



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 03:30 PM UTC

PDB ID : 1FRP / pdb_00001frp
Title : CRYSTAL STRUCTURE OF FRUCTOSE-1,6-BISPHOSPHATASE COM-
PLEXED WITH FRUCTOSE-2,6-BISPHOSPHATE, AMP AND ZN²⁺ AT
2.0 ANGSTROMS RESOLUTION. ASPECTS OF SYNERGISM BETWEEN
INHIBITORS
Authors : Xue, Y.; Huang, S.; Liang, J.-Y.; Zhang, Y.; Lipscomb, W.N.
Deposited on : 1994-08-26
Resolution : 2.00 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](#) ①) 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

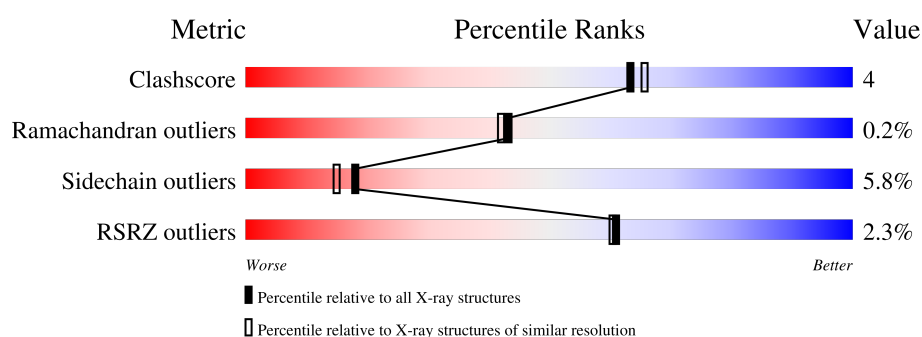
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	11152 (2.00-2.00)
Ramachandran outliers	187476	11031 (2.00-2.00)
Sidechain outliers	187428	11029 (2.00-2.00)
RSRZ outliers	180081	10067 (2.00-2.00)

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	335	2% 76% 16% • •
1	B	335	2% 73% 19% • •

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6789 atoms, of which 1566 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.

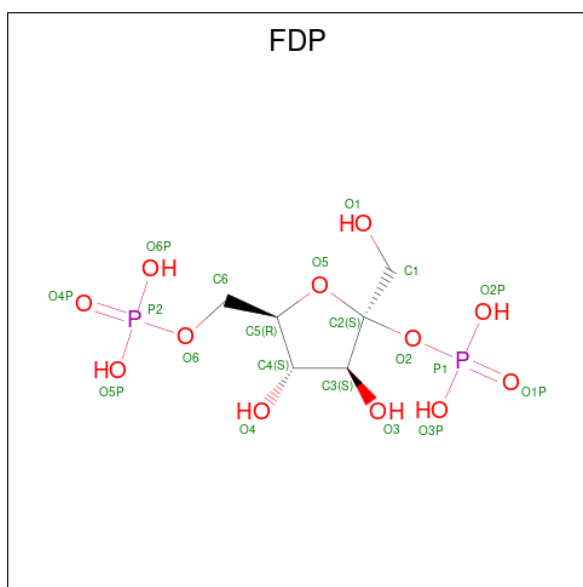
- Molecule 1 is a protein called FRUCTOSE 1,6-BISPHOSPHATASE.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	321	Total	C	H	N	O	S	0	0	1
			2990	1560	542	414	459	15			
1	B	321	Total	C	H	N	O	S	0	0	1
			2990	1560	542	414	459	15			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	20	GLN	GLU	conflict	UNP P00636
A	62	ALA	SER	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	62	ALA	SER	conflict	UNP P00636
B	96	THR	SER	conflict	UNP P00636
B	199	ASN	ASP	conflict	UNP P00636

- Molecule 2 is 2,6-di-O-phosphono-beta-D-fructofuranose (CCD ID: FDP) (formula: C₆H₁₄O₁₂P₂).

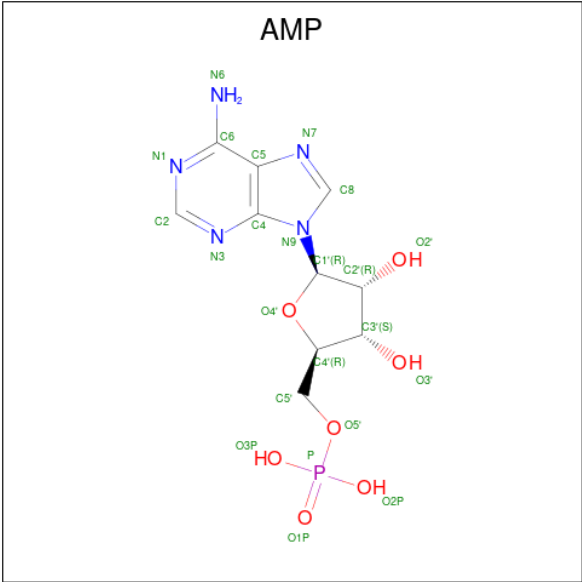


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	H	O	P	0	0
			22	6	2	12	2		
2	B	1	Total	C	H	O	P	0	0
			22	6	2	12	2		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

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

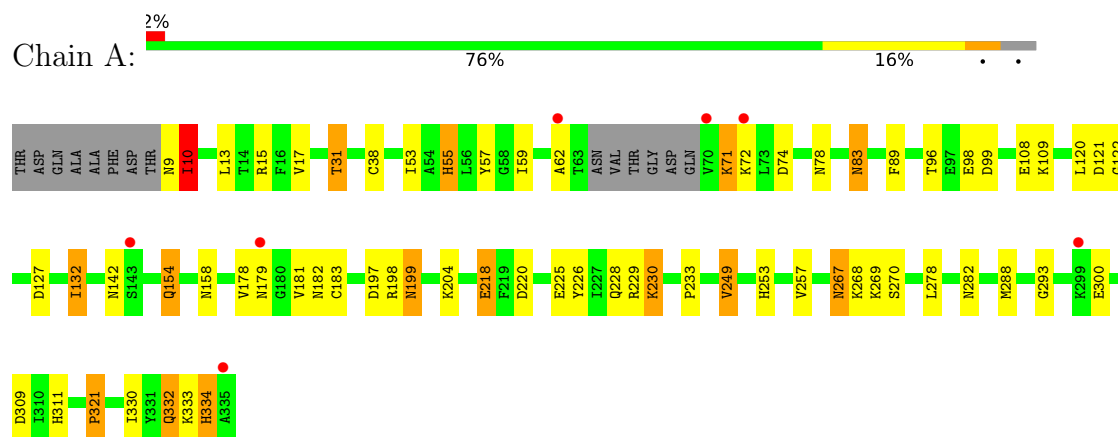
- Molecule 5 is water.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	128	Total	H	O	0	0
			384	256	128		
5	B	111	Total	H	O	0	0
			333	222	111		

