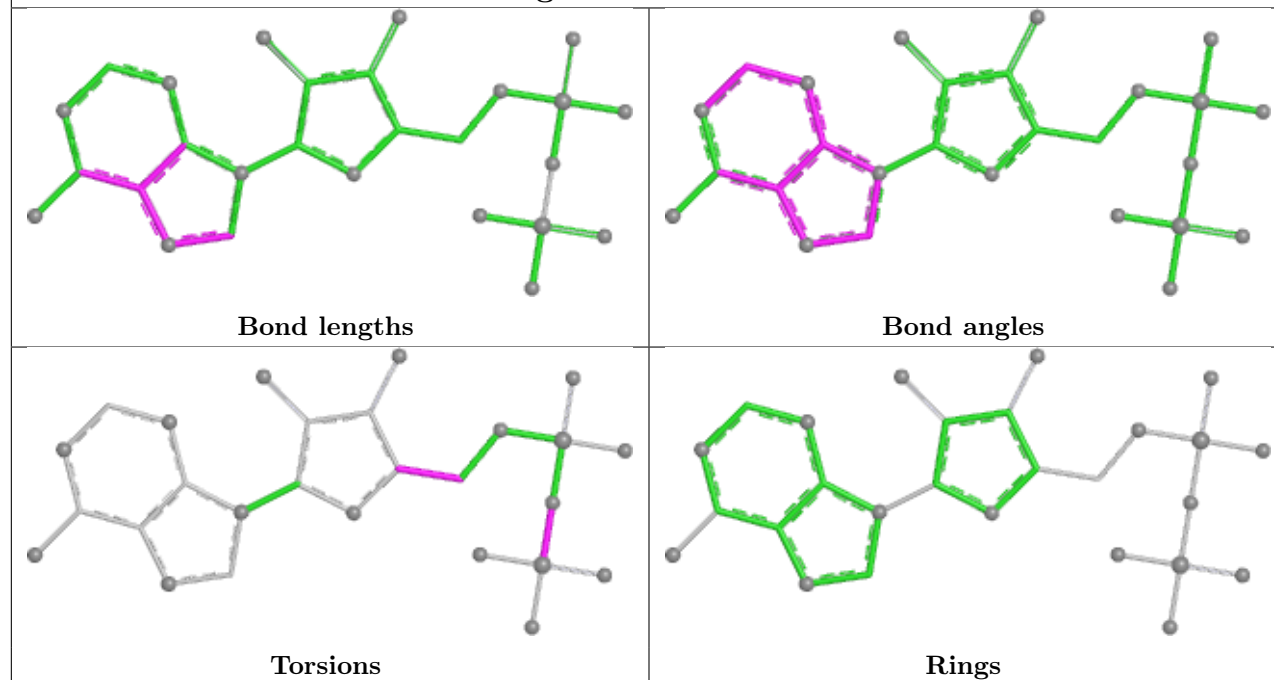
Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	500	ADP	1	0
3	I	500	ADP	1	0
3	J	500	ADP	1	0
3	F	500	ADP	1	0

