wwPDB X-ray Structure Validation Summary Report (i)

Feb 15, 2024 – 08:03 AM EST

PDB ID	:	3PQD
Title	:	Crystal structure of L-lactate dehydrogenase from Bacillus subtilis complexed with FBP and NAD+
Authors	:	Zhang, Y.; Garavito, R.M.
Deposited on	:	2010-11-26
Resolution	:	2.38 Å(reported)

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

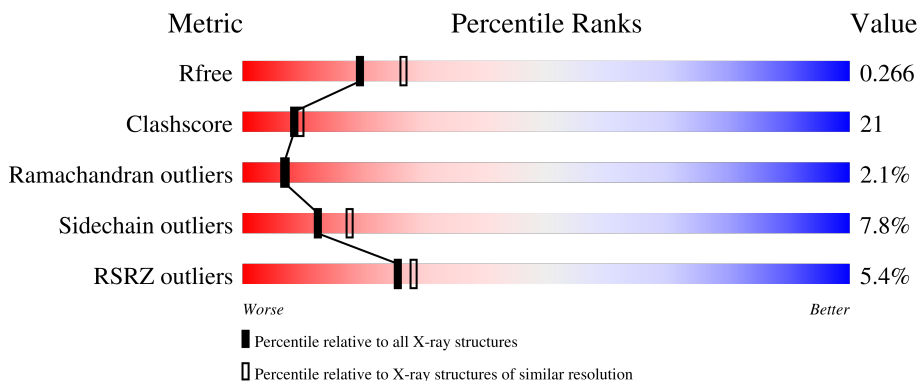|		
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 2.38 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.
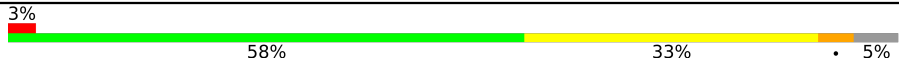
Metric	Percentile Ranks	Value
Rfree		0.266
Clashscore		21
Ramachandran outliers		2.1%
Sidechain outliers		7.8%
RSRZ outliers		5.4%

Worse   *Better*

▮ Percentile relative to all X-ray structures

▯ Percentile relative to X-ray structures of similar resolution

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R$_{free}$	130704	5509 (2.40-2.36)
Clashscore	141614	6082 (2.40-2.36)
Ramachandran outliers	138981	5973 (2.40-2.36)
Sidechain outliers	138945	5975 (2.40-2.36)
RSRZ outliers	127900	5397 (2.40-2.36)

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	326	3% / 56% / 36% / • 5%
1	B	326	2% / 61% / 29% / 5% •
1	C	326	5% / 57% / 32% / • 8%
1	D	326	11% / 47% / 39% / 6% 8%
1	E	326	3% / 60% / 33% / • 5%

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Mol	Chain	Length	Quality of chain
1	F	326	3% / 58% / 33% / 5%
1	G	326	5% / 57% / 30% / 5% / 7%
1	H	326	9% / 44% / 42% / 6% / 8%

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	FBP	C	327	-	-	X	-
2	FBP	D	328	X	-	-	-
2	FBP	F	327	X	-	-	-
2	FBP	G	327	X	-	-	-

2 Entry composition (i)

There are 4 unique types of molecules in this entry. The entry contains 19005 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 L-lactate dehydrogenase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	310	Total	C	N	O	S	0	0	0
			2367	1508	396	455	8			
1	B	312	Total	C	N	O	S	0	0	0
			2384	1520	399	457	8			
1	C	301	Total	C	N	O	S	0	0	0
			2300	1468	383	441	8			
1	D	301	Total	C	N	O	S	0	0	0
			2306	1475	382	441	8			
1	E	311	Total	C	N	O	S	0	0	0
			2379	1517	398	456	8			
1	F	311	Total	C	N	O	S	0	0	0
			2379	1517	398	456	8			
1	G	302	Total	C	N	O	S	0	0	0
			2315	1479	385	443	8			
1	H	301	Total	C	N	O	S	0	0	0
			2307	1475	383	441	8			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	321	HIS	-	expression tag	UNP P13714
A	322	HIS	-	expression tag	UNP P13714
A	323	HIS	-	expression tag	UNP P13714
A	324	HIS	-	expression tag	UNP P13714
A	325	HIS	-	expression tag	UNP P13714
A	326	HIS	-	expression tag	UNP P13714
B	321	HIS	-	expression tag	UNP P13714
B	322	HIS	-	expression tag	UNP P13714
B	323	HIS	-	expression tag	UNP P13714
B	324	HIS	-	expression tag	UNP P13714
B	325	HIS	-	expression tag	UNP P13714
B	326	HIS	-	expression tag	UNP P13714
C	321	HIS	-	expression tag	UNP P13714

