Full wwPDB X-ray Structure Validation Report (i)

Aug 26, 2023 – 07:54 PM EDT

PDB ID	:	3EZ2
Title	:	Partition protein-ADP complex
Authors	:	Schumacher, M.A.; Dunham, T.D.; Xu, W.; Funnell, B.
Deposited on	:	2008-10-22
Resolution	:	2.05 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 (i) 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 (i)) were used in the production of this report:

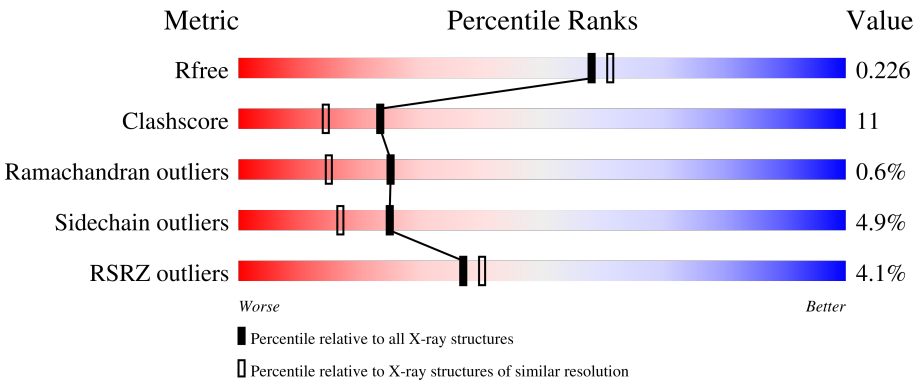
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.35
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.35

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 2.05 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}	130704	1692 (2.04-2.04)
Clashscore	141614	1773 (2.04-2.04)
Ramachandran outliers	138981	1752 (2.04-2.04)
Sidechain outliers	138945	1752 (2.04-2.04)
RSRZ outliers	127900	1672 (2.04-2.04)

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 <=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	398	6% 73% 21%
1	B	398	3% 80% 17%

2 Entry composition (i)

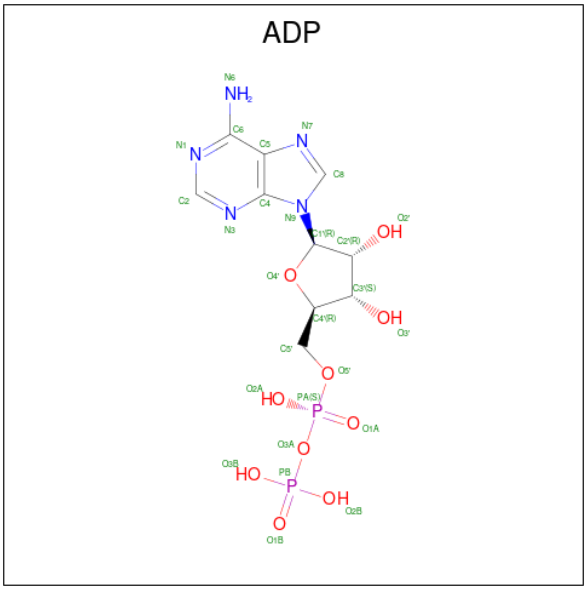
There are 6 unique types of molecules in this entry. The entry contains 6799 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Plasmid partition protein A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	388	3034	1930	517	571	16	0	0	0
1	B	394	3082	1958	526	582	16	0	0	0

- Molecule 2 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2$).

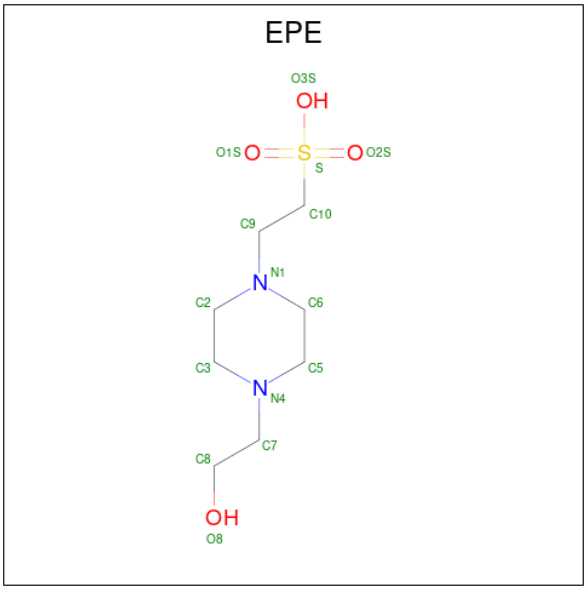


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	27	10	5	10	2	0	0
2	A	1	27	10	5	10	2	0	0
2	B	1	27	10	5	10	2	0	0
2	B	1	27	10	5	10	2	0	0

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

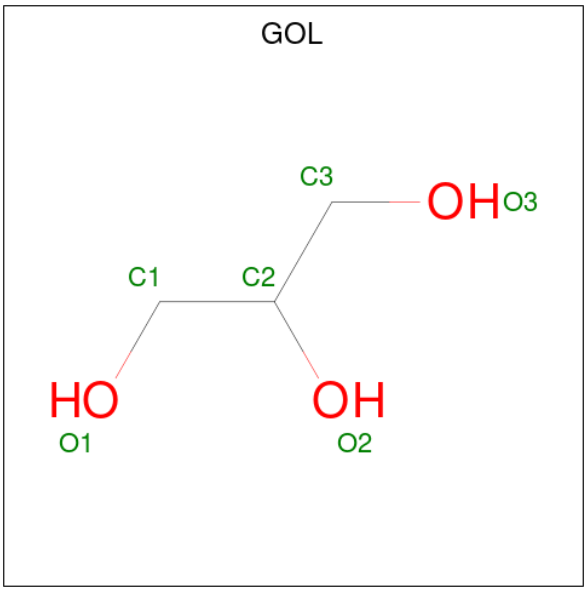
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total Mg 1 1	0	0
3	B	1	Total Mg 1 1	0	0

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: $C_8H_{18}N_2O_4S$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C N O S 15 8 2 4 1	0	0

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
5	B	1	6	3	3	0	0
			Total	C	O		
5	B	1	6	3	3	0	0

- Molecule 6 is water.

