



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 13, 2026 – 11:13 PM UTC

PDB ID : 1FBP / pdb_00001fbp
Title : CRYSTAL STRUCTURE OF FRUCTOSE-1,6-BISPHOSPHATASE COM-
PLEXED WITH FRUCTOSE 6-PHOSPHATE, AMP, AND MAGNESIUM
Authors : Ke, H.; Zhang, Y.; Lipscomb, W.N.
Deposited on : 1990-05-31
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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

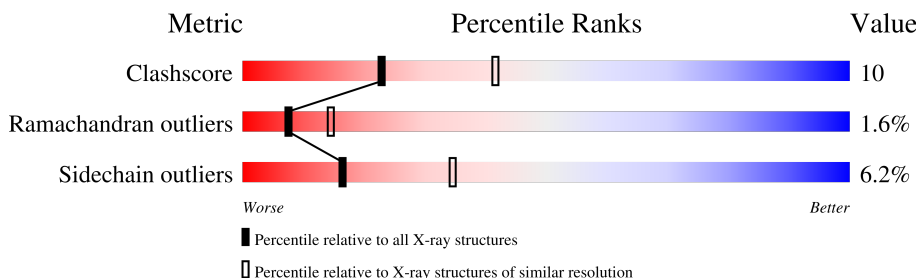
1 Overall quality at a glance

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))
Clashscore	190562	6492 (2.50-2.50)
Ramachandran outliers	187476	6378 (2.50-2.50)
Sidechain outliers	187428	6380 (2.50-2.50)

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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	335	
1	B	335	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	F6P	A	336	-	-	X	-

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 6016 atoms, of which 1076 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.

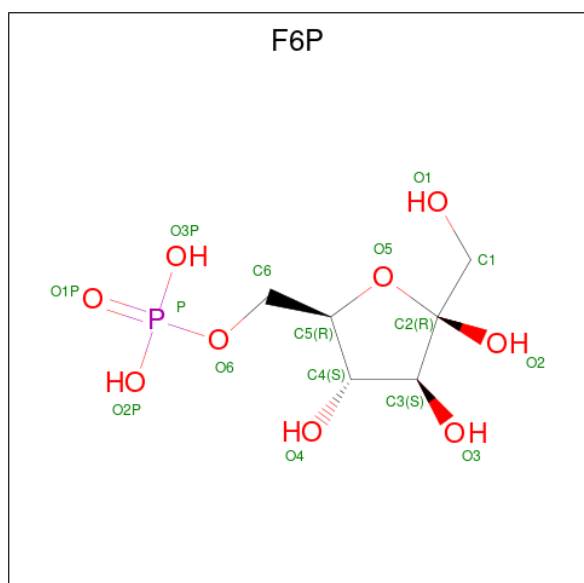
- Molecule 1 is a protein called FRUCTOSE 1,6-BISPHOSPHATASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	317	Total	C	H	N	O	S	0	0	1
			2968	1546	538	409	460	15			
1	B	317	Total	C	H	N	O	S	0	0	1
			2968	1546	538	409	460	15			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	GLN	GLU	conflict	UNP P00636
A	96	THR	SER	conflict	UNP P00636
A	199	ASN	ASP	conflict	UNP P00636
B	20	GLN	GLU	conflict	UNP P00636
B	96	THR	SER	conflict	UNP P00636
B	199	ASN	ASP	conflict	UNP P00636

- Molecule 2 is 6-O-phosphono-beta-D-fructofuranose (CCD ID: F6P) (formula: $C_6H_{13}O_9P$).

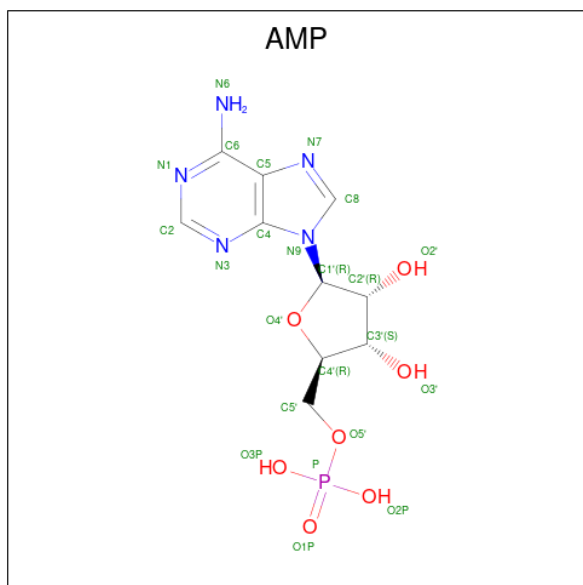


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	O	P	0	0
			16	6	9	1		
2	B	1	Total	C	O	P	0	0
			16	6	9	1		

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

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

- Molecule 4 is ADENOSINE MONOPHOSPHATE (CCD ID: AMP) (formula: C₁₀H₁₄N₅O₇P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			23	10	5	7	1		
4	B	1	Total	C	N	O	P	0	0
			23	10	5	7	1		