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Chain	Residue	Modelled	Actual	Comment	Reference
C	322	HIS	-	expression tag	UNP P13714
C	323	HIS	-	expression tag	UNP P13714
C	324	HIS	-	expression tag	UNP P13714
C	325	HIS	-	expression tag	UNP P13714
C	326	HIS	-	expression tag	UNP P13714
D	321	HIS	-	expression tag	UNP P13714
D	322	HIS	-	expression tag	UNP P13714
D	323	HIS	-	expression tag	UNP P13714
D	324	HIS	-	expression tag	UNP P13714
D	325	HIS	-	expression tag	UNP P13714
D	326	HIS	-	expression tag	UNP P13714
E	321	HIS	-	expression tag	UNP P13714
E	322	HIS	-	expression tag	UNP P13714
E	323	HIS	-	expression tag	UNP P13714
E	324	HIS	-	expression tag	UNP P13714
E	325	HIS	-	expression tag	UNP P13714
E	326	HIS	-	expression tag	UNP P13714
F	321	HIS	-	expression tag	UNP P13714
F	322	HIS	-	expression tag	UNP P13714
F	323	HIS	-	expression tag	UNP P13714
F	324	HIS	-	expression tag	UNP P13714
F	325	HIS	-	expression tag	UNP P13714
F	326	HIS	-	expression tag	UNP P13714
G	321	HIS	-	expression tag	UNP P13714
G	322	HIS	-	expression tag	UNP P13714
G	323	HIS	-	expression tag	UNP P13714
G	324	HIS	-	expression tag	UNP P13714
G	325	HIS	-	expression tag	UNP P13714
G	326	HIS	-	expression tag	UNP P13714
H	321	HIS	-	expression tag	UNP P13714
H	322	HIS	-	expression tag	UNP P13714
H	323	HIS	-	expression tag	UNP P13714
H	324	HIS	-	expression tag	UNP P13714
H	325	HIS	-	expression tag	UNP P13714
H	326	HIS	-	expression tag	UNP P13714

- Molecule 2 is 1,6-di-O-phosphono-beta-D-fructofuranose (three-letter code: FBP) (formula: $C_6H_{14}O_{12}P_2$).

FBP

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total 20	C 6	O 12	P 2	0	0
2	D	1	Total 20	C 6	O 12	P 2	0	0
2	F	1	Total 20	C 6	O 12	P 2	0	0
2	G	1	Total 20	C 6	O 12	P 2	0	0

- Molecule 3 is NICOTINAMIDE-ADENINE-DINUCLEOTIDE (three-letter code: NAD) (formula: $C_{21}H_{27}N_7O_{14}P_2$).

NAD
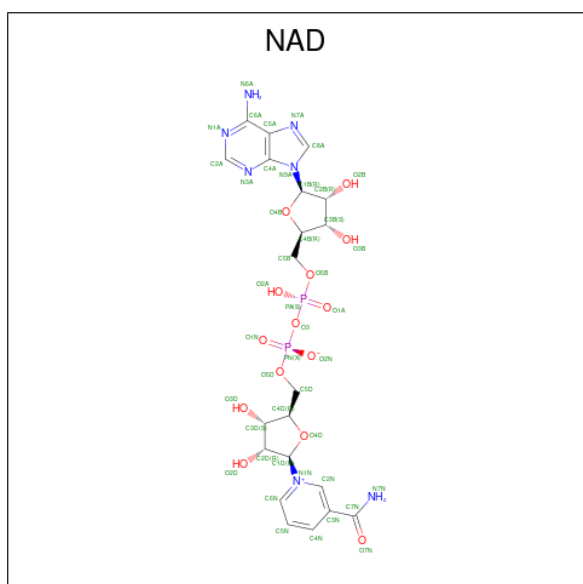
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	D	1	Total 44	C 21	N 7	O 14	P 2	0	0

- Molecule 4 is water.

| Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	22	Total 22	O 22	0	0
4	B	20	Total 20	O 20	0	0
4	C	24	Total 24	O 24	0	0
4	D	7	Total 7	O 7	0	0
4	E	13	Total 13	O 13	0	0
4	F	27	Total 27	O 27	0	0
4	G	20	Total 20	O 20	0	0
4	H	11	Total 11	O 11	0	0

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 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.