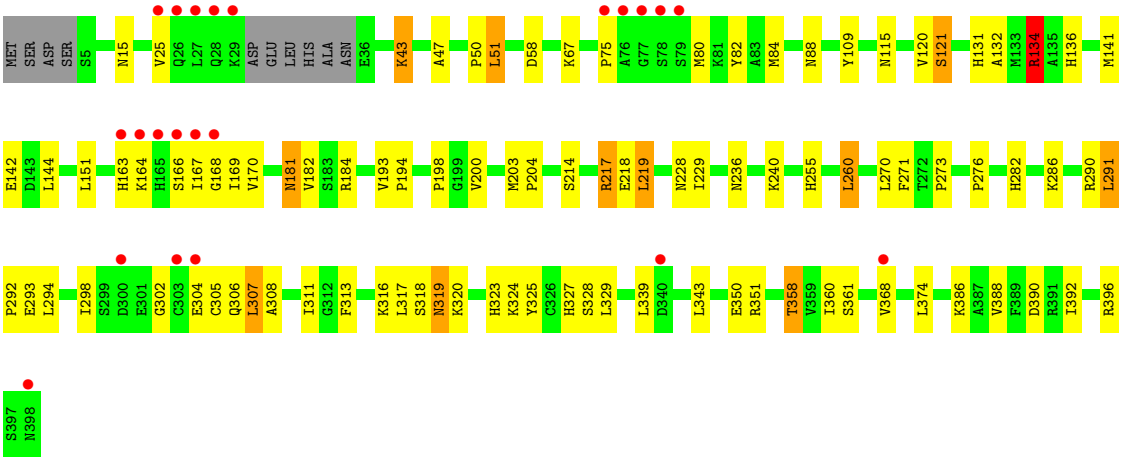
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
6	A	245	245	245	0	0
			Total	O		
6	B	301	301	301	0	0

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.

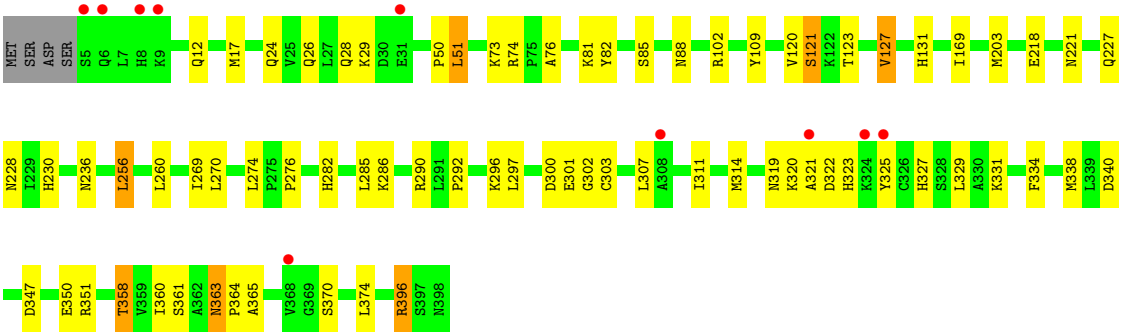
• Molecule 1: Plasmid partition protein A

Chain A: 6% 73% 21%



• Molecule 1: Plasmid partition protein A

Chain B: 3% 80% 17%



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	60.10Å 125.90Å 148.40Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.94 – 2.05 50.94 – 2.05	Depositor EDS
% Data completeness (in resolution range)	98.7 (50.94-2.05) 98.8 (50.94-2.05)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.08	Depositor
$< I/\sigma(I) >$ [1]	2.14 (at 2.05Å)	Xtriage
Refinement program	CNS 1.2	Depositor
R, R_{free}	0.191 , 0.232 0.185 , 0.226	Depositor DCC
R_{free} test set	7162 reflections (10.14%)	wwPDB-VP
Wilson B-factor (Å^2)	29.6	Xtriage
Anisotropy	0.259	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 57.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	6799	wwPDB-VP
Average B, all atoms (Å^2)	36.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.69% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: GOL, ADP, EPE, MG

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	0.58	0/3094	0.75	3/4186 (0.1%)
1	B	0.64	0/3144	0.75	5/4256 (0.1%)
All	All	0.61	0/6238	0.75	8/8442 (0.1%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	134	ARG	NE-CZ-NH1	10.25	125.42	120.30
1	A	134	ARG	NE-CZ-NH2	-8.46	116.07	120.30
1	B	102	ARG	NE-CZ-NH2	-6.97	116.81	120.30
1	B	102	ARG	NE-CZ-NH1	6.56	123.58	120.30
1	B	396	ARG	NE-CZ-NH2	-6.41	117.10	120.30
1	B	396	ARG	NE-CZ-NH1	5.95	123.28	120.30
1	B	203	MET	N-CA-C	-5.34	96.57	111.00
1	A	203	MET	N-CA-C	-5.21	96.95	111.00

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts (i)

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

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3034	0	3028	71	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	B	3082	0	3068	72	0
2	A	54	0	24	0	0
2	B	54	0	24	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	B	15	0	18	4	0
5	B	12	0	16	0	0
6	A	245	0	0	7	0
6	B	301	0	0	8	0
All	All	6799	0	6178	140	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 11.

All (140) 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:A:358:THR:HG22	1:A:361:SER:H	1.16	1.10
1:B:228:ASN:HD21	1:B:302:GLY:HA3	1.18	1.04
1:B:358:THR:HG22	1:B:361:SER:H	1.27	1.00
1:A:228:ASN:HD21	1:A:302:GLY:HA3	1.32	0.92
1:A:131:HIS:ND1	1:A:358:THR:HG21	1.89	0.87
1:B:73:LYS:NZ	4:B:3022:EPE:H51	1.92	0.83
1:B:131:HIS:ND1	1:B:358:THR:HG21	1.93	0.83
1:B:228:ASN:ND2	1:B:302:GLY:HA3	1.94	0.82
1:B:396:ARG:HD2	6:B:626:HOH:O	1.84	0.77
1:B:296:LYS:HE2	1:B:300:ASP:OD1	1.89	0.73
1:A:43:LYS:HE2	1:A:58:ASP:OD2	1.89	0.71
1:A:134:ARG:HG3	1:A:200:VAL:HG23	1.73	0.71
1:A:228:ASN:HD21	1:A:302:GLY:CA	2.02	0.71
1:A:358:THR:CG2	1:A:361:SER:H	1.98	0.70
1:B:73:LYS:HZ2	4:B:3022:EPE:H51	1.54	0.70
1:B:227:GLN:HE22	1:B:236:ASN:HD21	1.39	0.69
1:B:334:PHE:HB2	1:B:338:MET:HG2	1.73	0.68
1:A:368:VAL:HG13	1:A:368:VAL:O	1.94	0.68
1:A:25:VAL:HG11	1:A:169:ILE:HG12	1.76	0.66
1:B:358:THR:HG23	1:B:360:ILE:H	1.60	0.65
1:B:320:LYS:HE2	1:B:322:ASP:HB3	1.78	0.65
1:B:26:GLN:HE22	1:B:169:ILE:H	1.44	0.63
1:A:358:THR:HG22	1:A:361:SER:N	2.01	0.63
1:B:269:ILE:HD11	1:B:311:ILE:HD13	1.80	0.63