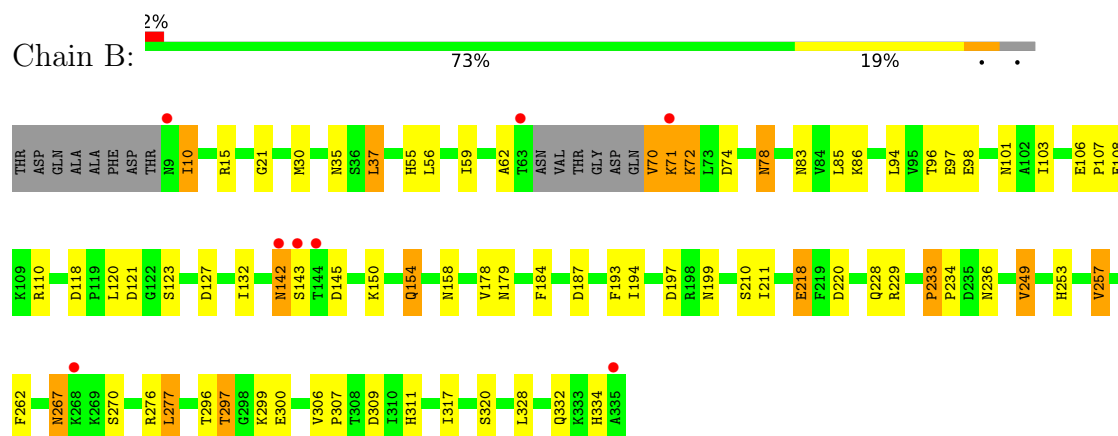
3 Residue-property plots [i](#)

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: FRUCTOSE 1,6-BISPHOSPHATASE



• Molecule 1: FRUCTOSE 1,6-BISPHOSPHATASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	60.95Å 166.30Å 80.00Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.00 10.00 – 2.00	Depositor EDS
% Data completeness (in resolution range)	(Not available) (10.00-2.00) 81.4 (10.00-2.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.91 (at 1.90Å)	Xtriage
Refinement program	X-PLOR	Depositor
R, R_{free}	0.189 , (Not available) 0.185 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	24.4	Xtriage
Anisotropy	0.393	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 61.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6789	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 16.95% 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

5.1 Standard geometry

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

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	0.99	8/2489 (0.3%)	1.69	32/3365 (1.0%)
1	B	1.01	7/2489 (0.3%)	1.72	42/3365 (1.2%)
All	All	1.00	15/4978 (0.3%)	1.70	74/6730 (1.1%)

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	2

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	311	HIS	CD2-NE2	-7.17	1.29	1.37
1	B	62	ALA	C-N	-7.02	1.23	1.33
1	B	311	HIS	CD2-NE2	-6.23	1.30	1.37
1	A	62	ALA	C-N	-6.17	1.24	1.33
1	A	55	HIS	CD2-NE2	-5.83	1.31	1.37
1	B	55	HIS	CD2-NE2	-5.76	1.31	1.37
1	A	253	HIS	CD2-NE2	-5.74	1.31	1.37
1	A	311	HIS	CG-ND1	-5.50	1.32	1.38
1	A	334	HIS	CD2-NE2	-5.42	1.31	1.37
1	B	334	HIS	CD2-NE2	-5.34	1.31	1.37
1	A	181	VAL	CA-CB	5.32	1.60	1.54
1	B	320	SER	CA-CB	-5.23	1.46	1.53
1	B	253	HIS	CD2-NE2	-5.14	1.32	1.37
1	B	211	ILE	CA-CB	5.13	1.60	1.55
1	A	178	VAL	CA-CB	5.07	1.60	1.54

All (74) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	142	ASN	CA-CB-CG	12.96	125.56	112.60
1	B	309	ASP	CA-CB-CG	10.35	122.95	112.60
1	B	142	ASN	OD1-CG-ND2	-10.12	112.48	122.60
1	A	83	ASN	CA-CB-CG	-9.45	103.15	112.60
1	A	199	ASN	CA-CB-CG	-9.17	103.43	112.60
1	B	142	ASN	CB-CG-ND2	8.55	129.22	116.40
1	B	220	ASP	CA-CB-CG	8.44	121.04	112.60
1	B	267	ASN	CA-CB-CG	8.29	120.89	112.60
1	B	74	ASP	CA-CB-CG	8.26	120.86	112.60
1	A	74	ASP	CA-CB-CG	8.14	120.74	112.60
1	A	309	ASP	CA-CB-CG	8.07	120.67	112.60
1	A	220	ASP	CA-CB-CG	8.01	120.61	112.60
1	B	35	ASN	OD1-CG-ND2	-7.97	114.63	122.60
1	B	270	SER	CA-C-N	7.73	127.36	119.56
1	B	270	SER	C-N-CA	7.73	127.36	119.56
1	B	306	VAL	N-CA-C	-7.54	100.09	107.55
1	B	257	VAL	N-CA-CB	-7.38	97.00	110.95
1	A	179	ASN	OD1-CG-ND2	-7.29	115.31	122.60
1	B	249	VAL	CG1-CB-CG2	-7.09	95.20	110.80
1	A	270	SER	CA-C-N	7.05	126.68	119.56
1	A	270	SER	C-N-CA	7.05	126.68	119.56
1	B	317	ILE	N-CA-C	-7.03	97.91	108.17
1	A	154	GLN	OE1-CD-NE2	-6.97	115.63	122.60
1	B	267	ASN	OD1-CG-ND2	-6.90	115.70	122.60
1	A	332	GLN	CA-CB-CG	-6.56	100.98	114.10
1	A	71	LYS	CA-C-O	6.38	129.63	120.51
1	B	132	ILE	O-C-N	-6.37	114.61	122.57
1	A	282	ASN	OD1-CG-ND2	-6.35	116.25	122.60
1	A	71	LYS	N-CA-C	-6.17	97.65	110.80
1	B	277	LEU	N-CA-C	6.14	117.64	111.07
1	A	228	GLN	OE1-CD-NE2	-6.11	116.49	122.60
1	A	31	THR	CA-CB-OG1	-5.96	100.66	109.60
1	A	267	ASN	OD1-CG-ND2	-5.95	116.65	122.60
1	B	332	GLN	OE1-CD-NE2	-5.95	116.65	122.60
1	B	35	ASN	CB-CG-ND2	5.88	125.22	116.40
1	A	142	ASN	OD1-CG-ND2	-5.87	116.73	122.60
1	B	267	ASN	O-C-N	-5.77	115.05	122.72
1	B	78	ASN	OD1-CG-ND2	-5.74	116.86	122.60
1	A	267	ASN	N-CA-C	-5.73	101.05	109.81
1	B	197	ASP	CA-CB-CG	5.72	118.32	112.60
1	B	145	ASP	N-CA-C	-5.69	100.70	108.38
1	B	118	ASP	CA-C-O	-5.63	114.63	119.36