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

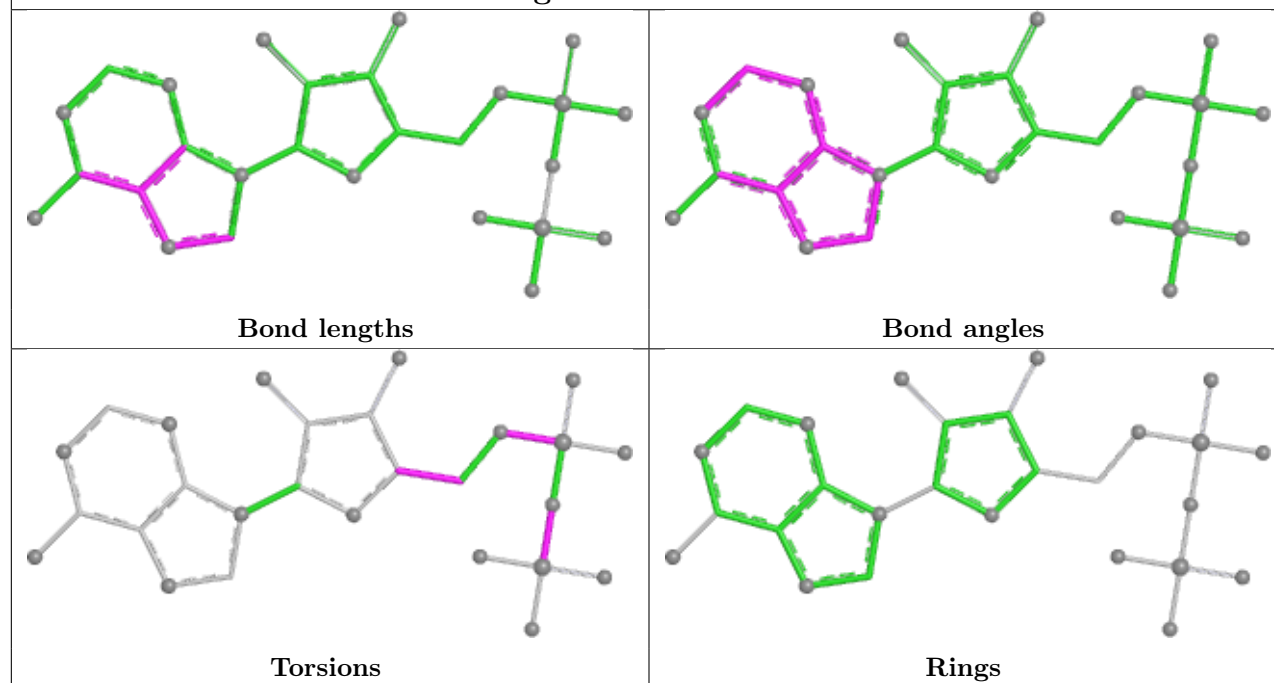
in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