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:26:GLN:NE2	1:B:169:ILE:H	1.96	0.62
1:A:329:LEU:HD13	1:B:17:MET:HE1	1.82	0.61
1:B:276:PRO:HB2	1:B:323:HIS:CD2	2.36	0.61
1:A:306:GLN:CD	1:A:306:GLN:H	2.05	0.60
1:B:73:LYS:HZ3	4:B:3022:EPE:H51	1.67	0.59
1:B:303:CYS:HB3	6:B:703:HOH:O	2.02	0.59
1:A:358:THR:HG23	1:A:360:ILE:H	1.66	0.58
1:B:227:GLN:HE22	1:B:236:ASN:ND2	2.00	0.58
1:A:255:HIS:HB2	6:B:404:HOH:O	2.03	0.58
1:A:163:HIS:HB3	1:A:166:SER:OG	2.04	0.57
1:B:363:ASN:HD22	1:B:364:PRO:CD	2.15	0.57
1:A:214:SER:OG	1:B:256:LEU:HD12	2.04	0.57
1:A:193:VAL:HG13	1:A:194:PRO:HD2	1.87	0.57
1:B:363:ASN:HD22	1:B:364:PRO:N	2.03	0.57
1:B:230:HIS:HE2	1:B:301:GLU:HG3	1.71	0.56
1:A:260:LEU:O	1:A:260:LEU:HD13	2.06	0.56
1:A:290:ARG:O	1:A:293:GLU:HB3	2.06	0.55
1:B:307:LEU:HB2	6:B:577:HOH:O	2.05	0.55
1:A:120:VAL:O	1:A:121:SER:CB	2.55	0.55
1:B:274:LEU:CD1	1:B:314:MET:HE1	2.37	0.55
1:A:167:ILE:HD12	1:A:168:GLY:O	2.07	0.55
1:B:228:ASN:ND2	1:B:302:GLY:CA	2.68	0.55
1:A:270:LEU:HG	1:A:307:LEU:HD11	1.90	0.54
1:A:236:ASN:N	1:A:236:ASN:HD22	2.04	0.54
1:B:85:SER:H	1:B:88:ASN:HD22	1.57	0.53
1:B:228:ASN:HD21	1:B:302:GLY:CA	2.07	0.53
1:B:363:ASN:ND2	1:B:365:ALA:H	2.07	0.53
1:A:217:ARG:NH1	1:A:229:ILE:HD13	2.24	0.53
1:A:396:ARG:HD2	6:A:403:HOH:O	2.08	0.53
1:A:170:VAL:HG11	1:A:204:PRO:HG2	1.91	0.52
1:A:169:ILE:HA	6:A:533:HOH:O	2.09	0.52
1:B:270:LEU:HG	1:B:307:LEU:HD22	1.91	0.52
1:A:50:PRO:O	1:A:51:LEU:HB2	2.09	0.51
1:A:319:ASN:ND2	1:A:324:LYS:CE	2.73	0.51
1:A:228:ASN:ND2	1:A:302:GLY:CA	2.73	0.51
1:A:182:VAL:O	1:A:240:LYS:NZ	2.42	0.51
1:B:286:LYS:O	1:B:290:ARG:HG2	2.11	0.51
1:A:319:ASN:HD22	1:A:324:LYS:HE3	1.75	0.51
1:B:274:LEU:HB2	1:B:314:MET:HE1	1.93	0.51
1:B:363:ASN:HD22	1:B:363:ASN:C	2.14	0.50
1:B:109:TYR:CE2	1:B:396:ARG:HD3	2.46	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:ARG:HG3	1:A:217:ARG:HH11	1.75	0.50
1:A:218:GLU:H	1:A:218:GLU:CD	2.14	0.49
1:B:350:GLU:HG3	2:B:502:ADP:C2	2.48	0.49
1:B:292:PRO:HG2	6:B:484:HOH:O	2.13	0.49
1:A:75:PRO:HA	1:A:80:MET:HG3	1.95	0.49
1:A:294:LEU:O	1:A:298:ILE:HG12	2.13	0.49
1:B:274:LEU:HD12	1:B:314:MET:HE1	1.94	0.48
1:B:363:ASN:HD22	1:B:364:PRO:HD2	1.78	0.48
1:A:47:ALA:O	6:A:400:HOH:O	2.20	0.48
1:B:26:GLN:O	1:B:29:LYS:HG2	2.14	0.47
1:B:120:VAL:O	1:B:121:SER:CB	2.62	0.47
1:A:317:LEU:HD13	1:A:318:SER:N	2.29	0.47
1:A:270:LEU:HG	1:A:307:LEU:HD21	1.96	0.47
1:B:85:SER:H	1:B:88:ASN:ND2	2.12	0.47
1:B:73:LYS:C	1:B:74:ARG:HG2	2.36	0.47
1:A:271:PHE:CD2	1:A:311:ILE:HB	2.50	0.46
1:A:329:LEU:HD13	1:B:17:MET:CE	2.45	0.46
1:A:386:LYS:HE2	1:A:390:ASP:OD1	2.15	0.46
1:B:82:TYR:CD1	4:B:3022:EPE:H101	2.51	0.46
1:A:109:TYR:CE2	1:A:396:ARG:HD3	2.50	0.46
1:B:340:ASP:HB2	6:B:687:HOH:O	2.15	0.46
1:A:319:ASN:HD22	1:A:324:LYS:CE	2.29	0.46
1:B:218:GLU:H	1:B:218:GLU:CD	2.20	0.46
1:A:167:ILE:HB	1:A:170:VAL:HG22	1.97	0.46
1:A:236:ASN:N	1:A:236:ASN:ND2	2.64	0.46
1:A:291:LEU:N	1:A:292:PRO:HD2	2.31	0.45
1:B:50:PRO:O	1:B:51:LEU:HB2	2.16	0.45
1:A:50:PRO:HB2	1:A:141:MET:HE1	1.97	0.45
1:A:219:LEU:HD12	1:A:219:LEU:HA	1.85	0.45
1:B:314:MET:HE3	1:B:338:MET:CE	2.47	0.45
1:A:82:TYR:HD2	1:A:84:MET:HE3	1.82	0.45
1:B:350:GLU:HG3	2:B:502:ADP:H2	1.80	0.45
1:B:274:LEU:HD12	1:B:314:MET:CE	2.46	0.45
1:B:297:LEU:O	1:B:301:GLU:HG2	2.17	0.45
1:A:167:ILE:HD12	1:A:168:GLY:N	2.32	0.44
1:A:292:PRO:HG2	6:A:484:HOH:O	2.16	0.44
1:A:25:VAL:HG11	1:A:169:ILE:CG1	2.44	0.44
1:A:273:PRO:HB3	1:A:313:PHE:CZ	2.52	0.44
1:A:276:PRO:HB2	1:A:323:HIS:CG	2.53	0.44
1:B:276:PRO:HB2	1:B:323:HIS:CG	2.53	0.44
1:B:230:HIS:NE2	1:B:301:GLU:HG3	2.32	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:325:TYR:CE2	1:B:329:LEU:HD11	2.53	0.44
1:A:181:ASN:ND2	1:A:240:LYS:HZ2	2.16	0.43
1:A:316:LYS:HD3	6:A:832:HOH:O	2.17	0.43
1:B:331:LYS:NZ	6:B:879:HOH:O	2.51	0.43
1:A:350:GLU:HG2	6:A:499:HOH:O	2.19	0.43
1:B:314:MET:HE2	1:B:314:MET:N	2.33	0.43
1:A:84:MET:HA	1:A:88:ASN:HD22	1.83	0.43
1:B:396:ARG:CD	6:B:626:HOH:O	2.55	0.43
1:A:170:VAL:HG11	1:A:204:PRO:CG	2.49	0.43
1:A:282:HIS:CE1	1:A:286:LYS:HE3	2.54	0.43
1:B:76:ALA:HB3	1:B:81:LYS:HG3	2.01	0.42
1:B:320:LYS:HG2	1:B:321:ALA:N	2.33	0.42
1:B:109:TYR:CD2	1:B:396:ARG:HD3	2.54	0.42
1:A:181:ASN:ND2	1:A:240:LYS:NZ	2.68	0.42
1:B:230:HIS:HE2	1:B:301:GLU:CG	2.30	0.42
1:B:260:LEU:O	1:B:260:LEU:HD23	2.19	0.42
1:A:134:ARG:HD2	1:A:198:PRO:O	2.19	0.42
1:B:297:LEU:O	1:B:297:LEU:HD12	2.20	0.42
1:A:388:VAL:O	1:A:392:ILE:HG13	2.20	0.42
1:A:132:ALA:O	1:A:136:HIS:HB2	2.20	0.42
1:A:184:ARG:HG3	1:A:240:LYS:O	2.19	0.42
1:B:282:HIS:NE2	1:B:286:LYS:HE3	2.35	0.42
1:B:358:THR:CG2	1:B:360:ILE:H	2.31	0.42
1:A:109:TYR:CD2	1:A:396:ARG:HD3	2.54	0.41
1:A:305:CYS:C	1:A:307:LEU:H	2.23	0.41
1:B:347:ASP:O	1:B:351:ARG:HG3	2.21	0.41
1:B:358:THR:CG2	1:B:361:SER:H	2.14	0.41
1:B:256:LEU:HA	1:B:256:LEU:HD22	1.88	0.41
1:B:285:LEU:HD23	1:B:285:LEU:HA	1.86	0.41
1:A:343:LEU:HD23	6:A:536:HOH:O	2.21	0.41
1:A:325:TYR:O	1:A:328:SER:HB2	2.21	0.41
1:A:368:VAL:O	1:A:368:VAL:CG1	2.65	0.41
1:B:123:THR:O	1:B:127:VAL:HB	2.21	0.41
1:B:24:GLN:O	1:B:28:GLN:HG3	2.22	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	384/398 (96%)	364 (95%)	16 (4%)	4 (1%)	15 6
1	B	392/398 (98%)	375 (96%)	16 (4%)	1 (0%)	41 31
All	All	776/796 (98%)	739 (95%)	32 (4%)	5 (1%)	25 15