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	233	PRO	CA-C-N	5.63	125.30	119.05
1	B	233	PRO	C-N-CA	5.63	125.30	119.05
1	B	178	VAL	N-CA-C	5.62	117.03	110.62
1	A	257	VAL	N-CA-CB	-5.59	101.22	110.56
1	A	278	LEU	N-CA-C	5.58	118.12	111.71
1	A	127	ASP	CA-CB-CG	5.55	118.15	112.60
1	A	10	ILE	N-CA-CB	-5.48	104.19	110.49
1	B	101	ASN	OD1-CG-ND2	-5.47	117.13	122.60
1	B	179	ASN	OD1-CG-ND2	-5.42	117.18	122.60
1	A	249	VAL	CG1-CB-CG2	-5.38	98.97	110.80
1	B	10	ILE	N-CA-C	-5.32	100.78	108.87
1	B	72	LYS	N-CA-C	-5.32	103.00	110.50
1	A	333	LYS	O-C-N	-5.31	115.53	122.59
1	A	233	PRO	CA-C-N	5.30	124.81	119.19
1	A	233	PRO	C-N-CA	5.30	124.81	119.19
1	A	267	ASN	CA-CB-CG	5.30	117.90	112.60
1	B	70	VAL	N-CA-C	-5.29	96.20	111.00
1	A	122	GLY	N-CA-C	-5.28	100.67	113.18
1	B	83	ASN	N-CA-C	5.25	117.08	111.36
1	B	228	GLN	OE1-CD-NE2	-5.22	117.38	122.60
1	B	108	GLU	CB-CA-C	-5.21	102.14	110.79
1	A	72	LYS	N-CA-C	-5.18	102.62	110.28
1	A	288	MET	CG-SD-CE	-5.13	89.60	100.90
1	B	267	ASN	N-CA-C	-5.09	101.71	109.65
1	A	132	ILE	O-C-N	-5.08	117.41	123.00
1	B	236	ASN	OD1-CG-ND2	-5.07	117.53	122.60
1	B	154	GLN	OE1-CD-NE2	-5.06	117.54	122.60
1	A	321	PRO	O-C-N	-5.05	116.73	122.18
1	B	106	GLU	CA-C-N	5.05	124.83	119.28
1	B	106	GLU	C-N-CA	5.05	124.83	119.28
1	B	276	ARG	CA-CB-CG	-5.04	104.03	114.10
1	B	127	ASP	N-CA-C	5.01	119.10	112.89

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	57	TYR	Sidechain
1	A	71	LYS	Mainchain

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	2448	542	2513	23	0
1	B	2448	542	2513	19	0
2	A	20	2	10	0	0
2	B	20	2	10	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
4	A	23	0	12	0	0
4	B	23	0	12	1	0
5	A	128	256	0	0	0
5	B	111	222	0	1	0
All	All	5223	1566	5070	40	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 4.

All (40) 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:96:THR:HG22	1:A:98:GLU:H	1.51	0.74
1:B:96:THR:HG22	1:B:98:GLU:H	1.57	0.69
1:A:78:ASN:OD1	1:A:96:THR:HG21	1.94	0.67
1:B:78:ASN:OD1	1:B:96:THR:HG21	1.98	0.63
1:A:182:ASN:HD22	1:A:198:ARG:HA	1.64	0.61
1:A:154:GLN:HE21	1:A:158:ASN:HD22	1.50	0.60
1:B:37:LEU:HD23	1:B:85:LEU:HD21	1.84	0.58
1:A:229:ARG:HH11	1:A:330:ILE:HD11	1.68	0.58
1:B:277:LEU:HD23	1:B:307:PRO:HB3	1.87	0.56
1:A:218:GLU:HB3	1:A:268:LYS:H	1.70	0.56
1:A:226:TYR:CZ	1:A:230:LYS:HD3	2.42	0.54
1:A:17:VAL:HG12	1:A:31:THR:HG23	1.90	0.54
1:A:53:ILE:HG22	1:B:187:ASP:HB2	1.89	0.53
1:B:94:LEU:HB2	1:B:103:ILE:HB	1.92	0.52
1:A:120:LEU:HD11	1:A:132:ILE:HD12	1.94	0.50
1:A:10:ILE:HD12	1:B:59:ILE:HB	1.92	0.50
1:A:55:HIS:HA	1:A:59:ILE:HG22	1.96	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:107:PRO:HA	1:B:110:ARG:HG3	1.95	0.47
1:A:96:THR:HG22	1:A:98:GLU:N	2.26	0.47
1:B:123:SER:HB2	5:B:417:HOH:O	2.15	0.47
1:A:267:ASN:OD1	1:A:269:LYS:HB2	2.17	0.45
1:A:230:LYS:HE3	1:A:230:LYS:HA	1.98	0.45
1:B:218:GLU:HB2	1:B:267:ASN:HB2	1.98	0.45
1:A:121:ASP:OD2	1:A:249:VAL:HG23	2.17	0.45
1:B:154:GLN:HE21	1:B:158:ASN:HD22	1.65	0.45
1:A:182:ASN:ND2	1:A:198:ARG:HA	2.31	0.44
1:A:13:LEU:HD23	1:A:38:CYS:HB2	1.99	0.44
1:B:121:ASP:OD2	1:B:249:VAL:HG23	2.18	0.44
1:B:297:THR:HG22	1:B:299:LYS:H	1.83	0.43
1:A:293:GLY:HA2	1:A:321:PRO:HD3	2.00	0.43
1:B:21:GLY:HA2	4:B:338:AMP:C5	2.53	0.43
1:A:89:PHE:CE1	1:A:109:LYS:HG2	2.55	0.42
1:A:53:ILE:HD12	1:A:53:ILE:HA	1.82	0.42
1:B:296:THR:HG21	1:B:328:LEU:HD21	2.01	0.42
1:A:183:CYS:HB2	1:A:197:ASP:HB3	2.02	0.41
1:A:225:GLU:OE1	1:A:334:HIS:HE1	2.03	0.41
1:B:210:SER:HB3	1:B:262:PHE:HA	2.03	0.41
1:B:10:ILE:HD11	1:B:194:ILE:HG12	2.02	0.41
1:B:184:PHE:HB3	1:B:193:PHE:HB3	2.03	0.40
1:B:233:PRO:HA	1:B:234:PRO:HD3	1.92	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	317/335 (95%)	307 (97%)	10 (3%)	0	100	100
1	B	317/335 (95%)	308 (97%)	8 (2%)	1 (0%)	36	35