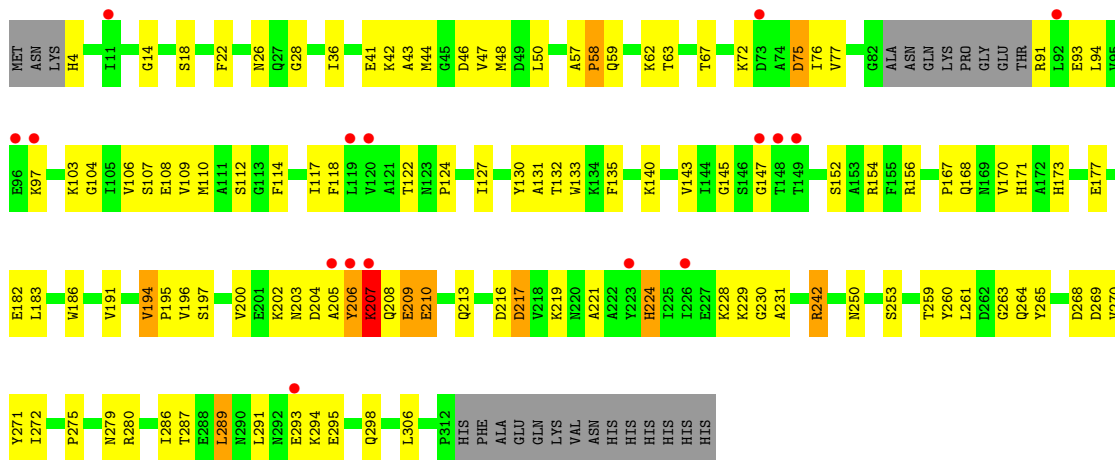- Molecule 1: L-lactate dehydrogenase
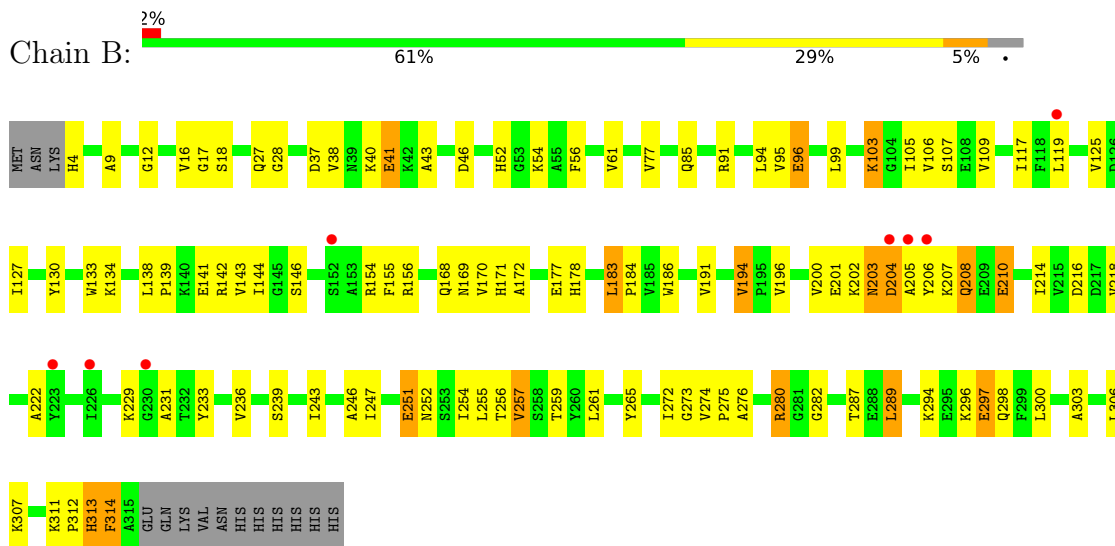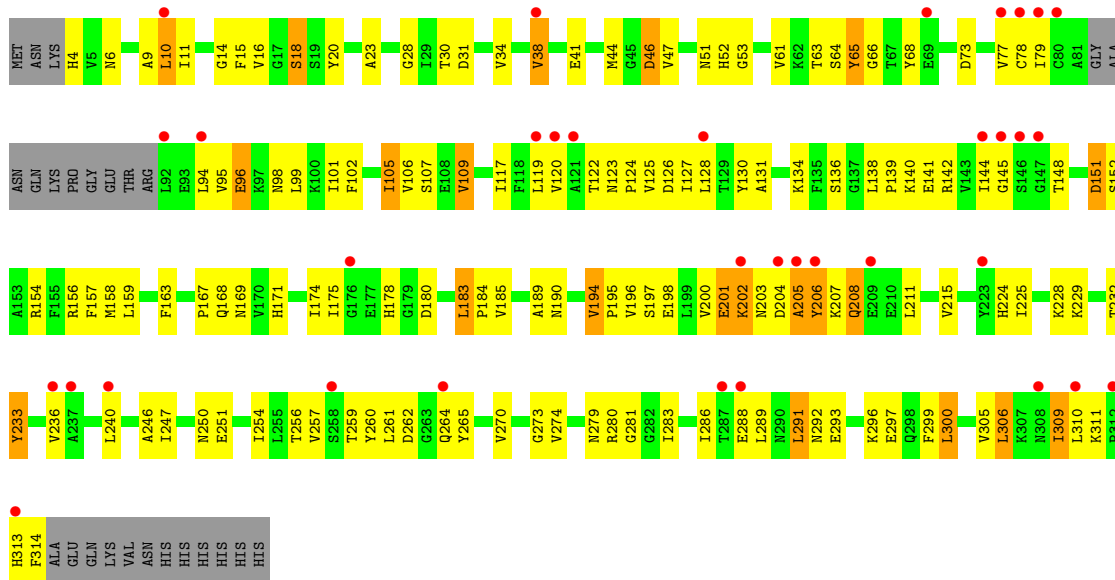
Chain A:

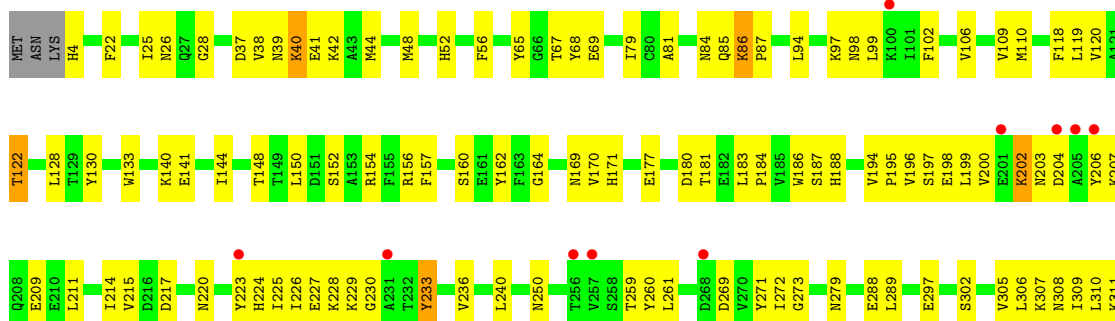- Molecule 1: L-lactate dehydrogenase

Chain B:

- Molecule 1: L-lactate dehydrogenase

Chain C:

• Molecule 1: L-lactate dehydrogenase

Chain D:

• Molecule 1: L-lactate dehydrogenase

Chain E:

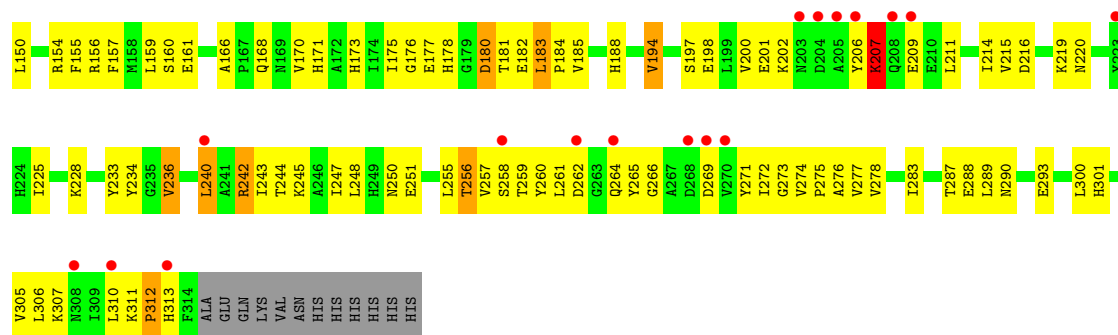• Molecule 1: L-lactate dehydrogenase

Chain F:

• Molecule 1: L-lactate dehydrogenase

Chain G:

• Molecule 1: L-lactate dehydrogenase

Chain H:

4 Data and refinement statistics ⓘ

Property	Value	Source
Space group	P 31	Depositor
Cell constants a, b, c, α, β, γ	171.04Å 171.04Å 96.27Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	29.45 – 2.38 29.45 – 2.38	Depositor EDS
% Data completeness (in resolution range)	99.5 (29.45-2.38) 99.5 (29.45-2.38)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.91 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6_289)	Depositor
R, R_{free}	0.214 , 0.269 0.210 , 0.266	Depositor DCC
R_{free} test set	3816 reflections (3.02%)	wwPDB-VP
Wilson B-factor (Å^2)	51.5	Xtriage
Anisotropy	0.011	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.33 , 43.6	EDS
L-test for twinning[2]	$< |L| > = 0.53, < L^2 > = 0.36$	Xtriage
Estimated twinning fraction	0.146 for -h,-k,l 0.000 for h,-h-k,-l 0.000 for -k,-h,-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	19005	wwPDB-VP
Average B, all atoms (Å^2)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.77% of the height of the origin peak. No significant pseudotranslation is detected.*