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	121	SER
1	A	121	SER
1	A	308	ALA
1	A	115	ASN
1	A	164	LYS

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	331/341 (97%)	309 (93%)	22 (7%)	16 9
1	B	336/341 (98%)	325 (97%)	11 (3%)	38 31
All	All	667/682 (98%)	634 (95%)	33 (5%)	25 17

All (33) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	15	ASN

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Mol	Chain	Res	Type
1	A	43	LYS
1	A	51	LEU
1	A	67	LYS
1	A	134	ARG
1	A	142	GLU
1	A	144	LEU
1	A	151	LEU
1	A	181	ASN
1	A	217	ARG
1	A	219	LEU
1	A	260	LEU
1	A	291	LEU
1	A	304	GLU
1	A	307	LEU
1	A	319	ASN
1	A	320	LYS
1	A	327	HIS
1	A	339	LEU
1	A	351	ARG
1	A	358	THR
1	A	374	LEU
1	B	12	GLN
1	B	51	LEU
1	B	127	VAL
1	B	221	ASN
1	B	256	LEU
1	B	319	ASN
1	B	327	HIS
1	B	358	THR
1	B	363	ASN
1	B	370	SER
1	B	374	LEU

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	12	GLN
1	A	15	ASN
1	A	39	GLN
1	A	88	ASN
1	A	138	HIS
1	A	163	HIS

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Mol	Chain	Res	Type
1	A	181	ASN
1	A	227	GLN
1	A	228	ASN
1	A	236	ASN
1	A	282	HIS
1	A	319	ASN
1	A	398	ASN
1	B	26	GLN
1	B	88	ASN
1	B	221	ASN
1	B	236	ASN
1	B	319	ASN
1	B	363	ASN
1	B	376	ASN

5.3.3 RNA (i)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains (i)

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

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 9 ligands modelled in this entry, 2 are monoatomic - leaving 7 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	EPE	B	3022	-	15,15,15	1.26	1 (6%)	18,20,20	1.61	3 (16%)
5	GOL	B	445	-	5,5,5	0.29	0	5,5,5	0.41	0
2	ADP	A	501	3	24,29,29	2.18	8 (33%)	29,45,45	2.28	7 (24%)
2	ADP	A	509	-	24,29,29	2.06	6 (25%)	29,45,45	2.20	10 (34%)
2	ADP	B	502	3	24,29,29	2.00	6 (25%)	29,45,45	2.25	6 (20%)
5	GOL	B	545	-	5,5,5	0.42	0	5,5,5	0.32	0
2	ADP	B	507	-	24,29,29	2.08	5 (20%)	29,45,45	2.21	10 (34%)