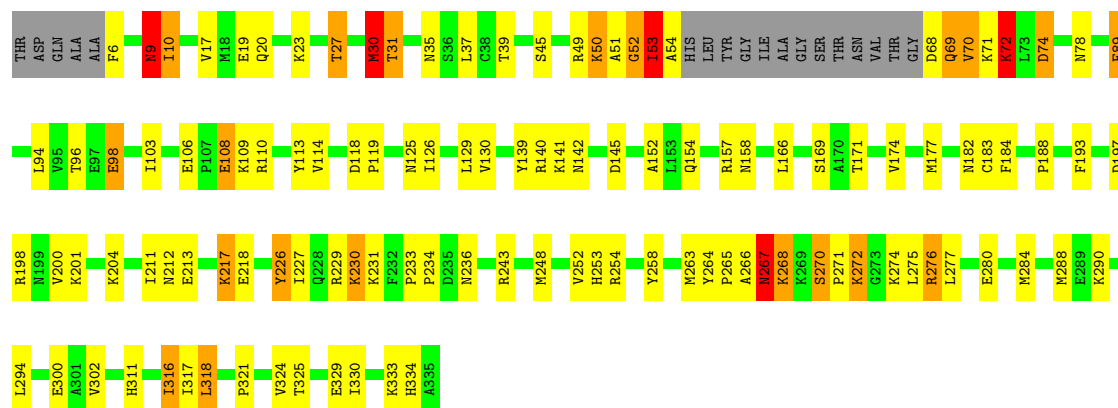
3 Residue-property plots

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. 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. 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.

Note EDS was not executed.

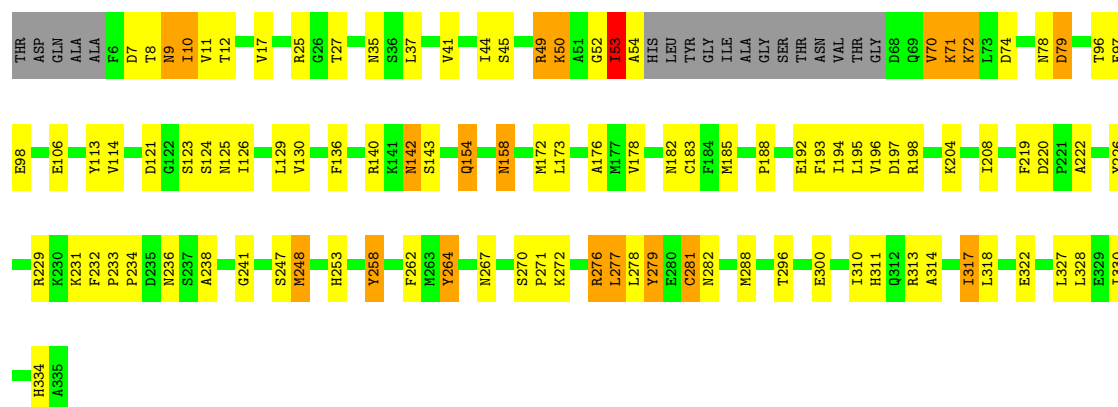
• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATASE

Chain A: 



• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATASE

Chain B: 



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	61.60Å 166.60Å 80.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	(Not available) – 2.50	Depositor
% Data completeness (in resolution range)	(Not available) ((Not available)-2.50)	Depositor
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR	Depositor
R, R_{free}	0.215 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	6016	wwPDB-VP
Average B, all atoms (Å ²)	21.0	wwPDB-VP

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MG, AMP, F6P

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	0.93	7/2470 (0.3%)	1.79	46/3339 (1.4%)
1	B	0.93	5/2470 (0.2%)	1.80	49/3339 (1.5%)
All	All	0.93	12/4940 (0.2%)	1.79	95/6678 (1.4%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	5
1	B	0	3
All	All	0	8

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	53	ILE	C-N	-7.29	1.23	1.33
1	B	53	ILE	C-N	-6.98	1.23	1.33
1	B	311	HIS	CD2-NE2	-6.35	1.30	1.37
1	A	311	HIS	CD2-NE2	-6.32	1.30	1.37
1	A	334	HIS	CG-ND1	-5.51	1.32	1.38
1	B	253	HIS	CD2-NE2	-5.36	1.31	1.37
1	A	253	HIS	CD2-NE2	-5.34	1.31	1.37
1	B	334	HIS	CD2-NE2	-5.26	1.32	1.37
1	B	253	HIS	CG-ND1	-5.24	1.32	1.38
1	A	334	HIS	CD2-NE2	-5.13	1.32	1.37
1	A	317	ILE	CA-CB	5.12	1.61	1.54
1	A	311	HIS	CG-ND1	-5.07	1.32	1.38