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[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: FBP, NAD

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	0.35	0/2412	0.57	0/3269
1	B	0.38	0/2431	0.56	0/3296
1	C	0.39	2/2343 (0.1%)	0.57	3/3175 (0.1%)
1	D	0.29	0/2351	0.51	0/3187
1	E	0.34	0/2426	0.52	0/3289
1	F	0.37	0/2426	0.55	0/3289
1	G	0.35	0/2360	0.55	0/3198
1	H	0.30	0/2352	0.50	0/3187
All	All	0.35	2/19101 (0.0%)	0.54	3/25890 (0.0%)

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	C	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	207	LYS	C-N	5.54	1.46	1.34
1	C	206	TYR	C-N	-5.23	1.22	1.34

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	207	LYS	CA-C-N	-8.14	99.30	117.20
1	C	207	LYS	O-C-N	6.36	132.88	122.70
1	C	206	TYR	C-N-CA	5.55	135.57	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	207	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	2367	0	2359	115	0
1	B	2384	0	2367	87	0
1	C	2300	0	2289	95	0
1	D	2306	0	2290	127	0
1	E	2379	0	2362	104	0
1	F	2379	0	2362	94	0
1	G	2315	0	2298	85	0
1	H	2307	0	2292	141	0
2	C	20	0	10	13	0
2	D	20	0	10	2	0
2	F	20	0	10	2	0
2	G	20	0	10	0	0
3	D	44	0	26	9	0
4	A	22	0	0	4	0
4	B	20	0	0	1	0
4	C	24	0	0	1	0
4	D	7	0	0	0	0
4	E	13	0	0	0	0
4	F	27	0	0	2	0
4	G	20	0	0	0	0
4	H	11	0	0	0	0
All	All	19005	0	18685	779	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 21.

The worst 5 of 779 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:H:98:ASN:HA	1:H:101:ILE:CD1	1.59	1.30
1:C:207:LYS:HG3	1:C:208:GLN:N	1.49	1.28
1:C:207:LYS:CG	1:C:208:GLN:H	1.41	1.25
1:H:98:ASN:CA	1:H:101:ILE:HD11	1.81	1.11
1:A:238:MET:HG3	1:D:53:GLY:HA3	1.36	1.04

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	308/326 (94%)	281 (91%)	26 (8%)	1 (0%)	41	53
1	B	310/326 (95%)	276 (89%)	27 (9%)	7 (2%)	6	6
1	C	297/326 (91%)	258 (87%)	37 (12%)	2 (1%)	22	30
1	D	297/326 (91%)	251 (84%)	36 (12%)	10 (3%)	3	3
1	E	309/326 (95%)	273 (88%)	30 (10%)	6 (2%)	8	9
1	F	309/326 (95%)	271 (88%)	32 (10%)	6 (2%)	8	9
1	G	298/326 (91%)	266 (89%)	23 (8%)	9 (3%)	4	3
1	H	297/326 (91%)	255 (86%)	32 (11%)	10 (3%)	3	3
All	All	2425/2608 (93%)	2131 (88%)	243 (10%)	51 (2%)	7	7

5 of 51 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	204	ASP
1	D	202	LYS
1	D	208	GLN
1	F	204	ASP
1	G	205	ALA

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	252/267 (94%)	234 (93%)	18 (7%)	14	21
1	B	253/267 (95%)	233 (92%)	20 (8%)	12	17
1	C	245/267 (92%)	226 (92%)	19 (8%)	12	17
1	D	246/267 (92%)	221 (90%)	25 (10%)	7	9
1	E	253/267 (95%)	238 (94%)	15 (6%)	19	29
1	F	253/267 (95%)	231 (91%)	22 (9%)	10	14
1	G	247/267 (92%)	230 (93%)	17 (7%)	15	22
1	H	246/267 (92%)	226 (92%)	20 (8%)	11	16
All	All	1995/2136 (93%)	1839 (92%)	156 (8%)	12	17

5 of 156 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	293	GLU
1	H	112	SER
1	G	2	ASN
1	G	202	LYS
1	H	216	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 24 such sidechains are listed below:

Mol	Chain	Res	Type
1	F	85	GLN
1	G	168	GLN
1	G	2	ASN
1	G	252	ASN
1	C	98	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 monosaccharides in this entry.

5.6 Ligand geometry ⓘ

5 ligands are modelled in this entry.