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	EPE	B	3022	-	-	0/9/19/19	0/1/1/1
5	GOL	B	445	-	-	0/4/4/4	-
2	ADP	A	501	3	-	0/12/32/32	0/3/3/3
2	ADP	A	509	-	-	1/12/32/32	0/3/3/3
2	ADP	B	502	3	-	0/12/32/32	0/3/3/3
5	GOL	B	545	-	-	0/4/4/4	-
2	ADP	B	507	-	-	2/12/32/32	0/3/3/3

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	509	ADP	C4-N3	6.44	1.44	1.35
2	B	507	ADP	C4-N3	6.24	1.44	1.35
2	A	501	ADP	C4-N3	6.01	1.43	1.35
2	B	507	ADP	C2-N3	4.94	1.40	1.32
2	A	501	ADP	C2-N3	4.50	1.39	1.32
2	A	509	ADP	C2-N3	4.28	1.39	1.32
2	B	502	ADP	C4-N3	4.19	1.41	1.35
2	B	502	ADP	C2-N3	4.18	1.38	1.32
4	B	3022	EPE	C10-S	3.77	1.82	1.77
2	A	501	ADP	O4'-C1'	3.51	1.46	1.41
2	B	502	ADP	C2'-C1'	-3.39	1.48	1.53
2	A	509	ADP	PB-O3B	3.17	1.67	1.54
2	B	507	ADP	PB-O3B	3.15	1.67	1.54
2	B	502	ADP	O4'-C1'	3.11	1.45	1.41
2	A	501	ADP	C8-N7	-3.00	1.29	1.34
2	B	502	ADP	PB-O3B	2.71	1.65	1.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	501	ADP	C2-N1	2.67	1.38	1.33
2	B	507	ADP	O4'-C1'	2.51	1.44	1.41
2	A	501	ADP	PB-O2B	-2.51	1.45	1.54
2	A	509	ADP	O4'-C1'	2.45	1.44	1.41
2	B	502	ADP	C8-N7	-2.32	1.30	1.34
2	A	509	ADP	C2-N1	2.23	1.38	1.33
2	A	509	ADP	PB-O2B	-2.23	1.46	1.54
2	B	507	ADP	PB-O2B	-2.22	1.46	1.54
2	A	501	ADP	C3'-C4'	2.05	1.58	1.53
2	A	501	ADP	PA-O2A	-2.05	1.45	1.55

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	501	ADP	O2B-PB-O1B	6.80	137.31	110.68
2	B	502	ADP	O2B-PB-O1B	6.55	136.33	110.68
2	B	507	ADP	O2B-PB-O1B	5.92	133.85	110.68
2	A	509	ADP	O2B-PB-O1B	5.91	133.82	110.68
4	B	3022	EPE	O1S-S-C10	5.07	113.03	106.92
2	B	502	ADP	O3A-PB-O1B	-5.05	83.16	111.19
2	A	509	ADP	O3A-PB-O1B	-4.96	83.68	111.19
2	B	507	ADP	O3A-PB-O1B	-4.91	83.95	111.19
2	A	501	ADP	C3'-C2'-C1'	4.48	107.73	100.98
2	B	507	ADP	C3'-C2'-C1'	4.46	107.70	100.98
2	A	501	ADP	O3A-PB-O1B	-4.45	86.51	111.19
2	A	509	ADP	C3'-C2'-C1'	4.32	107.48	100.98
2	B	502	ADP	O2B-PB-O3A	-3.94	91.42	104.64
2	A	501	ADP	O2B-PB-O3A	-3.85	91.72	104.64
2	B	502	ADP	O4'-C1'-C2'	-3.84	101.31	106.93
2	B	507	ADP	O2B-PB-O3A	-3.63	92.46	104.64
2	B	502	ADP	C3'-C2'-C1'	3.60	106.39	100.98
2	A	509	ADP	O2B-PB-O3A	-3.46	93.03	104.64
2	A	501	ADP	O4'-C1'-C2'	-2.95	102.61	106.93
2	A	501	ADP	O3B-PB-O3A	-2.95	94.76	104.64
2	A	509	ADP	O3B-PB-O3A	-2.87	95.03	104.64
2	B	507	ADP	C1'-N9-C4	-2.77	121.78	126.64
2	A	509	ADP	C1'-N9-C4	-2.72	121.86	126.64
2	B	507	ADP	O3B-PB-O3A	-2.69	95.62	104.64
2	B	507	ADP	C4-C5-N7	2.52	112.03	109.40
2	B	507	ADP	PA-O3A-PB	2.44	141.21	132.83
2	B	507	ADP	N3-C2-N1	-2.40	124.93	128.68
2	A	509	ADP	PA-O3A-PB	2.37	140.95	132.83

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	509	ADP	O4'-C1'-C2'	-2.36	103.47	106.93
2	A	509	ADP	N3-C2-N1	-2.31	125.07	128.68
4	B	3022	EPE	O3S-S-O2S	-2.29	105.67	111.27
2	A	509	ADP	C4-C5-N7	2.24	111.74	109.40
4	B	3022	EPE	O3S-S-O1S	-2.18	105.95	111.27
2	A	501	ADP	C4-C5-N7	2.17	111.66	109.40
2	B	507	ADP	O4'-C1'-C2'	-2.17	103.75	106.93
2	B	502	ADP	C4-C5-N7	2.09	111.57	109.40

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	507	ADP	O4'-C4'-C5'-O5'
2	A	509	ADP	O4'-C4'-C5'-O5'
2	B	507	ADP	C4'-C5'-O5'-PA