All (95) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	272	LYS	N-CA-C	-12.69	96.48	112.72
1	A	254	ARG	NE-CZ-NH2	-8.90	111.19	119.20
1	A	267	ASN	CA-CB-CG	8.81	121.41	112.60
1	A	50	LYS	N-CA-C	-8.59	90.05	107.41
1	A	6	PHE	N-CA-C	-7.96	88.70	111.00
1	B	248	MET	CG-SD-CE	-7.94	83.43	100.90
1	B	50	LYS	N-CA-C	-7.76	103.42	113.12
1	B	154	GLN	OE1-CD-NE2	-7.35	115.25	122.60
1	B	281	CYS	N-CA-C	7.30	118.88	111.07
1	B	98	GLU	N-CA-C	7.23	121.20	112.38
1	A	174	VAL	N-CA-C	-7.18	98.06	108.11
1	A	142	ASN	OD1-CG-ND2	-7.18	115.42	122.60
1	B	7	ASP	N-CA-C	7.13	119.95	109.69
1	B	258	TYR	N-CA-CB	-7.04	101.17	110.88
1	B	49	ARG	NE-CZ-NH2	-7.00	112.90	119.20
1	B	238	ALA	N-CA-C	-6.90	101.38	109.93
1	A	317	ILE	N-CA-C	-6.89	97.52	107.78
1	B	220	ASP	CA-CB-CG	6.82	119.42	112.60
1	A	27	THR	CA-CB-OG1	-6.79	99.42	109.60
1	A	10	ILE	N-CA-C	6.71	123.29	109.34
1	A	70	VAL	N-CA-C	-6.67	95.46	109.34
1	A	110	ARG	N-CA-C	6.50	119.71	109.96
1	A	9	ASN	OD1-CG-ND2	-6.43	116.17	122.60
1	A	98	GLU	N-CA-C	6.39	120.34	112.54
1	B	125	ASN	OD1-CG-ND2	-6.38	116.22	122.60
1	A	158	ASN	CA-CB-CG	6.37	118.97	112.60
1	B	282	ASN	OD1-CG-ND2	-6.37	116.23	122.60
1	A	277	LEU	N-CA-C	6.27	117.91	111.14
1	B	219	PHE	CA-CB-CG	6.27	120.07	113.80
1	B	10	ILE	CB-CA-C	6.26	118.75	111.55
1	A	145	ASP	N-CA-C	6.24	118.35	110.24
1	A	53	ILE	CB-CA-C	-6.20	99.20	111.60
1	A	52	GLY	CA-C-N	6.16	132.78	121.70
1	A	52	GLY	C-N-CA	6.16	132.78	121.70
1	B	276	ARG	CA-CB-CG	-6.15	101.80	114.10
1	A	39	THR	CA-CB-OG1	-6.13	100.40	109.60
1	A	53	ILE	N-CA-CB	6.12	121.90	111.50
1	B	317	ILE	N-CA-C	-6.10	98.74	107.77
1	B	314	ALA	CA-C-N	5.95	126.29	119.92
1	B	314	ALA	C-N-CA	5.95	126.29	119.92
1	A	154	GLN	OE1-CD-NE2	-5.94	116.66	122.60
1	B	154	GLN	CG-CD-NE2	5.92	125.28	116.40
1	A	268	LYS	CB-CG-CD	-5.89	97.74	111.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	72	LYS	N-CA-C	-5.86	106.05	113.43
1	A	27	THR	CA-CB-CG2	5.84	120.43	110.50
1	B	282	ASN	CA-C-O	-5.81	113.03	118.73
1	B	158	ASN	CA-CB-CG	5.74	118.34	112.60
1	B	247	SER	N-CA-C	-5.74	98.74	108.26
1	B	277	LEU	N-CA-C	5.74	117.21	111.07
1	B	272	LYS	N-CA-C	-5.73	105.60	112.59
1	A	53	ILE	CA-CB-CG2	-5.69	100.82	110.50
1	A	9	ASN	CB-CG-ND2	5.69	124.94	116.40
1	B	44	ILE	N-CA-C	-5.64	104.86	111.00
1	B	142	ASN	OD1-CG-ND2	-5.63	116.97	122.60
1	A	30	MET	CA-CB-CG	-5.62	102.87	114.10
1	A	37	LEU	N-CA-CB	5.51	118.22	110.12
1	B	35	ASN	OD1-CG-ND2	-5.49	117.11	122.60
1	A	31	THR	CA-CB-OG1	-5.44	101.43	109.60
1	B	121	ASP	O-C-N	5.42	129.51	122.89
1	B	262	PHE	N-CA-C	-5.39	100.23	109.24
1	B	53	ILE	CB-CA-C	-5.39	100.81	111.60
1	A	108	GLU	CB-CA-C	-5.39	101.69	110.85
1	A	158	ASN	OD1-CG-ND2	-5.35	117.25	122.60
1	B	97	GLU	CB-CG-CD	5.35	121.69	112.60
1	A	140	ARG	N-CA-C	-5.32	101.79	110.20
1	A	35	ASN	OD1-CG-ND2	-5.27	117.33	122.60
1	A	37	LEU	CB-CA-C	-5.25	102.08	110.79
1	A	290	LYS	CA-C-O	-5.20	114.22	120.10
1	B	236	ASN	OD1-CG-ND2	-5.18	117.42	122.60
1	B	176	ALA	CA-C-O	5.17	126.05	120.32
1	A	118	ASP	CB-CA-C	-5.16	104.44	110.17
1	A	169	SER	CA-CB-OG	5.15	121.39	111.10
1	B	53	ILE	N-CA-CB	5.14	120.24	111.50
1	A	89	PHE	N-CA-C	-5.14	106.31	112.58
1	B	231	LYS	CB-CG-CD	-5.13	99.49	111.30
1	B	264	TYR	CA-C-N	5.13	125.13	120.21
1	B	264	TYR	C-N-CA	5.13	125.13	120.21
1	B	322	GLU	N-CA-C	5.12	116.86	111.28
1	B	106	GLU	CA-C-N	5.12	124.73	119.05
1	B	106	GLU	C-N-CA	5.12	124.73	119.05
1	B	17	VAL	N-CA-CB	-5.12	104.83	110.51
1	A	236	ASN	CA-CB-CG	-5.11	107.49	112.60
1	A	20	GLN	OE1-CD-NE2	-5.11	117.49	122.60
1	A	174	VAL	O-C-N	5.10	128.77	123.26
1	B	79	ASP	N-CA-C	5.08	117.21	111.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	222	ALA	N-CA-C	-5.06	105.47	111.69
1	B	97	GLU	CA-CB-CG	-5.05	104.00	114.10
1	A	157	ARG	N-CA-CB	-5.05	102.44	110.22
1	B	270	SER	CA-C-N	5.05	125.12	119.87
1	B	270	SER	C-N-CA	5.05	125.12	119.87
1	B	279	TYR	N-CA-C	5.05	120.28	113.72
1	B	114	VAL	N-CA-C	-5.01	100.43	107.75
1	A	141	LYS	N-CA-C	-5.01	102.87	110.28
1	A	106	GLU	CA-C-N	5.00	124.78	119.28
1	A	106	GLU	C-N-CA	5.00	124.78	119.28