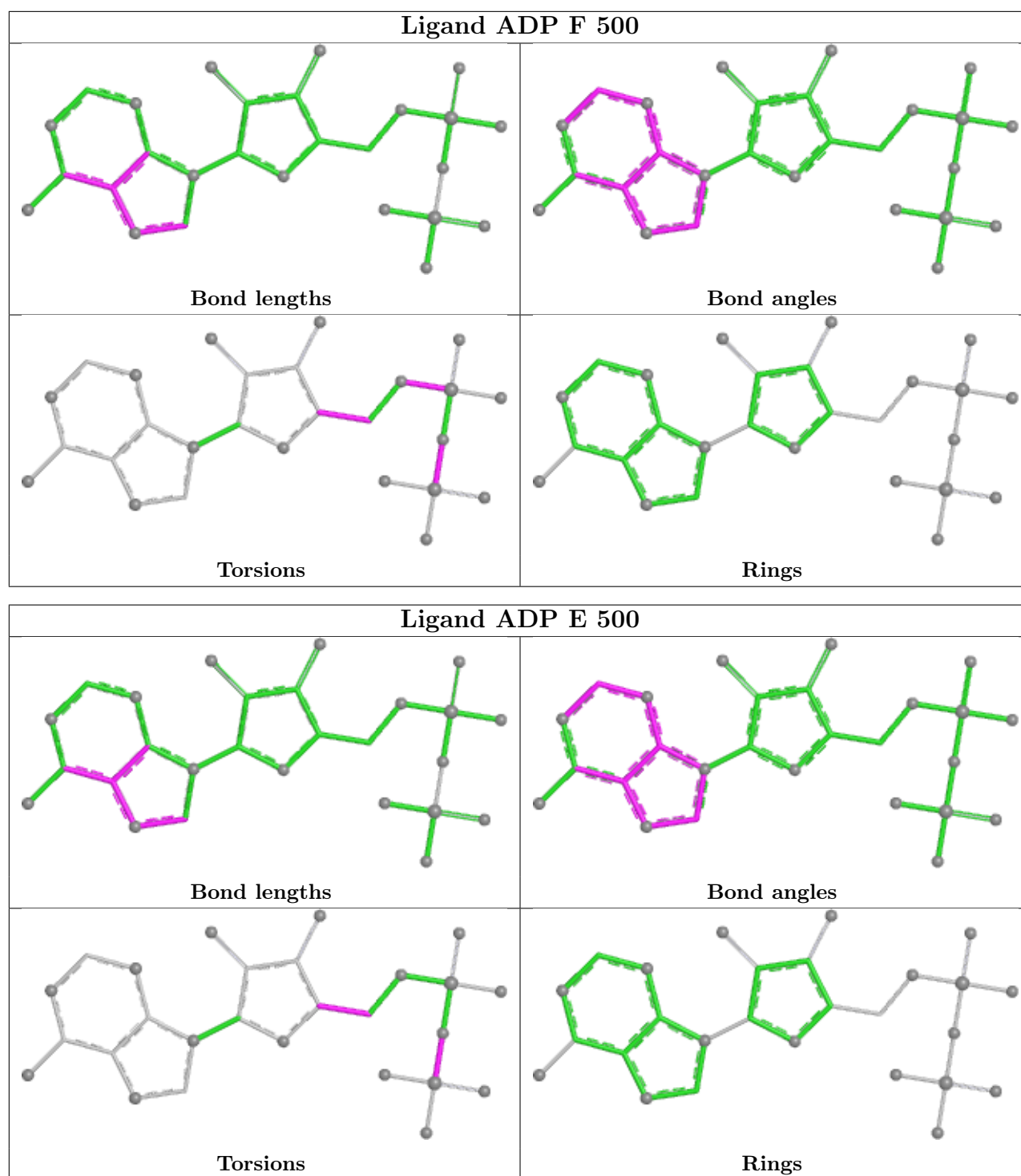


Ligand ADP I 500



Ligand ADP J 500





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

There are no chain breaks in this entry.

6 Fit of model and data ⓘ

6.1 Protein, DNA and RNA chains ⓘ

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	A	457/459 (99%)	0.07	3 (0%) 84 81	35, 50, 69, 100	0
1	B	456/459 (99%)	0.10	8 (1%) 67 64	34, 47, 65, 109	0
1	E	457/459 (99%)	0.40	18 (3%) 43 38	44, 59, 84, 135	0
1	F	451/459 (98%)	0.93	39 (8%) 16 14	54, 88, 126, 147	0
1	I	451/459 (98%)	0.81	48 (10%) 11 9	42, 78, 124, 141	0
1	J	453/459 (98%)	0.59	13 (2%) 53 49	47, 69, 96, 125	0
2	C	22/24 (91%)	-0.27	0 100 100	46, 54, 79, 102	0
2	D	22/24 (91%)	-0.09	2 (9%) 15 13	31, 54, 72, 113	2 (9%)
2	G	21/24 (87%)	0.13	1 (4%) 35 31	61, 77, 107, 134	0
2	H	22/24 (91%)	0.59	0 100 100	62, 123, 141, 153	0
2	K	22/24 (91%)	0.30	0 100 100	73, 89, 112, 120	0
2	L	22/24 (91%)	0.25	0 100 100	73, 91, 101, 125	0
All	All	2856/2898 (98%)	0.47	132 (4%) 37 33	31, 62, 114, 153	2 (0%)

All (132) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	I	130	PRO	4.1
1	J	373	SER	4.0
1	I	433	VAL	4.0
1	F	108	GLY	3.9
1	F	116	ARG	3.8
1	E	371	ALA	3.6
1	I	376	ALA	3.6
1	F	109	GLY	3.6
1	I	344	PHE	3.6
1	F	114	MET	3.5
1	B	373	SER	3.5