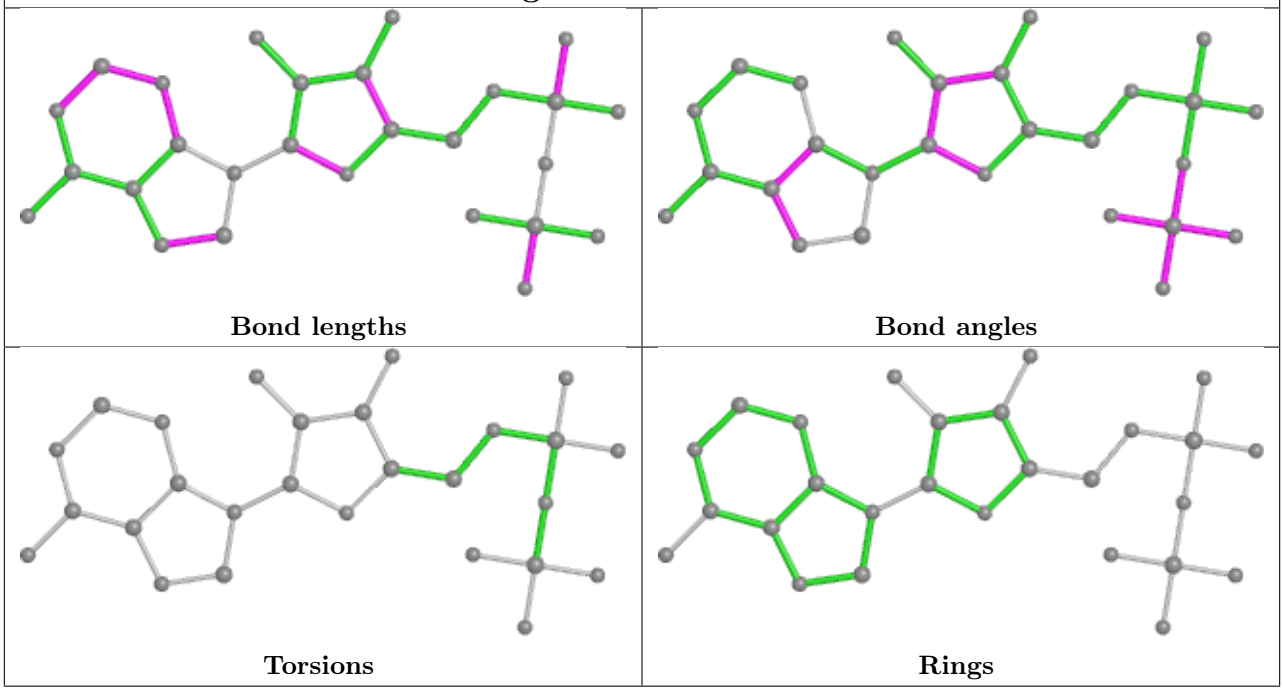
There are no ring outliers.

2 monomers are involved in 6 short contacts:

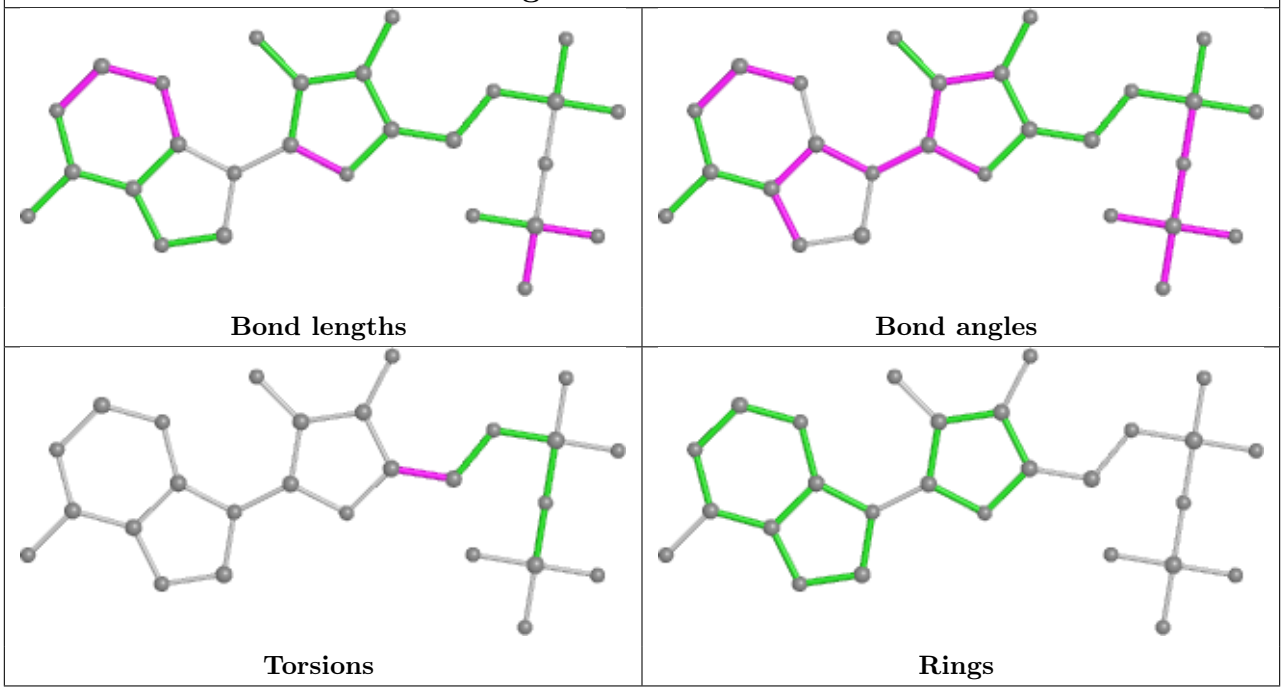
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	3022	EPE	4	0
2	B	502	ADP	2	0

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 then 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.