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	113	TYR	Sidechain
1	A	139	TYR	Sidechain
1	A	226	TYR	Sidechain
1	A	258	TYR	Sidechain
1	A	264	TYR	Sidechain
1	B	226	TYR	Sidechain
1	B	258	TYR	Sidechain
1	B	264	TYR	Sidechain

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	A	2430	538	2486	68	0
1	B	2430	538	2486	40	0
2	A	16	0	11	13	0
2	B	16	0	11	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	23	0	12	4	0
4	B	23	0	12	4	0
All	All	4940	1076	5018	104	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 10.

All (104) 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:27:THR:HB	4:A:337:AMP:O3P	1.34	1.26
1:A:274:LYS:NZ	2:A:336:F6P:C6	2.02	1.23
1:A:274:LYS:NZ	2:A:336:F6P:H61	1.54	1.20
1:A:274:LYS:HZ3	2:A:336:F6P:H61	0.97	1.09
1:A:275:LEU:HD21	2:A:336:F6P:O2	1.53	1.09
1:A:274:LYS:NZ	2:A:336:F6P:H62	1.75	0.99
1:A:274:LYS:HZ3	2:A:336:F6P:C6	1.67	0.98
1:A:274:LYS:HZ2	2:A:336:F6P:C6	1.83	0.91
1:A:27:THR:CB	4:A:337:AMP:O3P	2.22	0.88
1:A:276:ARG:HG3	1:A:276:ARG:HH11	1.40	0.86
1:A:218:GLU:HB3	1:A:267:ASN:HB2	1.61	0.82
1:B:27:THR:OG1	4:B:337:AMP:O3P	2.00	0.79
1:A:243:ARG:NH2	2:B:336:F6P:O1P	2.12	0.79
1:B:9:ASN:HB3	1:B:194:ILE:HG12	1.67	0.77
1:B:78:ASN:OD1	1:B:96:THR:HG21	1.85	0.77
1:A:125:ASN:HB3	1:A:130:VAL:HB	1.68	0.75
1:A:217:LYS:NZ	1:A:217:LYS:HB2	2.07	0.70
1:A:204:LYS:HA	1:A:321:PRO:HD2	1.74	0.70
1:A:248:MET:HB2	2:A:336:F6P:H12	1.73	0.70
1:A:78:ASN:OD1	1:A:96:THR:HG21	1.92	0.69
1:B:70:VAL:HA	1:B:126:ILE:HD12	1.75	0.68
1:A:274:LYS:HZ2	2:A:336:F6P:H62	1.48	0.67
1:B:229:ARG:NH2	1:B:330:ILE:HD11	2.10	0.67
1:B:195:LEU:HD21	1:B:198:ARG:HG2	1.78	0.65
1:B:277:LEU:HA	1:B:281:CYS:HB2	1.78	0.64
1:B:9:ASN:OD1	1:B:12:THR:HG23	1.98	0.64
1:A:316:ILE:HD11	1:A:318:LEU:HD23	1.82	0.61
1:A:30:MET:HB3	4:A:337:AMP:C2	2.35	0.60
1:A:212:ASN:ND2	2:A:336:F6P:O2P	2.33	0.60
1:A:218:GLU:HG2	1:A:268:LYS:HB2	1.83	0.59
1:B:182:ASN:HD22	1:B:198:ARG:HA	1.66	0.59
1:A:217:LYS:HB2	1:A:217:LYS:HZ2	1.70	0.57
1:A:302:VAL:HG21	1:A:316:ILE:HD12	1.85	0.57
1:A:96:THR:HG22	1:A:98:GLU:H	1.70	0.57
1:A:226:TYR:CZ	1:A:230:LYS:HD3	2.40	0.55
1:B:296:THR:HG21	1:B:328:LEU:HD21	1.88	0.55
1:A:50:LYS:HG2	1:B:188:PRO:HD2	1.87	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:MET:N	2:A:336:F6P:O1	2.40	0.54
1:A:17:VAL:HG12	1:A:31:THR:HG23	1.92	0.52
1:A:188:PRO:HD2	1:B:50:LYS:HG2	1.91	0.51
1:A:50:LYS:NZ	1:A:54:ALA:N	2.58	0.51
4:B:337:AMP:O4'	4:B:337:AMP:N3	2.43	0.51
1:A:276:ARG:HG3	1:A:276:ARG:NH1	2.12	0.51
4:A:337:AMP:N3	4:A:337:AMP:O4'	2.44	0.51
1:B:182:ASN:ND2	1:B:198:ARG:HA	2.26	0.50
1:A:227:ILE:HG22	1:A:231:LYS:HE2	1.93	0.49
1:A:252:VAL:HG11	1:A:284:MET:SD	2.53	0.49