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	634/670 (95%)	615 (97%)	18 (3%)	1 (0%)	43	42

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	71	LYS

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	265/277 (96%)	253 (96%)	12 (4%)	24	23
1	B	265/277 (96%)	246 (93%)	19 (7%)	13	10
All	All	530/554 (96%)	499 (94%)	31 (6%)	18	15

All (31) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	10	ILE
1	A	15	ARG
1	A	83	ASN
1	A	99	ASP
1	A	108	GLU
1	A	199	ASN
1	A	204	LYS
1	A	218	GLU
1	A	230	LYS
1	A	300	GLU
1	A	332	GLN
1	B	15	ARG
1	B	30	MET
1	B	37	LEU
1	B	56	LEU
1	B	70	VAL

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Mol	Chain	Res	Type
1	B	71	LYS
1	B	72	LYS
1	B	86	LYS
1	B	97	GLU
1	B	120	LEU
1	B	142	ASN
1	B	143	SER
1	B	150	LYS
1	B	199	ASN
1	B	218	GLU
1	B	229	ARG
1	B	257	VAL
1	B	297	THR
1	B	300	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	9	ASN
1	A	32	GLN
1	A	35	ASN
1	A	55	HIS
1	A	154	GLN
1	A	182	ASN
1	A	334	HIS
1	B	9	ASN
1	B	55	HIS
1	B	154	GLN
1	B	179	ASN
1	B	228	GLN

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 [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	$\# Z > 2$
2	FDP	B	336	3	19,20,20	0.98	1 (5%)	29,32,32	1.68	9 (31%)
2	FDP	A	336	3	19,20,20	0.96	1 (5%)	29,32,32	1.78	9 (31%)
4	AMP	A	338	-	25,25,25	1.08	2 (8%)	37,38,38	1.59	6 (16%)
4	AMP	B	338	-	25,25,25	1.13	3 (12%)	37,38,38	1.79	8 (21%)

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
2	FDP	B	336	3	-	3/12/34/34	0/1/1/1
2	FDP	A	336	3	-	3/12/34/34	0/1/1/1
4	AMP	A	338	-	-	0/10/26/26	0/3/3/3
4	AMP	B	338	-	-	1/10/26/26	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	338	AMP	C1'-N9	2.56	1.53	1.46
4	B	338	AMP	C8-N7	2.52	1.36	1.31
4	A	338	AMP	C8-N7	2.34	1.36	1.31
4	A	338	AMP	C2-N1	2.28	1.38	1.33
2	A	336	FDP	O1-C1	2.28	1.49	1.42
4	B	338	AMP	C2-N1	2.24	1.37	1.33

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	336	FDP	O1-C1	2.18	1.49	1.42

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	338	AMP	N3-C2-N1	-4.93	121.11	128.58
4	B	338	AMP	C5-C4-N3	-4.71	120.23	126.72
2	A	336	FDP	O1-C1-C2	4.55	126.68	111.54
2	B	336	FDP	O1-C1-C2	4.24	125.64	111.54
4	A	338	AMP	N3-C2-N1	-4.04	122.47	128.58
4	A	338	AMP	C5-C4-N3	-3.90	121.35	126.72
2	A	336	FDP	O5-C2-C3	-3.57	98.25	105.42
4	A	338	AMP	O2P-P-O5'	3.47	115.73	106.67
2	B	336	FDP	O5-C2-C3	-3.44	98.51	105.42
4	B	338	AMP	C6-C5-C4	3.35	121.76	117.18
4	B	338	AMP	O2P-P-O5'	3.21	115.05	106.67
4	A	338	AMP	C6-C5-C4	3.16	121.49	117.18
2	A	336	FDP	O5-C2-C1	3.07	115.41	107.94
4	B	338	AMP	C6-C5-N7	-2.67	126.94	132.09
2	B	336	FDP	O5-C2-C1	2.60	114.26	107.94
2	B	336	FDP	O5-C5-C6	2.59	115.60	109.50
2	A	336	FDP	O3P-P1-O2	2.49	115.56	105.85
4	A	338	AMP	C6-C5-N7	-2.45	127.37	132.09
2	B	336	FDP	O3P-P1-O2	2.39	115.16	105.85
2	A	336	FDP	C6-C5-C4	-2.36	106.72	115.21
2	B	336	FDP	C6-C5-C4	-2.33	106.82	115.21
2	A	336	FDP	O5-C5-C6	2.33	114.98	109.50
4	B	338	AMP	N9-C8-N7	-2.31	110.66	113.94
2	A	336	FDP	C2-O5-C5	2.29	114.47	108.14
2	B	336	FDP	O5P-P2-O6	2.24	112.52	106.67
2	A	336	FDP	O5P-P2-O6	2.23	112.48	106.67
2	B	336	FDP	C2-O5-C5	2.16	114.12	108.14
4	A	338	AMP	N9-C8-N7	-2.15	110.89	113.94
4	B	338	AMP	N3-C4-N9	2.12	130.76	127.17
2	A	336	FDP	O2-C2-C1	2.10	115.65	109.63
4	B	338	AMP	O3P-P-O5'	2.09	112.12	106.67
2	B	336	FDP	O4-C4-C5	2.01	116.87	111.08

There are no chirality outliers.

All (7) torsion outliers are listed below:

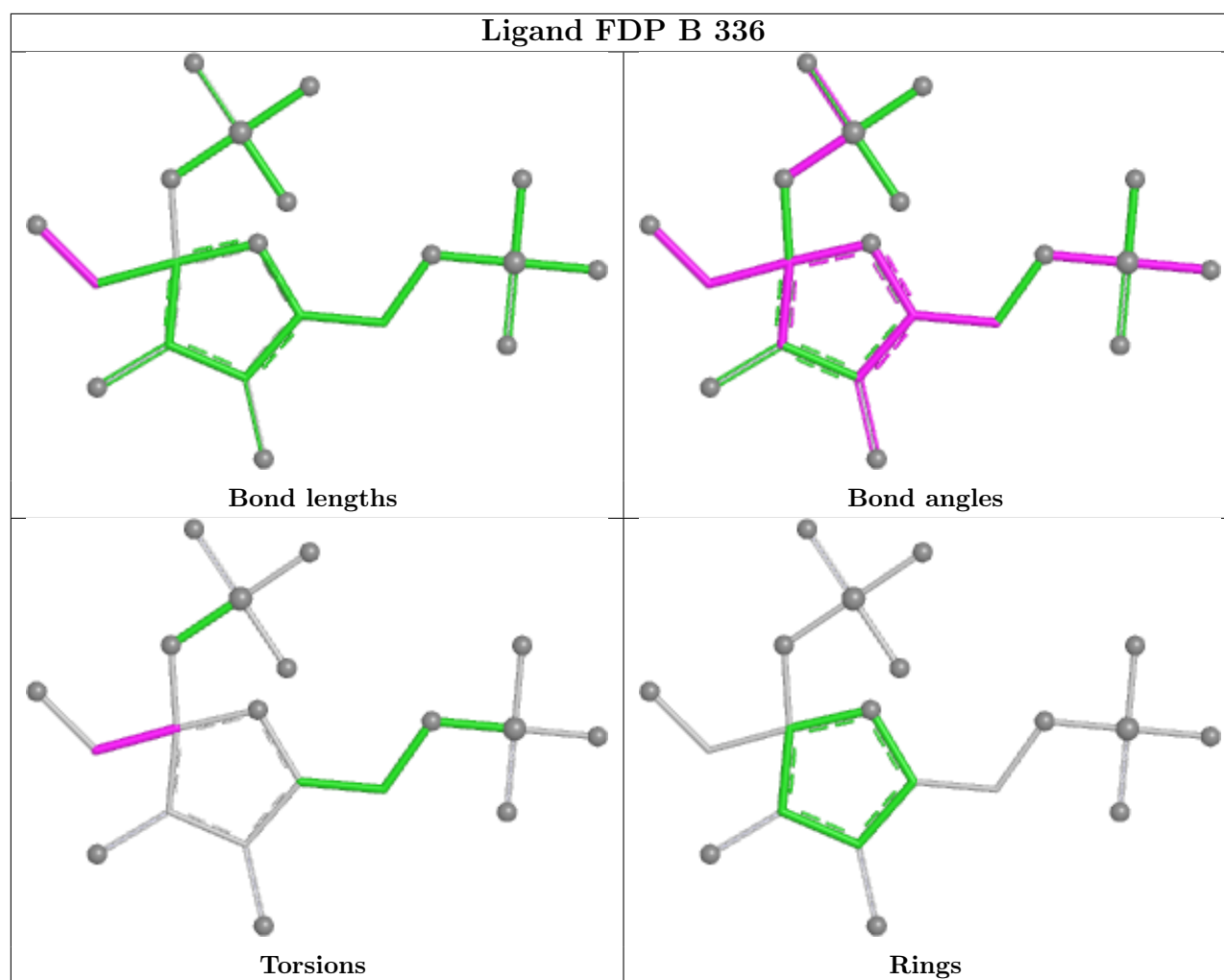
Mol	Chain	Res	Type	Atoms
2	A	336	FDP	O1-C1-C2-O2
2	A	336	FDP	O1-C1-C2-C3
2	A	336	FDP	O1-C1-C2-O5
2	B	336	FDP	O1-C1-C2-O2
2	B	336	FDP	O1-C1-C2-C3
2	B	336	FDP	O1-C1-C2-O5
4	B	338	AMP	O4'-C4'-C5'-O5'

There are no ring outliers.

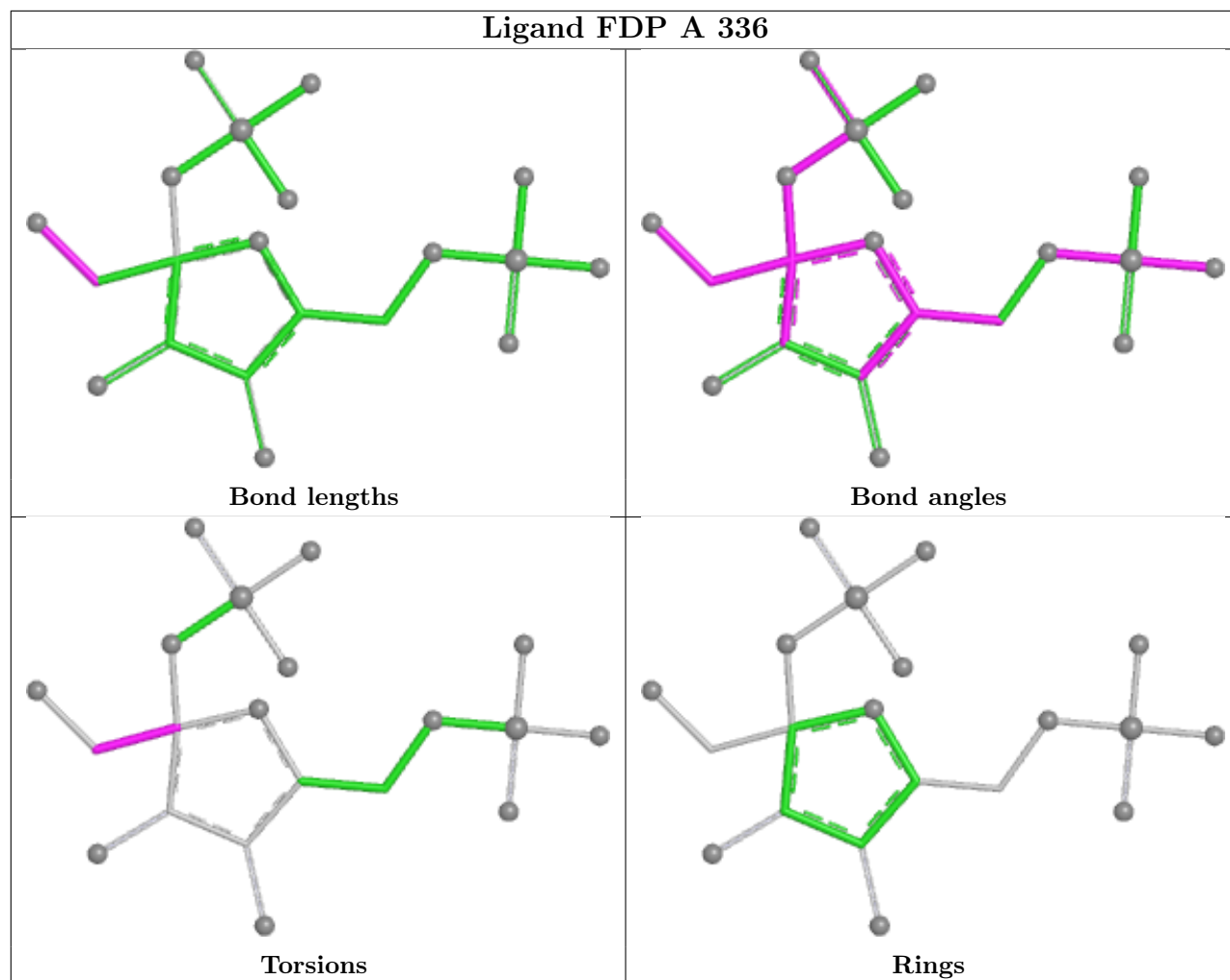
1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	338	AMP	1	0