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Mol	Chain	Res	Type	RSRZ
1	J	406	GLY	3.5
1	E	121	HIS	3.4
1	I	385	LEU	3.4
1	I	161	MET	3.4
1	I	238	LEU	3.3
1	I	316	PHE	3.2
1	I	397	PRO	3.2
1	B	197	ARG	3.1
1	F	438	TRP	3.1
2	D	5[A]	A	3.1
1	J	20	GLU	3.1
1	I	230	PRO	3.1
1	F	452	ARG	3.1
1	E	373	SER	3.1
1	I	301	ALA	3.0
1	E	117	ASP	3.0
1	I	369	PRO	2.9
1	E	372	ASN	2.9
1	F	408	ILE	2.9
1	B	371	ALA	2.9
1	I	274	ASP	2.9
1	F	237	SER	2.9
1	E	206	GLU	2.9
1	J	78	CYS	2.9
1	F	369	PRO	2.7
1	F	104	LEU	2.7
1	F	376	ALA	2.7
1	F	161	MET	2.7
1	J	454	ARG	2.7
1	I	355	ILE	2.7
1	F	456	LEU	2.7
1	F	112	PHE	2.7
1	F	77	LEU	2.7
1	I	348	GLU	2.7
1	B	457	LYS	2.6
1	A	276	GLU	2.6
1	I	105	THR	2.6
1	F	445	LYS	2.6
1	I	210	THR	2.6
2	D	6[A]	U	2.6
1	I	408	ILE	2.6
1	F	453	VAL	2.6

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Mol	Chain	Res	Type	RSRZ
1	J	153	ASP	2.6
1	I	229	ILE	2.6
1	F	96	ARG	2.5
1	A	210	THR	2.5
1	I	373	SER	2.5
1	E	107	CYS	2.5
1	F	441	LEU	2.5
1	I	374	SER	2.5
1	E	1	MET	2.5
1	A	85	ASP	2.4
1	I	226	LYS	2.4
1	F	455	LEU	2.4
1	F	120	GLN	2.4
1	F	351	GLN	2.4
1	I	260	ALA	2.4
1	F	318	LEU	2.4
1	B	395	MET	2.4
1	I	264	VAL	2.4
1	I	432	ALA	2.4
1	F	25	THR	2.3
1	F	162	GLY	2.3
1	B	172	ARG	2.3
1	F	446	ILE	2.3
1	F	107	CYS	2.3
1	E	56	ALA	2.3
1	J	370	PRO	2.3
1	I	347	PRO	2.3
1	E	105	THR	2.3
1	F	210	THR	2.3
1	I	320	TRP	2.3
1	E	108	GLY	2.3
1	E	106	LEU	2.3
1	B	85	ASP	2.3
1	E	278	ARG	2.3
1	I	356	ILE	2.3
1	F	410	LEU	2.3
1	E	127	VAL	2.3
1	I	298	THR	2.3
1	I	443	GLY	2.3
1	F	87	VAL	2.3
1	I	437	ALA	2.2
1	B	1	MET	2.2

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Mol	Chain	Res	Type	RSRZ
1	E	161	MET	2.2
1	F	373	SER	2.2
1	F	422	PRO	2.2
1	F	110	GLN	2.2
1	F	272	HIS	2.2
1	J	2	THR	2.2
1	I	414	ASP	2.2
1	E	70	PHE	2.2
1	F	432	ALA	2.2
1	I	439	LYS	2.2
1	F	121	HIS	2.1
1	F	2	THR	2.1
1	I	20	GLU	2.1
1	E	114	MET	2.1
1	I	435	HIS	2.1
1	I	350	ALA	2.1
1	J	114	MET	2.1
2	G	6	U	2.1
1	I	441	LEU	2.1
1	F	232	LEU	2.1
1	I	85	ASP	2.1
1	I	401	LEU	2.1
1	I	227	GLY	2.1
1	J	76	VAL	2.0
1	I	220	PHE	2.0
1	I	268	ALA	2.0
1	I	340	LEU	2.0
1	J	85	ASP	2.0
1	I	359	MET	2.0
1	I	110	GLN	2.0
1	I	345	CYS	2.0
1	J	204	ALA	2.0
1	I	318	LEU	2.0
1	F	15	LEU	2.0
1	E	210	THR	2.0
1	I	377	THR	2.0
1	J	111	PRO	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