1:A:288:MET:HG3	1:A:318:LEU:HB2	1.95	0.49
1:A:51:ALA:HB3	1:B:185:MET:HE3	1.95	0.48
1:A:30:MET:HE1	1:A:177:MET:HE3	1.95	0.48
1:A:182:ASN:HD22	1:A:198:ARG:HA	1.79	0.47
1:A:183:CYS:HB2	1:A:197:ASP:HB3	1.96	0.47
1:A:218:GLU:CG	1:A:268:LYS:HB2	2.43	0.47
1:A:274:LYS:HZ1	2:A:336:F6P:H62	1.74	0.47
1:B:140:ARG:HH12	4:B:337:AMP:H3'	1.79	0.47
1:A:71:LYS:HA	1:A:74:ASP:OD1	2.15	0.47
1:A:266:ALA:CB	1:A:271:PRO:HA	2.44	0.47
1:A:229:ARG:HE	1:A:330:ILE:HD11	1.81	0.46
1:A:333:LYS:O	1:A:333:LYS:HG2	2.15	0.46
1:B:50:LYS:HZ2	1:B:54:ALA:N	2.14	0.46
1:B:278:LEU:HD12	1:B:310:ILE:HA	1.98	0.46
1:A:129:LEU:HD11	1:B:172:MET:HB2	1.98	0.46
1:A:217:LYS:HB3	1:B:232:PHE:CE2	2.51	0.46
1:A:294:LEU:HD12	1:A:324:VAL:HB	1.97	0.46
1:A:325:THR:O	1:A:329:GLU:HG3	2.15	0.46
1:A:89:PHE:CD2	1:A:109:LYS:HA	2.51	0.46
1:B:194:ILE:O	1:B:196:VAL:HG13	2.16	0.46
1:A:266:ALA:HB1	1:A:271:PRO:HA	1.97	0.45
1:B:288:MET:HG3	1:B:318:LEU:HD13	1.97	0.45
1:B:126:ILE:O	1:B:129:LEU:HD23	2.16	0.45
1:B:71:LYS:HA	1:B:74:ASP:OD1	2.16	0.45
1:A:69:GLN:OE1	1:A:72:LYS:NZ	2.48	0.44
1:A:114:VAL:HG11	1:A:152:ALA:HA	1.99	0.44
1:B:113:TYR:OH	4:B:337:AMP:H5'1	2.17	0.44
1:B:267:ASN:O	1:B:271:PRO:HA	2.17	0.43
1:B:12:THR:HG22	1:B:192:GLU:HG3	2.00	0.43
1:B:229:ARG:HH22	1:B:330:ILE:HD11	1.82	0.43
1:A:96:THR:HG23	1:A:119:PRO:HD3	2.01	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:317:ILE:HG21	1:B:327:LEU:HD23	2.01	0.43
1:B:233:PRO:HA	1:B:234:PRO:HD3	1.89	0.43
1:B:248:MET:N	2:B:336:F6P:O3	2.43	0.43
1:A:270:SER:C	1:A:272:LYS:H	2.26	0.43
1:A:45:SER:O	1:A:49:ARG:HD3	2.19	0.43
1:A:70:VAL:HA	1:A:126:ILE:HD12	2.01	0.42
1:A:183:CYS:SG	1:A:200:VAL:HG21	2.59	0.42
1:A:211:ILE:HD12	1:A:263:MET:HB2	2.01	0.42
1:A:213:GLU:CD	1:A:231:LYS:HZ1	2.27	0.42
1:A:19:GLU:HB3	1:A:23:LYS:NZ	2.35	0.42
1:B:37:LEU:HD21	1:B:136:PHE:CD2	2.54	0.42
1:A:71:LYS:O	1:A:72:LYS:HB2	2.19	0.42
1:B:52:GLY:O	1:B:53:ILE:HG13	2.20	0.42
1:B:154:GLN:HE21	1:B:158:ASN:HD22	1.67	0.41
1:A:166:LEU:O	1:A:171:THR:HA	2.20	0.41
1:A:50:LYS:CG	1:B:188:PRO:HD2	2.51	0.41
1:A:94:LEU:HB2	1:A:103:ILE:HB	2.01	0.41
1:B:208:ILE:HA	1:B:241:GLY:O	2.21	0.41
1:B:276:ARG:HD2	1:B:279:TYR:OH	2.21	0.41
1:B:204:LYS:HE3	1:B:204:LYS:HB2	1.91	0.41
1:A:184:PHE:HB3	1:A:193:PHE:HB3	2.03	0.41
1:A:233:PRO:HA	1:A:234:PRO:HD2	1.83	0.40
1:A:248:MET:CA	2:A:336:F6P:O1	2.70	0.40
1:B:183:CYS:HB2	1:B:197:ASP:HB3	2.02	0.40
1:B:10:ILE:HG23	1:B:11:VAL:HG23	2.02	0.40
1:B:41:VAL:HG12	1:B:193:PHE:HZ	1.87	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	313/335 (93%)	290 (93%)	16 (5%)	7 (2%)	5	9
1	B	313/335 (93%)	286 (91%)	24 (8%)	3 (1%)	12	24
All	All	626/670 (93%)	576 (92%)	40 (6%)	10 (2%)	7	14