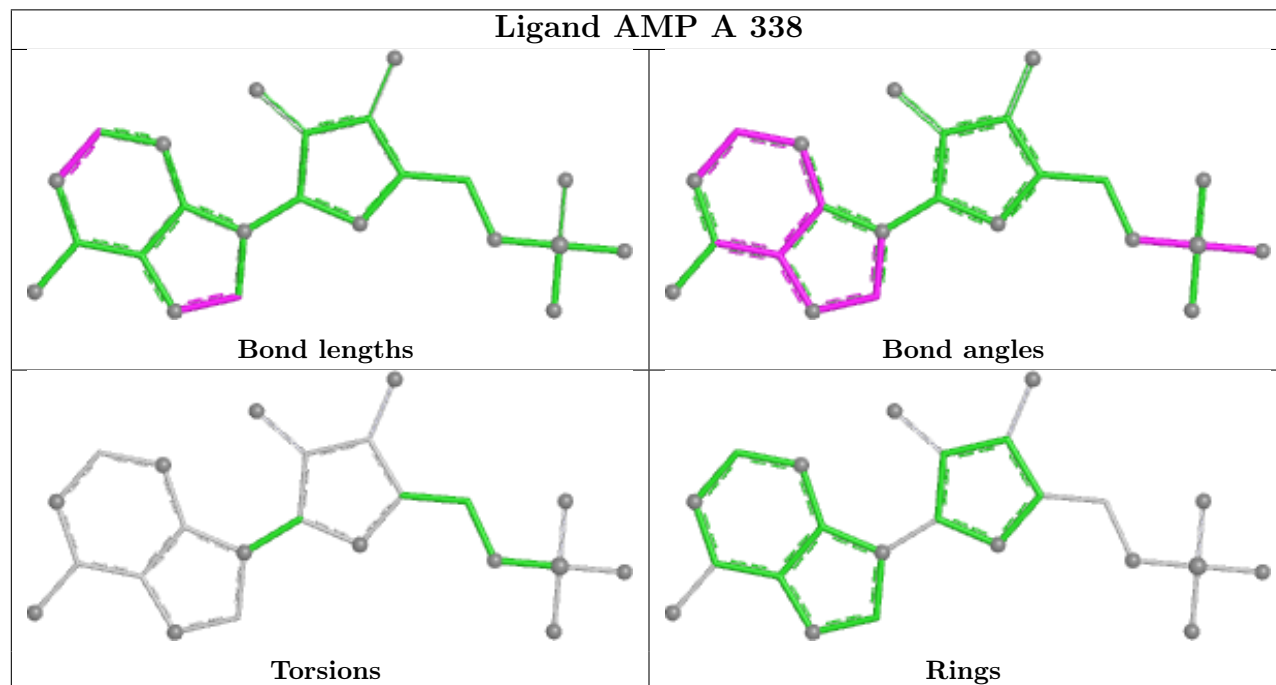
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. 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.

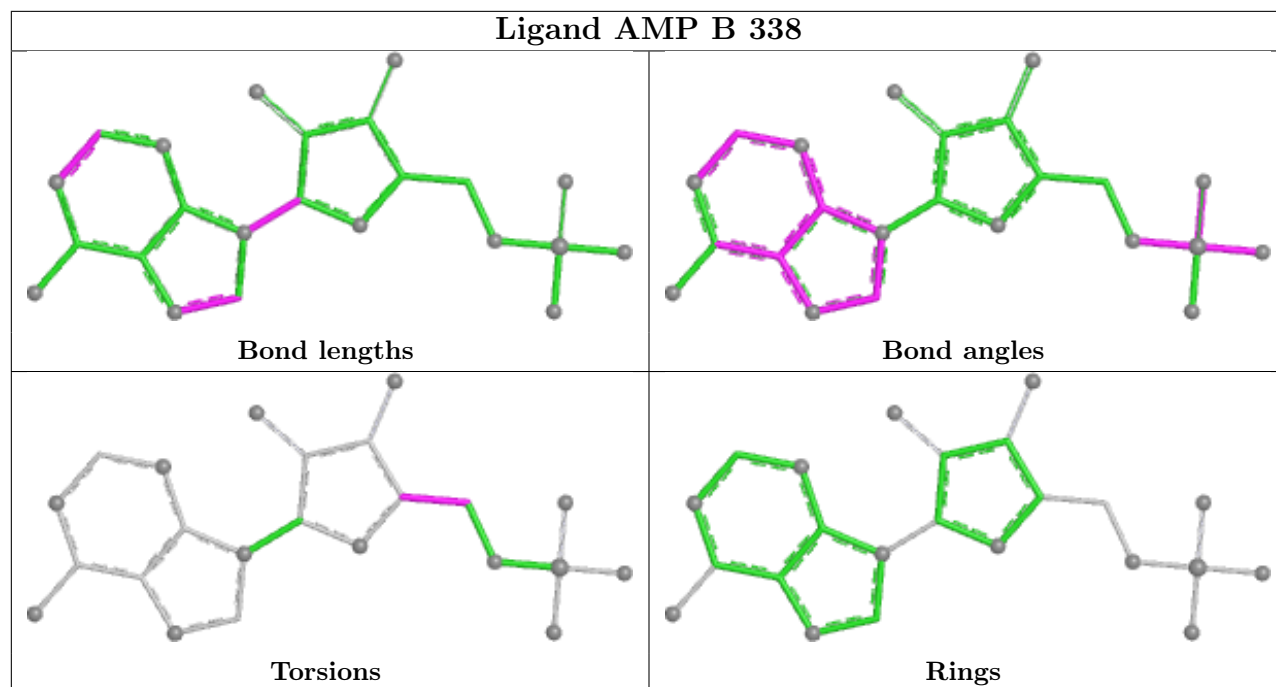


Ligand FDP A 336



Ligand AMP A 338





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	321/335 (95%)	-0.41	7 (2%) 62 61	8, 21, 49, 89	0
1	B	321/335 (95%)	-0.36	8 (2%) 58 58	8, 21, 52, 89	0
All	All	642/670 (95%)	-0.39	15 (2%) 61 60	8, 21, 51, 89	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	63	THR	9.9
1	B	142	ASN	3.3
1	A	70	VAL	2.9
1	B	144	THR	2.9
1	B	335	ALA	2.7
1	A	143	SER	2.6
1	A	62	ALA	2.6
1	A	72	LYS	2.5
1	B	71	LYS	2.5
1	A	179	ASN	2.5
1	B	268	LYS	2.4
1	B	143	SER	2.4
1	B	9	ASN	2.2
1	A	335	ALA	2.1
1	A	299	LYS	2.1