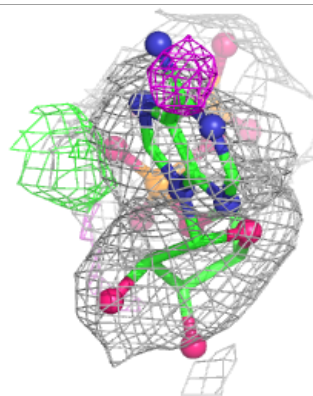
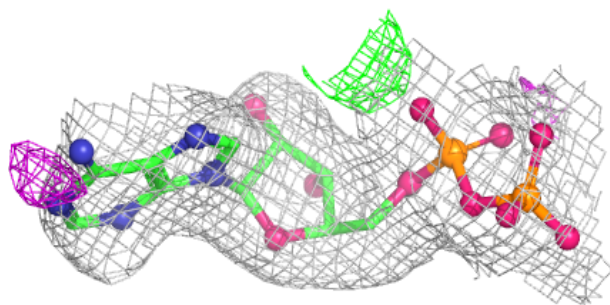
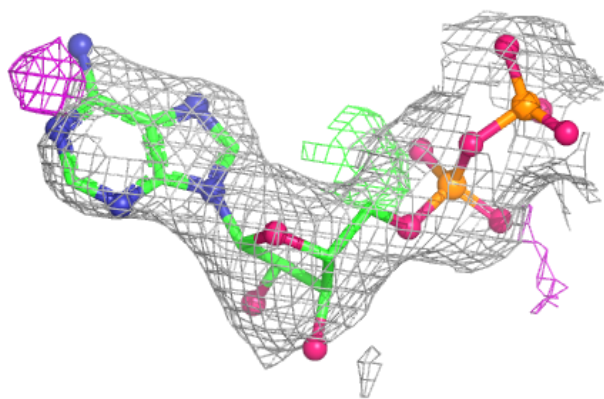
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
4	BEF	I	501	4/4	0.88	0.10	47,49,50,53	0
4	BEF	J	501	4/4	0.90	0.08	47,48,49,50	0
3	ADP	F	500	27/27	0.92	0.09	53,67,74,80	0
4	BEF	F	501	4/4	0.92	0.08	55,56,57,58	0
4	BEF	E	501	4/4	0.94	0.07	44,47,47,50	0
3	ADP	I	500	27/27	0.95	0.09	42,53,59,60	0
3	ADP	J	500	27/27	0.96	0.07	46,52,55,56	0
3	ADP	A	500	27/27	0.96	0.07	36,45,49,51	0
3	ADP	E	500	27/27	0.96	0.06	41,46,50,53	0
4	BEF	A	501	4/4	0.96	0.06	37,40,41,41	0
3	ADP	B	500	27/27	0.97	0.07	28,40,43,48	0
4	BEF	B	501	4/4	0.97	0.06	31,35,35,36	0
5	MG	A	502	1/1	0.99	0.07	40,40,40,40	0
5	MG	B	502	1/1	0.99	0.04	34,34,34,34	0
5	MG	E	502	1/1	0.99	0.02	47,47,47,47	0
5	MG	J	502	1/1	0.99	0.03	51,51,51,51	0
5	MG	F	502	1/1	0.99	0.04	53,53,53,53	0
5	MG	I	502	1/1	1.00	0.05	49,49,49,49	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.