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	10	ILE
1	A	53	ILE
1	B	70	VAL
1	A	72	LYS
1	B	9	ASN
1	B	178	VAL
1	A	52	GLY
1	A	267	ASN
1	A	270	SER

5.3.2 Protein sidechains ⓘ

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	266/278 (96%)	249 (94%)	17 (6%)	16	33
1	B	266/278 (96%)	250 (94%)	16 (6%)	17	36
All	All	532/556 (96%)	499 (94%)	33 (6%)	16	34

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

Mol	Chain	Res	Type
1	A	9	ASN
1	A	30	MET
1	A	53	ILE
1	A	68	ASP
1	A	69	GLN
1	A	72	LYS

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Mol	Chain	Res	Type
1	A	74	ASP
1	A	108	GLU
1	A	201	LYS
1	A	217	LYS
1	A	230	LYS
1	A	265	PRO
1	A	276	ARG
1	A	280	GLU
1	A	300	GLU
1	A	316	ILE
1	A	318	LEU
1	B	8	THR
1	B	25	ARG
1	B	45	SER
1	B	49	ARG
1	B	53	ILE
1	B	71	LYS
1	B	72	LYS
1	B	79	ASP
1	B	123	SER
1	B	124	SER
1	B	130	VAL
1	B	142	ASN
1	B	143	SER
1	B	173	LEU
1	B	300	GLU
1	B	313	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	35	ASN
1	A	142	ASN
1	A	154	GLN
1	A	182	ASN
1	A	332	GLN
1	B	32	GLN
1	B	125	ASN
1	B	154	GLN
1	B	182	ASN
1	B	267	ASN
1	B	282	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 2 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	AMP	B	337	-	25,25,25	2.37	5 (20%)	37,38,38	2.33	10 (27%)
4	AMP	A	337	-	25,25,25	2.38	5 (20%)	37,38,38	2.33	10 (27%)
2	F6P	B	336	-	15,16,16	1.04	1 (6%)	16,25,25	0.86	0
2	F6P	A	336	-	15,16,16	1.05	1 (6%)	16,25,25	0.86	0

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	AMP	B	337	-	-	6/10/26/26	0/3/3/3
4	AMP	A	337	-	-	6/10/26/26	0/3/3/3
2	F6P	B	336	-	-	0/9/28/28	0/1/1/1
2	F6P	A	336	-	-	0/9/28/28	0/1/1/1

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	337	AMP	C3'-C4'	-5.84	1.38	1.53
4	B	337	AMP	C3'-C4'	-5.83	1.38	1.53
4	A	337	AMP	O3'-C3'	4.56	1.54	1.43
4	B	337	AMP	O3'-C3'	4.51	1.54	1.43
4	B	337	AMP	O4'-C4'	4.45	1.54	1.45
4	A	337	AMP	O4'-C4'	4.45	1.54	1.45
4	A	337	AMP	P-O5'	-4.33	1.46	1.60
4	B	337	AMP	P-O5'	-4.32	1.46	1.60
4	A	337	AMP	O5'-C5'	3.94	1.59	1.44
4	B	337	AMP	O5'-C5'	3.92	1.59	1.44
2	A	336	F6P	C6-C5	-2.08	1.45	1.51
2	B	336	F6P	C6-C5	-2.07	1.45	1.51

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	337	AMP	C2'-C3'-C4'	7.51	117.12	102.61
4	B	337	AMP	C2'-C3'-C4'	7.49	117.08	102.61
4	B	337	AMP	C3'-C2'-C1'	-5.82	90.45	101.46
4	A	337	AMP	C3'-C2'-C1'	-5.81	90.47	101.46
4	B	337	AMP	O4'-C1'-N9	-4.17	100.08	108.09
4	A	337	AMP	O4'-C1'-N9	-4.15	100.11	108.09
4	B	337	AMP	O2'-C2'-C1'	-3.75	97.21	110.10
4	A	337	AMP	O2'-C2'-C1'	-3.73	97.27	110.10
4	B	337	AMP	O3P-P-O5'	3.67	116.24	106.67
4	A	337	AMP	O3P-P-O5'	3.66	116.21	106.67
4	A	337	AMP	O4'-C4'-C3'	-3.15	98.91	105.15
4	B	337	AMP	O4'-C4'-C3'	-3.13	98.95	105.15
4	A	337	AMP	O3P-P-O2P	2.99	119.03	107.80
4	B	337	AMP	O3P-P-O2P	2.98	118.99	107.80
4	B	337	AMP	O3P-P-O1P	-2.61	100.66	110.83
4	A	337	AMP	O3P-P-O1P	-2.61	100.66	110.83
4	A	337	AMP	C2-N1-C6	2.51	122.85	118.73
4	B	337	AMP	C2-N1-C6	2.51	122.85	118.73
4	B	337	AMP	C2'-C1'-N9	-2.44	107.24	113.30
4	A	337	AMP	C2'-C1'-N9	-2.42	107.29	113.30

There are no chirality outliers.