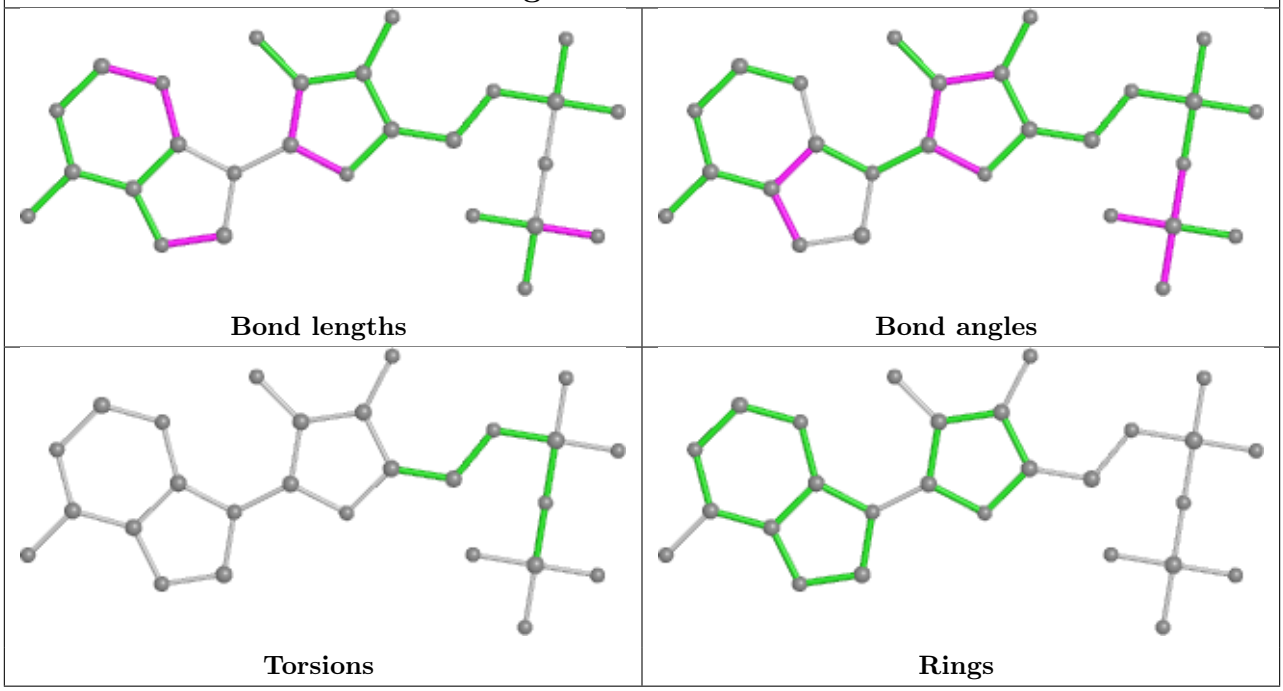
Ligand ADP A 501



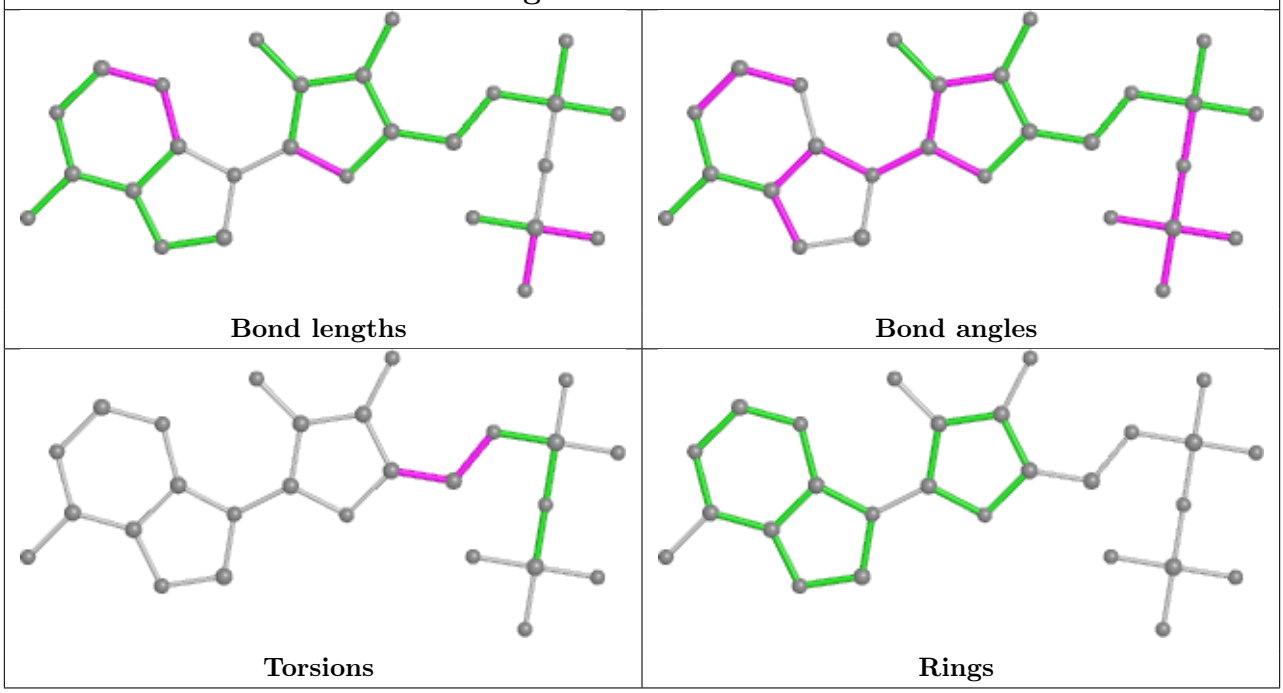
Ligand ADP A 509



Ligand ADP B 502



Ligand ADP B 507



5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.

6 Fit of model and data (i)

6.1 Protein, DNA and RNA chains (i)

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 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	388/398 (97%)	-0.07	22 (5%)	23	25	17, 33, 76, 109	0
1	B	394/398 (98%)	-0.25	10 (2%)	57	61	15, 29, 62, 91	0
All	All	782/796 (98%)	-0.16	32 (4%)	37	40	15, 31, 68, 109	0

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	27	LEU	6.2
1	A	164	LYS	6.0
1	A	76	ALA	5.9
1	A	77	GLY	5.4
1	A	79	SER	5.0
1	B	321	ALA	4.7
1	A	28	GLN	4.2
1	A	165	HIS	4.2
1	B	325	TYR	3.5
1	A	167	ILE	3.4
1	B	6	GLN	3.3
1	A	78	SER	3.3
1	B	5	SER	3.2
1	B	324	LYS	3.2
1	A	168	GLY	3.1
1	A	163	HIS	2.9
1	A	368	VAL	2.9
1	A	25	VAL	2.7
1	A	166	SER	2.6
1	B	368	VAL	2.6
1	B	31	GLU	2.5
1	A	75	PRO	2.5
1	A	29	LYS	2.4
1	A	26	GLN	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	398	ASN	2.3
1	A	303	CYS	2.3
1	A	340	ASP	2.3
1	B	8	HIS	2.2
1	B	9	LYS	2.2
1	A	304	GLU	2.2
1	A	300	ASP	2.1
1	B	308	ALA	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 monosaccharides in this entry.

6.4 Ligands (i)

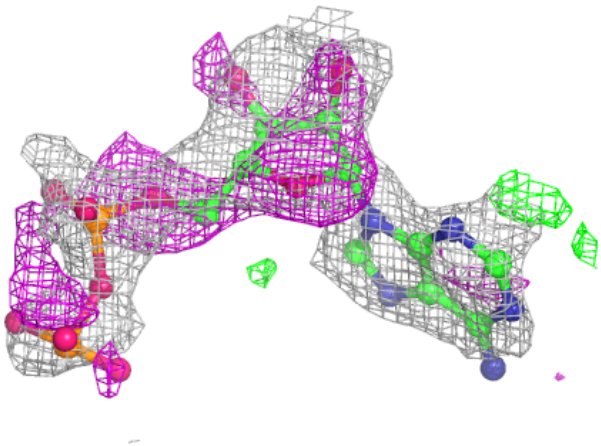
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