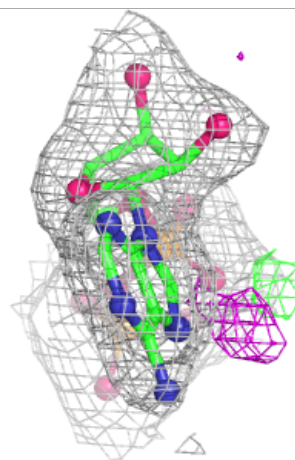
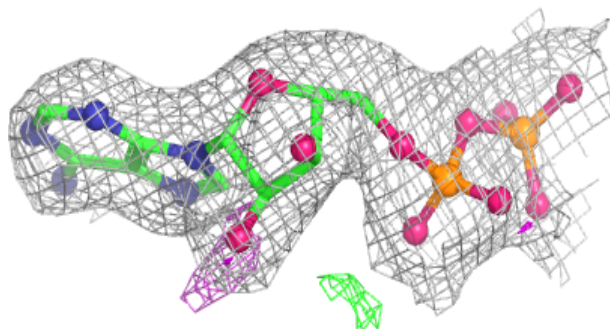
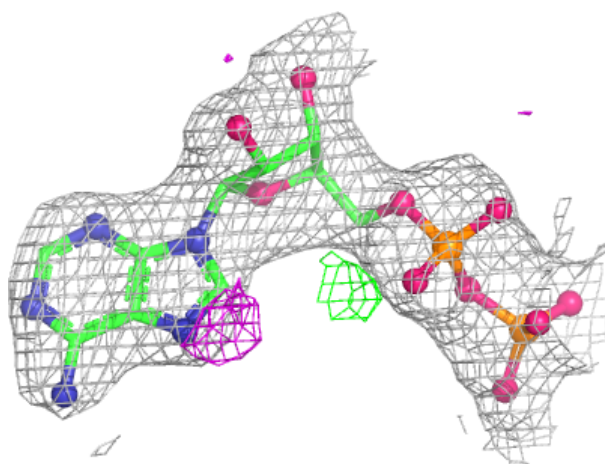
Electron density around ADP F 500:

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



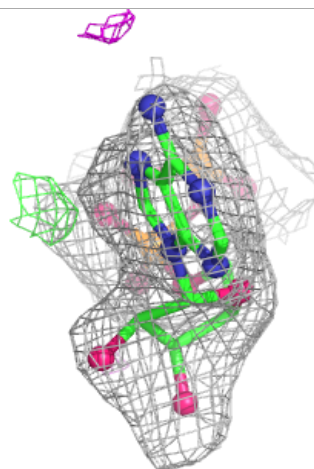
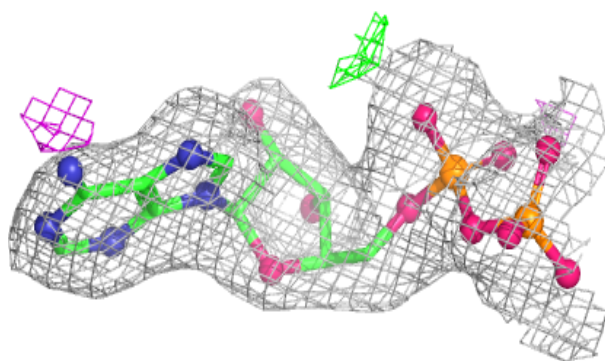
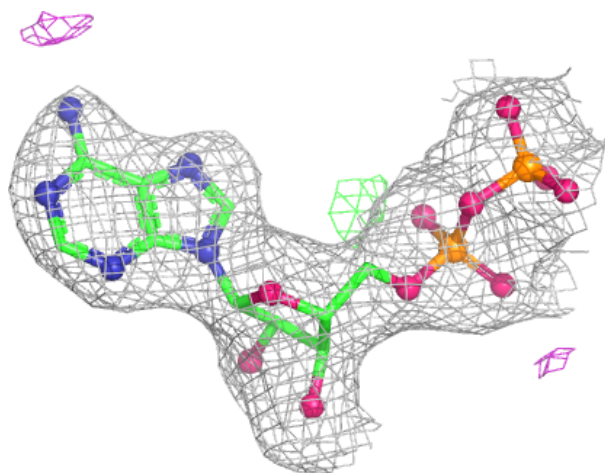
Electron density around ADP I 500:

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



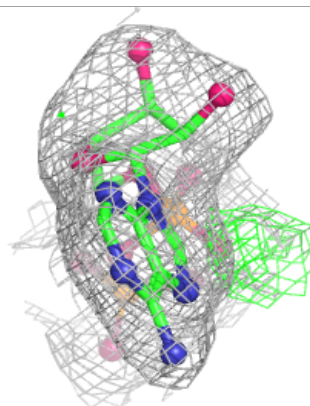
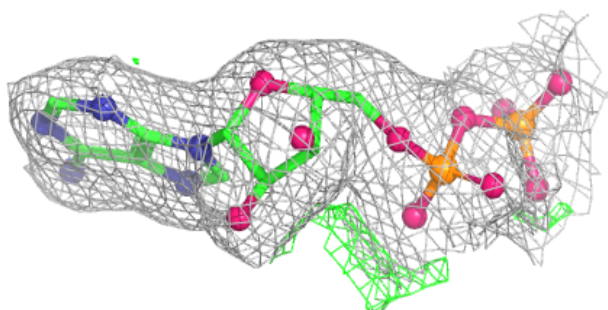
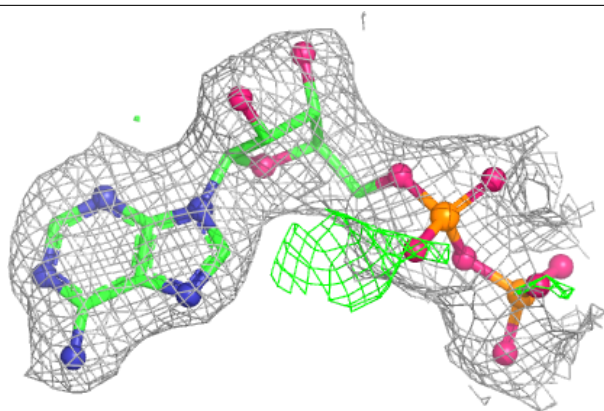
Electron density around ADP J 500:

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

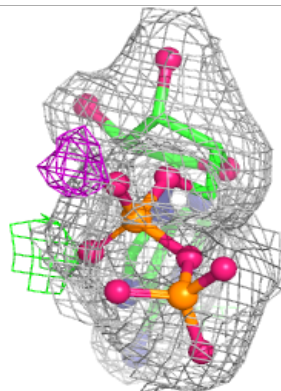
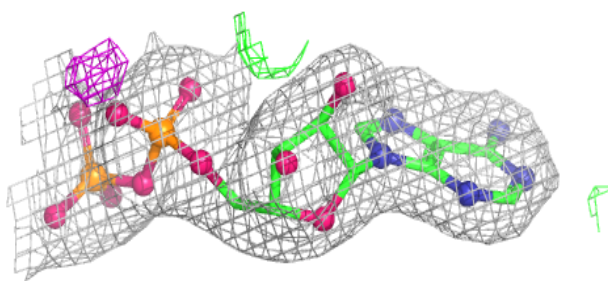
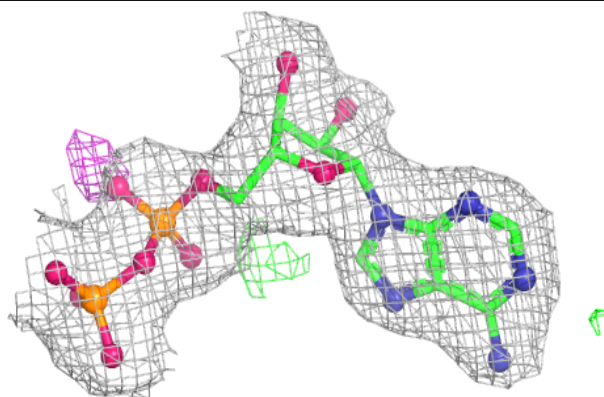