All (12) torsion outliers are listed below:

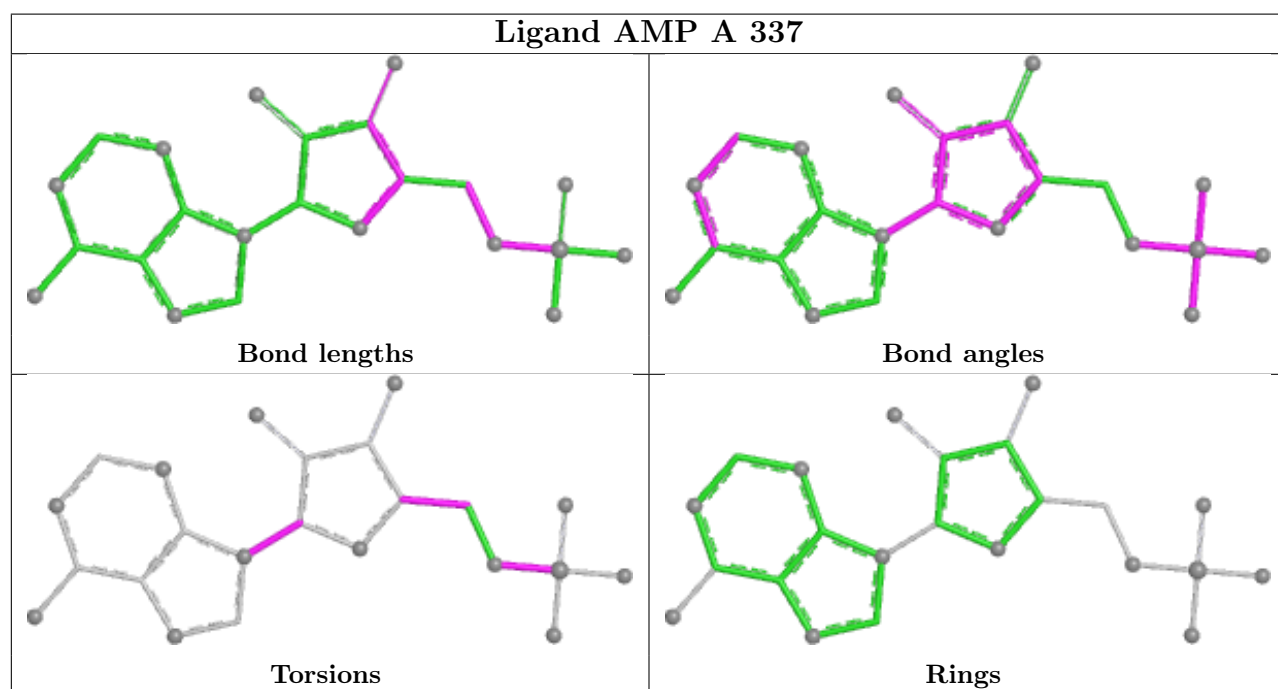
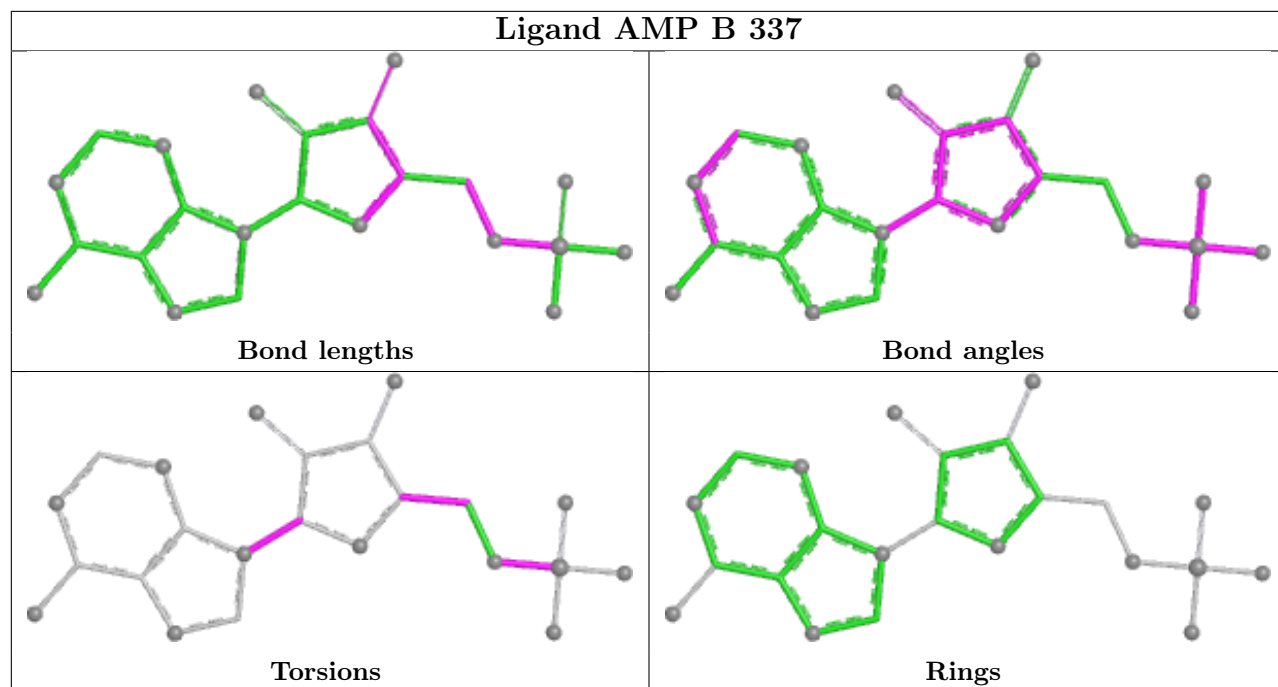
Mol	Chain	Res	Type	Atoms
4	A	337	AMP	C5'-O5'-P-O1P
4	A	337	AMP	C5'-O5'-P-O2P
4	A	337	AMP	O4'-C1'-N9-C4
4	B	337	AMP	C5'-O5'-P-O1P
4	B	337	AMP	O4'-C1'-N9-C4
4	A	337	AMP	O4'-C1'-N9-C8
4	B	337	AMP	O4'-C1'-N9-C8
4	A	337	AMP	O4'-C4'-C5'-O5'
4	B	337	AMP	O4'-C4'-C5'-O5'
4	B	337	AMP	C5'-O5'-P-O2P
4	B	337	AMP	C3'-C4'-C5'-O5'
4	A	337	AMP	C3'-C4'-C5'-O5'