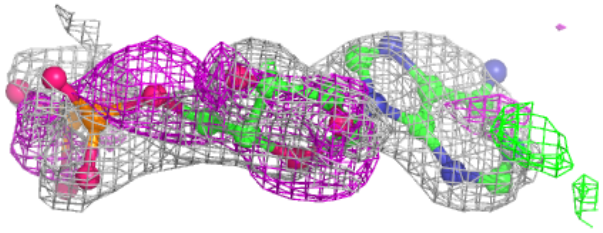
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	ADP	A	509	27/27	0.62	0.37	36,73,131,131	0
2	ADP	B	507	27/27	0.71	0.22	36,53,116,119	0
5	GOL	B	545	6/6	0.71	0.15	51,61,63,66	0
5	GOL	B	445	6/6	0.86	0.17	44,51,54,65	0
4	EPE	B	3022	15/15	0.88	0.28	30,80,89,93	0
3	MG	A	399	1/1	0.91	0.23	29,29,29,29	0
2	ADP	A	501	27/27	0.96	0.13	19,29,36,36	0
2	ADP	B	502	27/27	0.97	0.11	20,26,32,33	0
3	MG	B	399	1/1	0.99	0.18	26,26,26,26	0

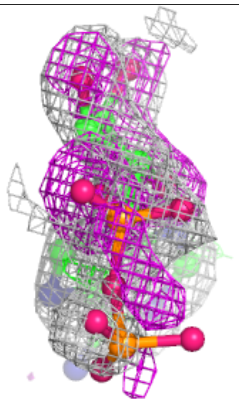
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around ADP A 509:

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

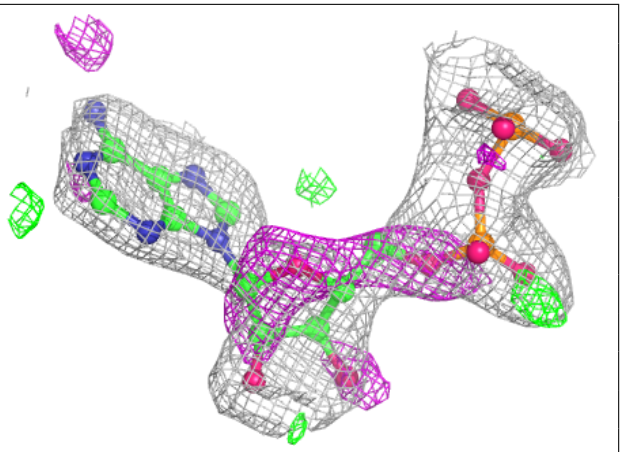


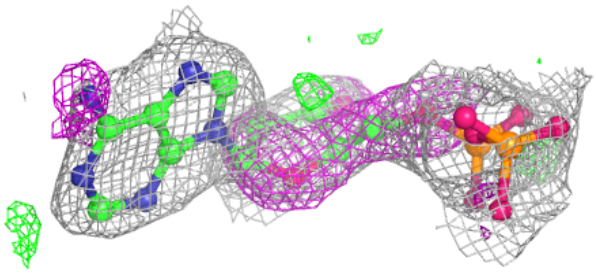


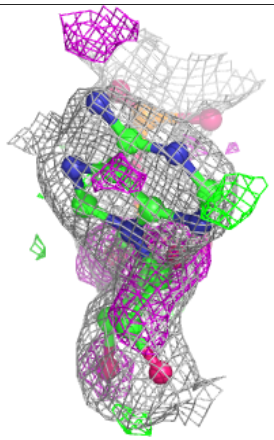


Electron density around ADP B 507:

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

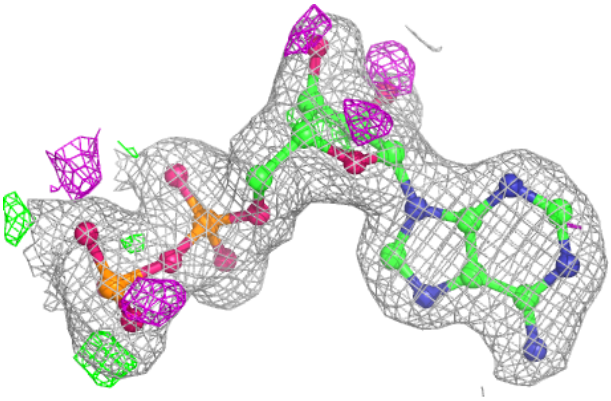


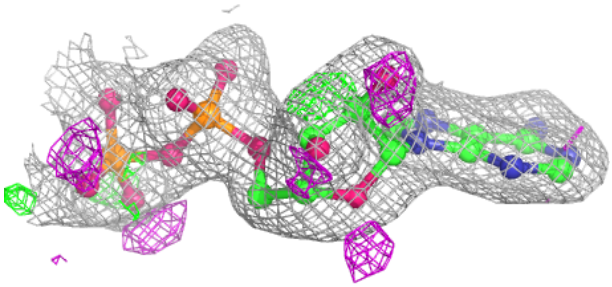




Electron density around ADP A 501:

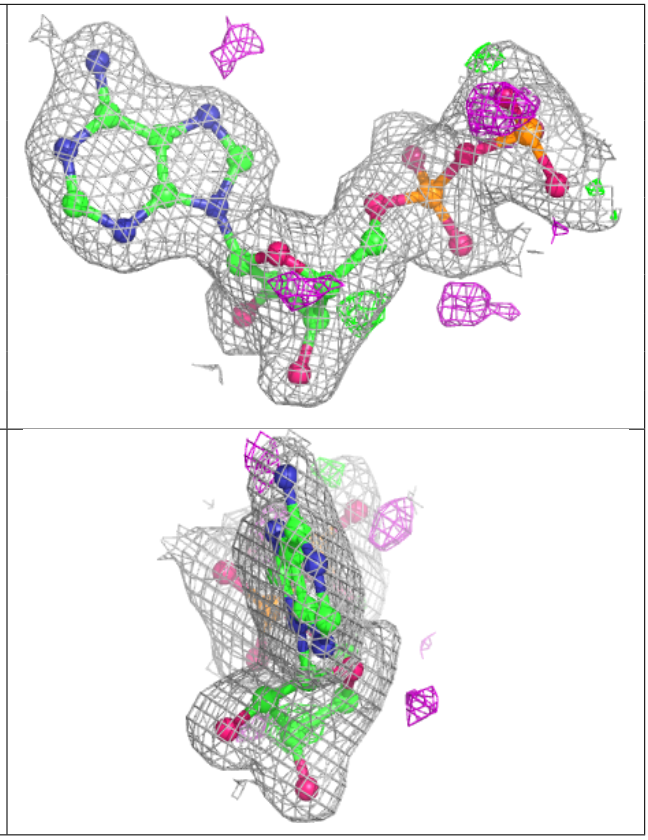
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





Electron density around ADP B 502:

$2mF_o$-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.