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	FBP	G	327	-	18,20,20	1.03	2 (11%)	23,32,32	1.38	4 (17%)
2	FBP	C	327	-	18,20,20	1.06	1 (5%)	23,32,32	1.82	6 (26%)
2	FBP	D	328	-	18,20,20	0.93	1 (5%)	23,32,32	1.02	1 (4%)
3	NAD	D	327	-	42,48,48	1.81	4 (9%)	50,73,73	1.39	6 (12%)
2	FBP	F	327	-	18,20,20	0.97	2 (11%)	23,32,32	1.46	3 (13%)

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	FBP	G	327	-	1/1/6/6	4/13/32/32	0/1/1/1
2	FBP	D	328	-	1/1/6/6	8/13/32/32	0/1/1/1
2	FBP	C	327	-	-	2/13/32/32	0/1/1/1
3	NAD	D	327	-	-	9/26/62/62	0/5/5/5
2	FBP	F	327	-	1/1/6/6	6/13/32/32	0/1/1/1

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	327	NAD	O7N-C7N	9.39	1.42	1.24
3	D	327	NAD	C2A-N3A	4.05	1.38	1.32
2	C	327	FBP	O2-C2	2.88	1.45	1.40
2	G	327	FBP	O2-C2	2.78	1.45	1.40
2	D	328	FBP	O2-C2	2.65	1.45	1.40

The worst 5 of 20 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	D	327	NAD	N3A-C2A-N1A	-5.42	120.21	128.68
2	G	327	FBP	P1-O1-C1	4.45	130.54	118.30
2	F	327	FBP	P1-O1-C1	4.34	130.26	118.30
2	C	327	FBP	O6P-P2-O6	4.33	118.26	106.73
3	D	327	NAD	PN-O3-PA	-3.52	120.73	132.83

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	D	328	FBP	C2
2	F	327	FBP	C2
2	G	327	FBP	C2

5 of 29 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	327	FBP	C6-O6-P2-O6P
2	D	328	FBP	C1-O1-P1-O2P
2	D	328	FBP	O1-C1-C2-C3
2	F	327	FBP	O1-C1-C2-O2
2	F	327	FBP	O1-C1-C2-C3

There are no ring outliers.

4 monomers are involved in 26 short contacts:

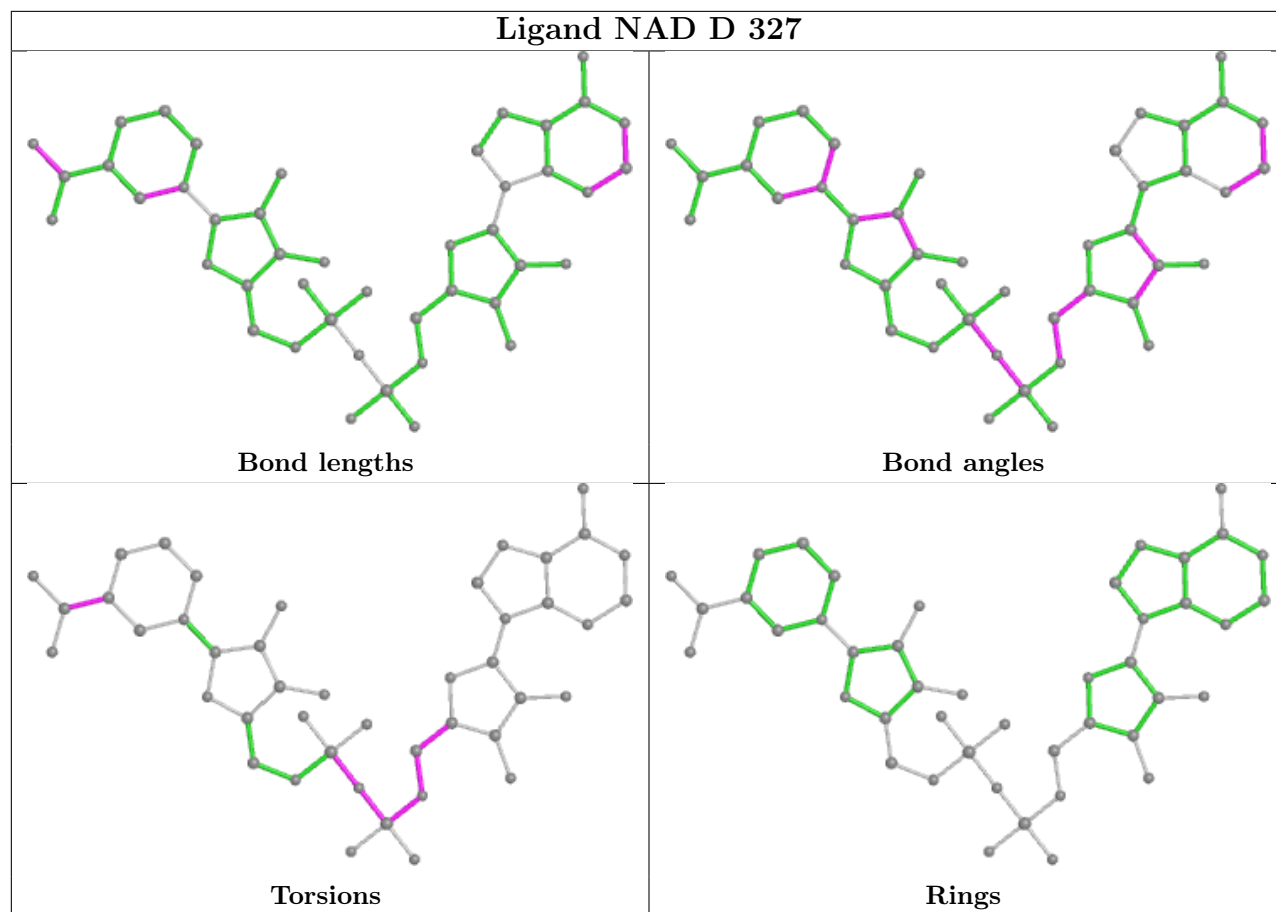| Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	327	FBP	13	0
2	D	328	FBP	2	0
3	D	327	NAD	9	0
2	F	327	FBP	2	0