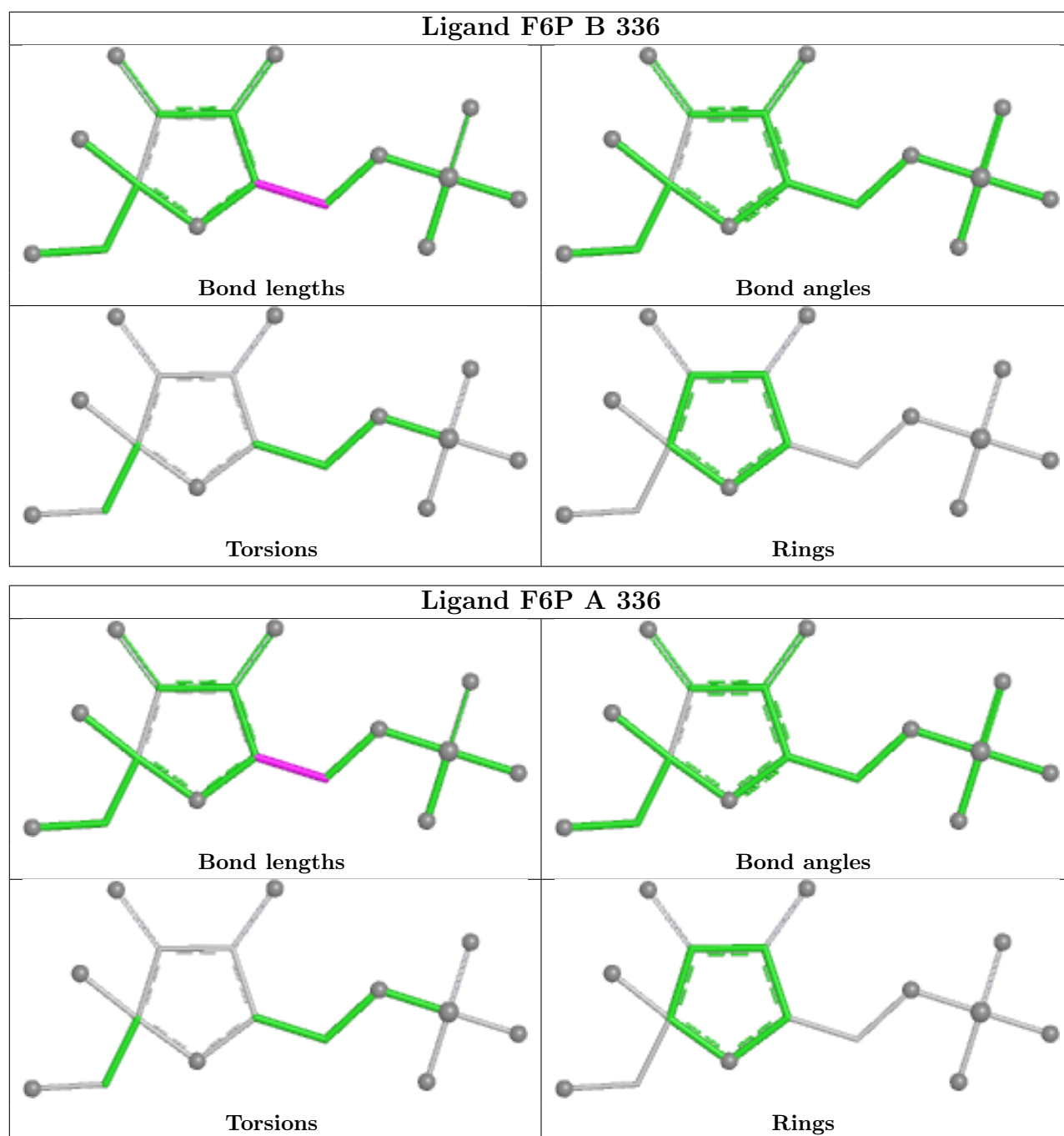
There are no ring outliers.

4 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	337	AMP	4	0
4	A	337	AMP	4	0
2	B	336	F6P	2	0
2	A	336	F6P	13	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

EDS was not executed - this section is therefore empty.

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

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.