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

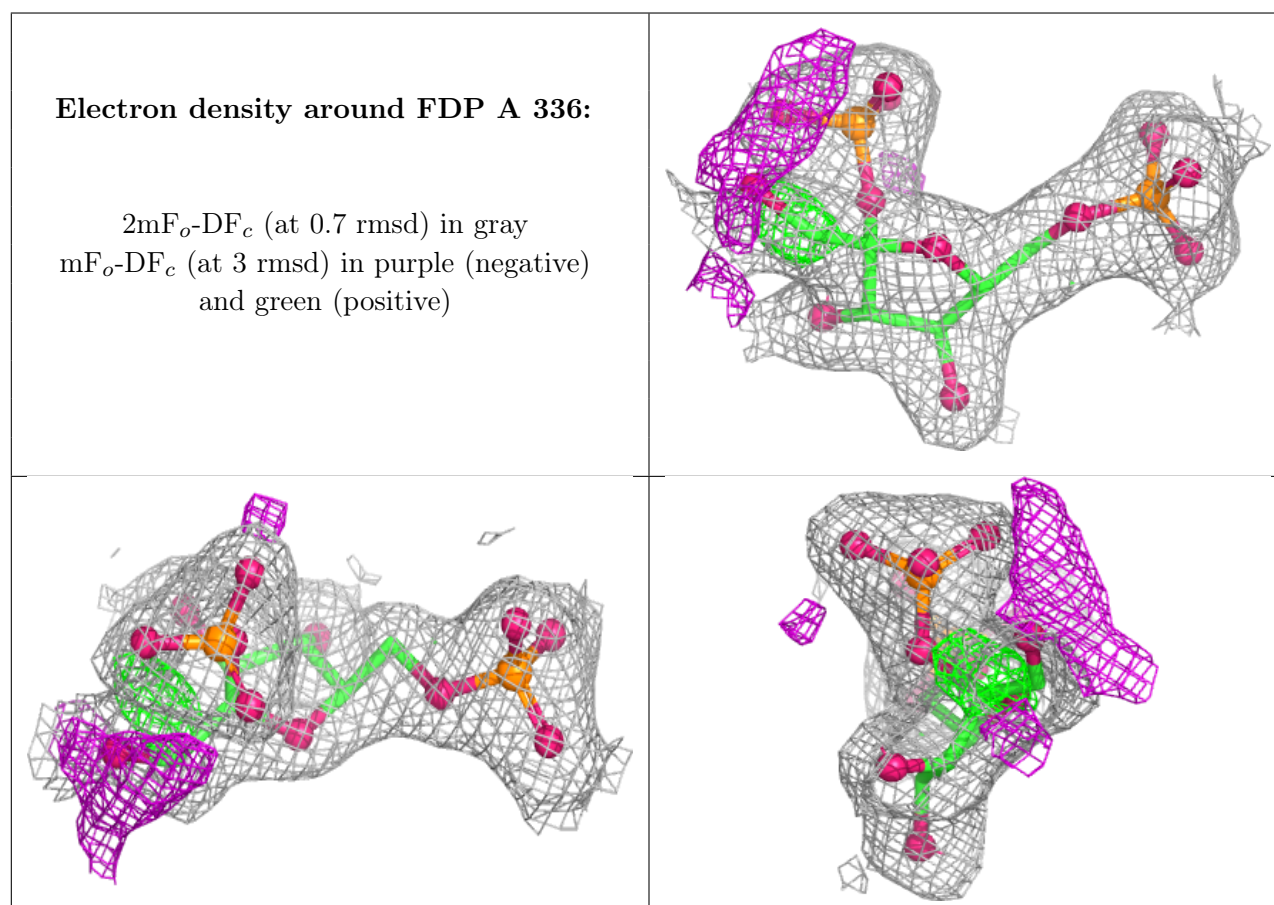
There are no oligosaccharides in this entry.

6.4 Ligands ⓘ

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.

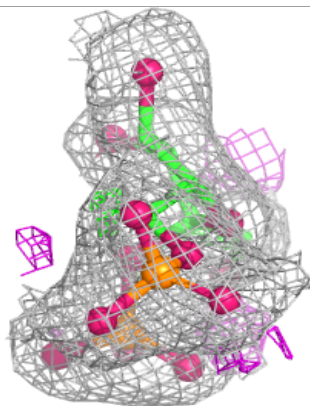
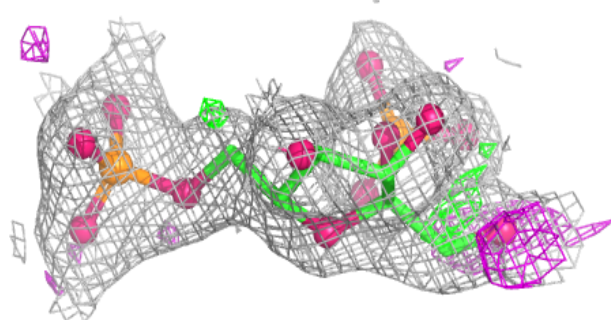
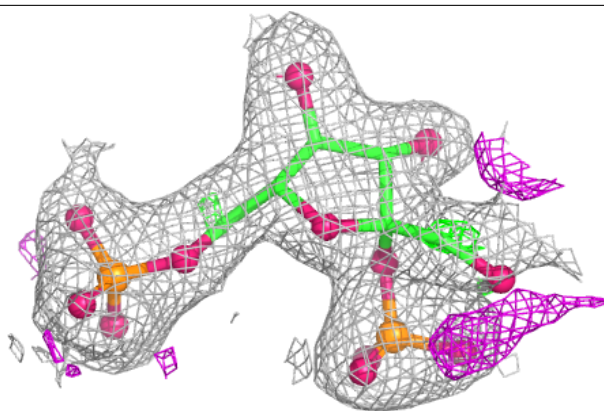
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	ZN	A	337	1/1	0.91	0.07	49,49,49,49	0
3	ZN	B	337	1/1	0.92	0.09	50,50,50,50	0
2	FDP	A	336	20/20	0.96	0.07	0,21,28,36	0
2	FDP	B	336	20/20	0.97	0.06	0,23,29,35	0
4	AMP	A	338	23/23	0.97	0.05	17,25,28,28	0
4	AMP	B	338	23/23	0.97	0.05	24,25,30,31	0