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
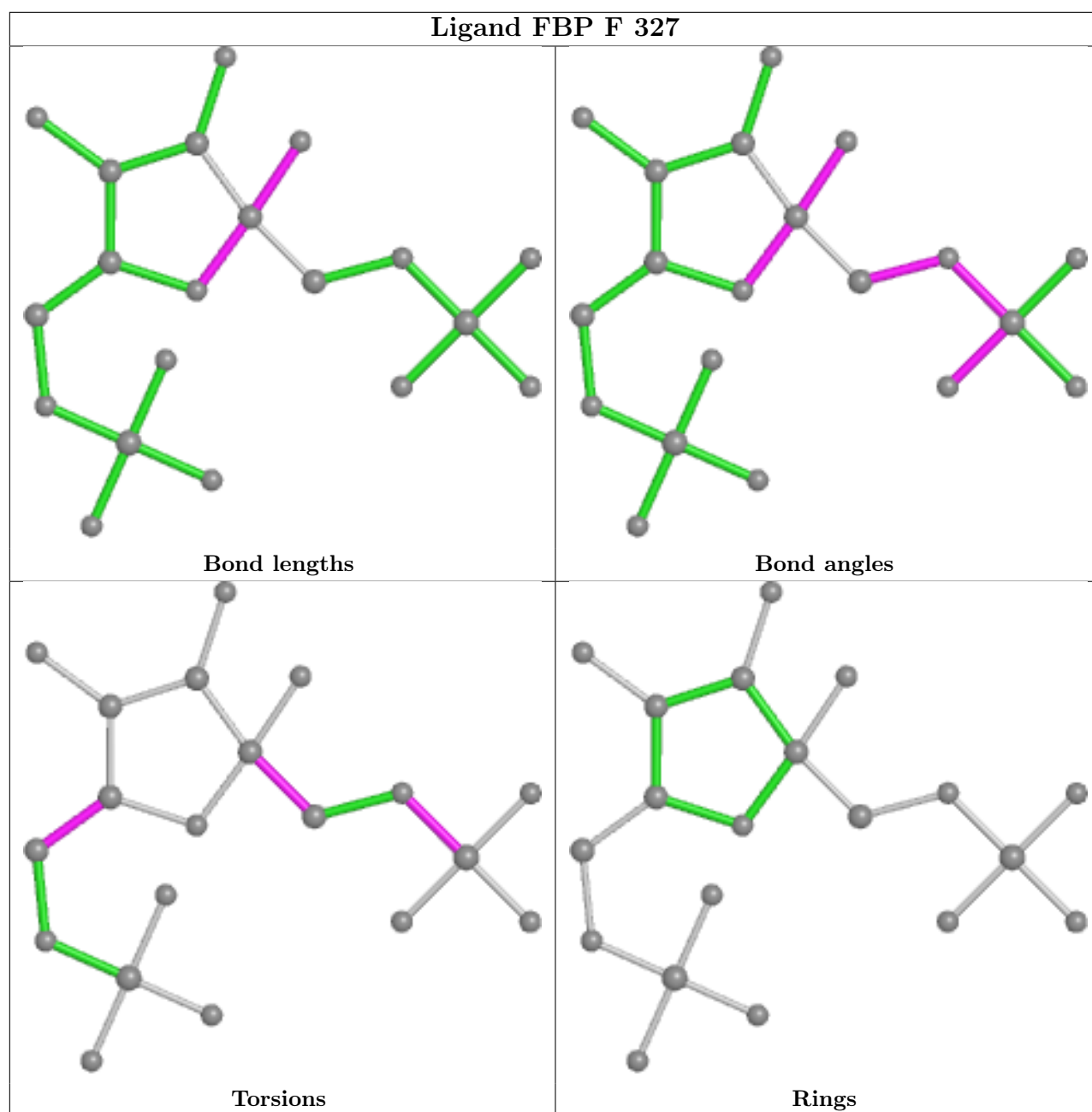
addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. 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 FBP G 327