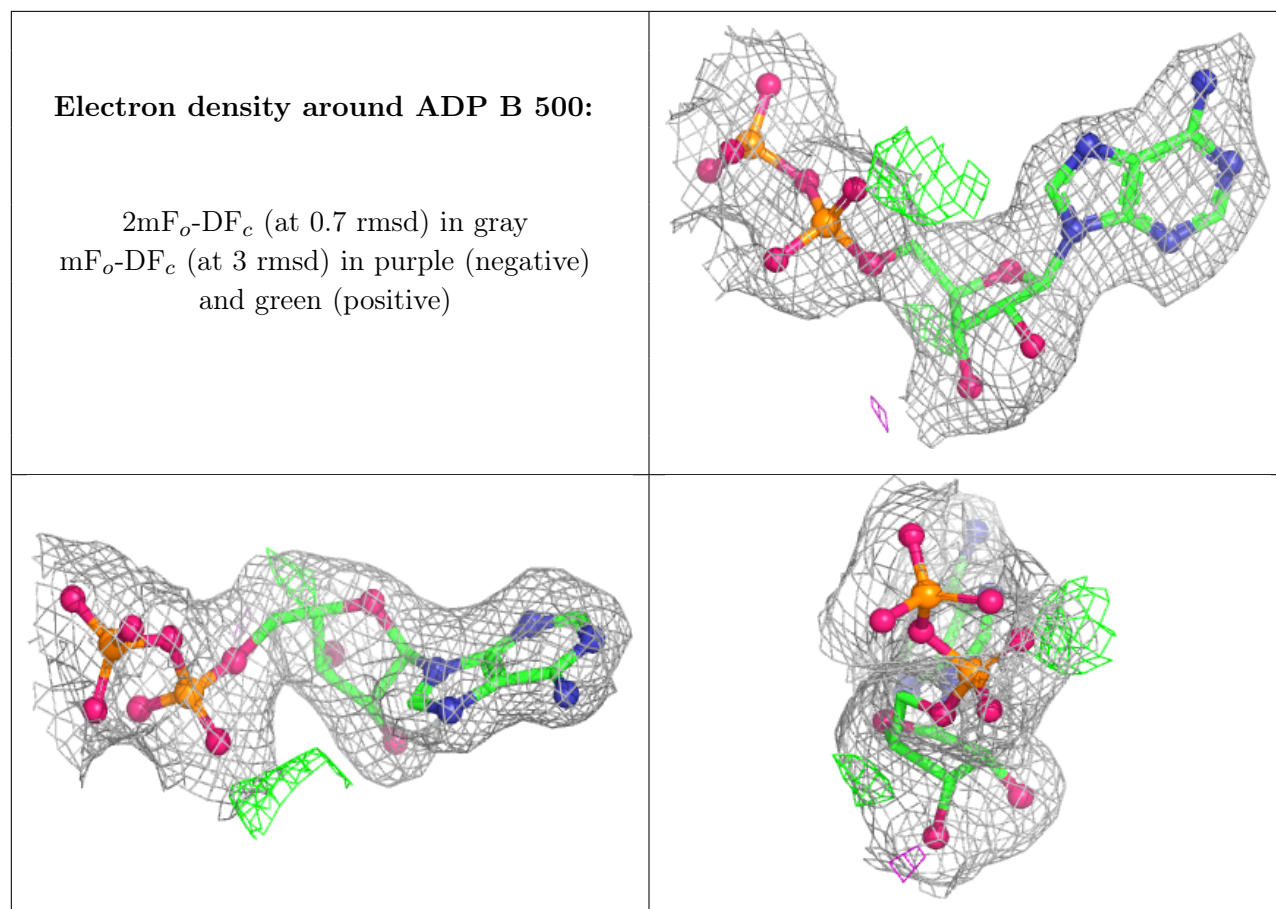
Electron density around ADP A 500:

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

**Electron density around ADP E 500:**

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





6.5 Other polymers ⓘ

There are no such residues in this entry.