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



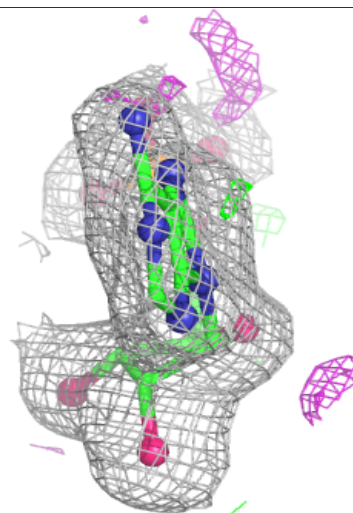
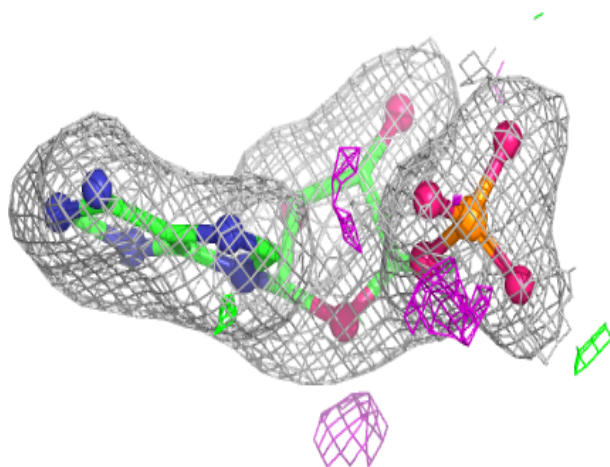
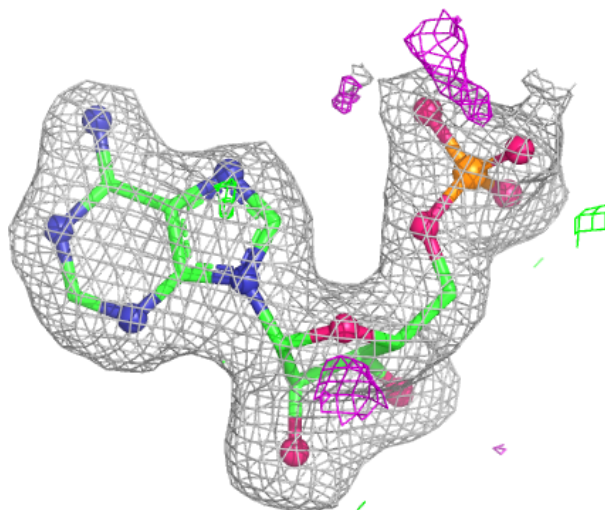
Electron density around FDP B 336:

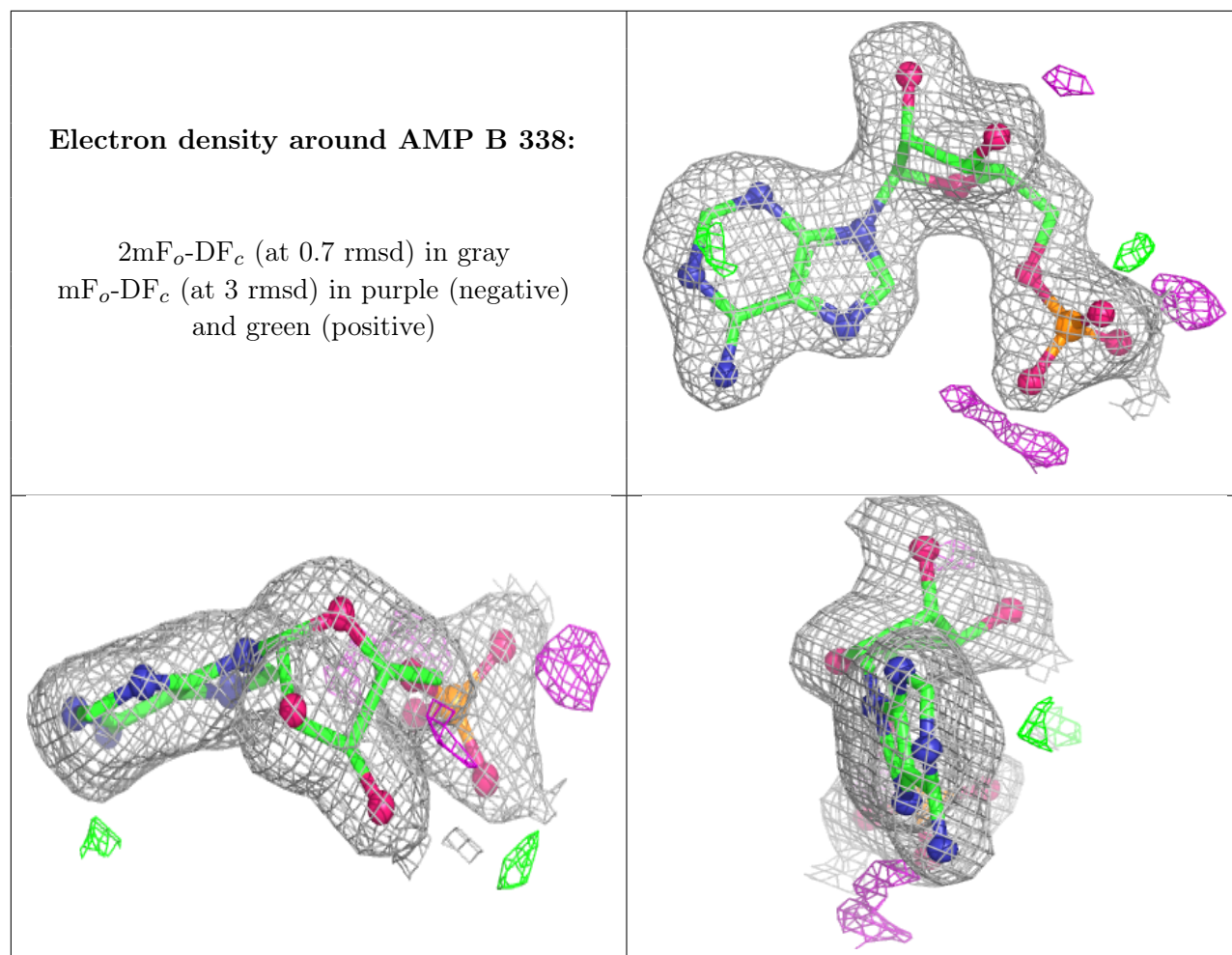
$2mF_o - DF_c$ (at 0.7 rmsd) in gray
 $mF_o - DF_c$ (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around AMP A 338:

$2mF_o-DF_c$ (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.