Bond lengths

Bond angles

Torsions

Rings

Ligand FBP C 327

Bond lengths

Bond angles

Torsions

Rings

Ligand FBP D 328

Bond lengths

Bond angles

Torsions

Rings

Ligand NAD D 327

Bond lengths

Bond angles

Torsions

Rings

Ligand FBP F 327

Bond lengths

Bond angles

Torsions

Rings
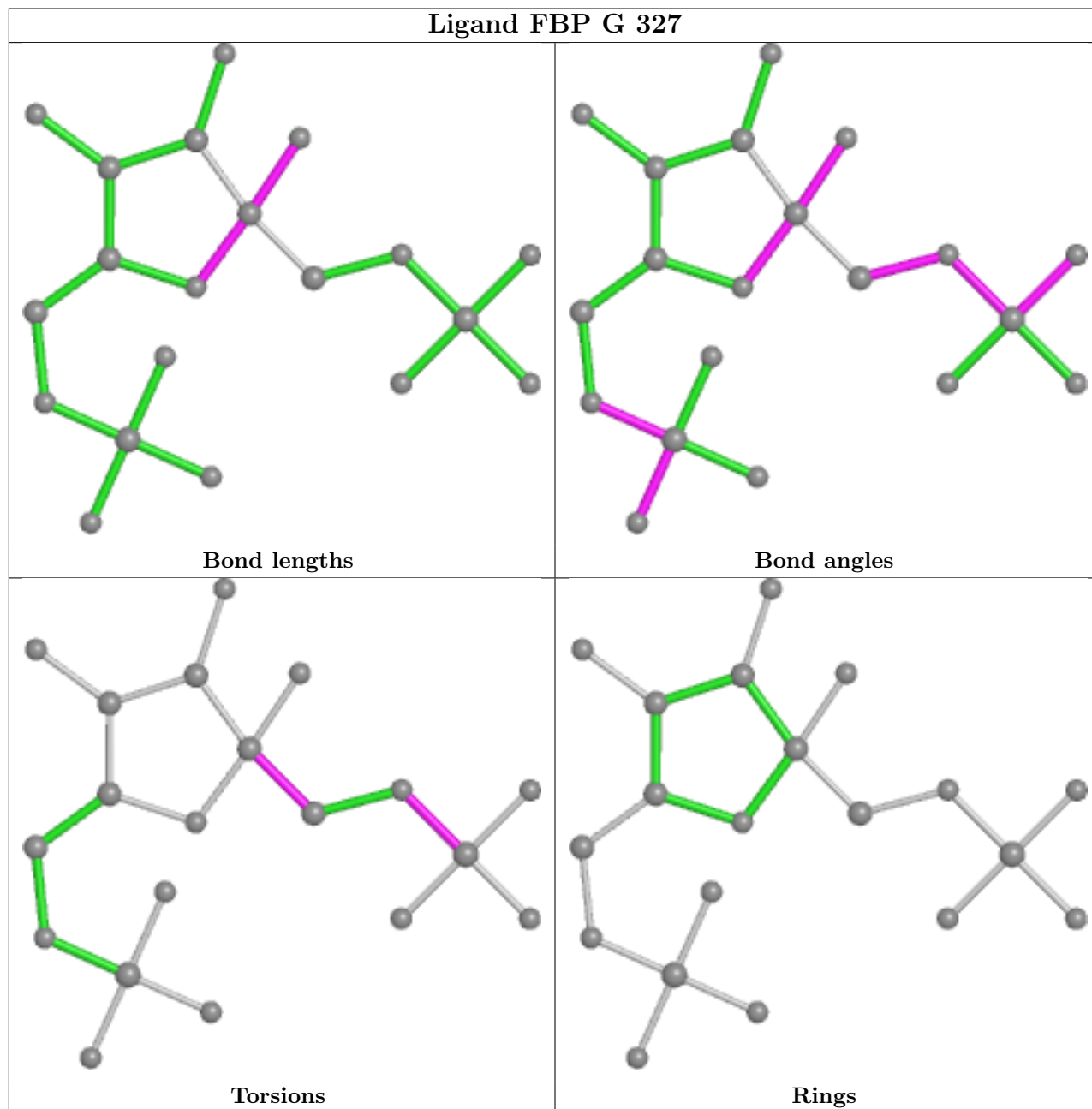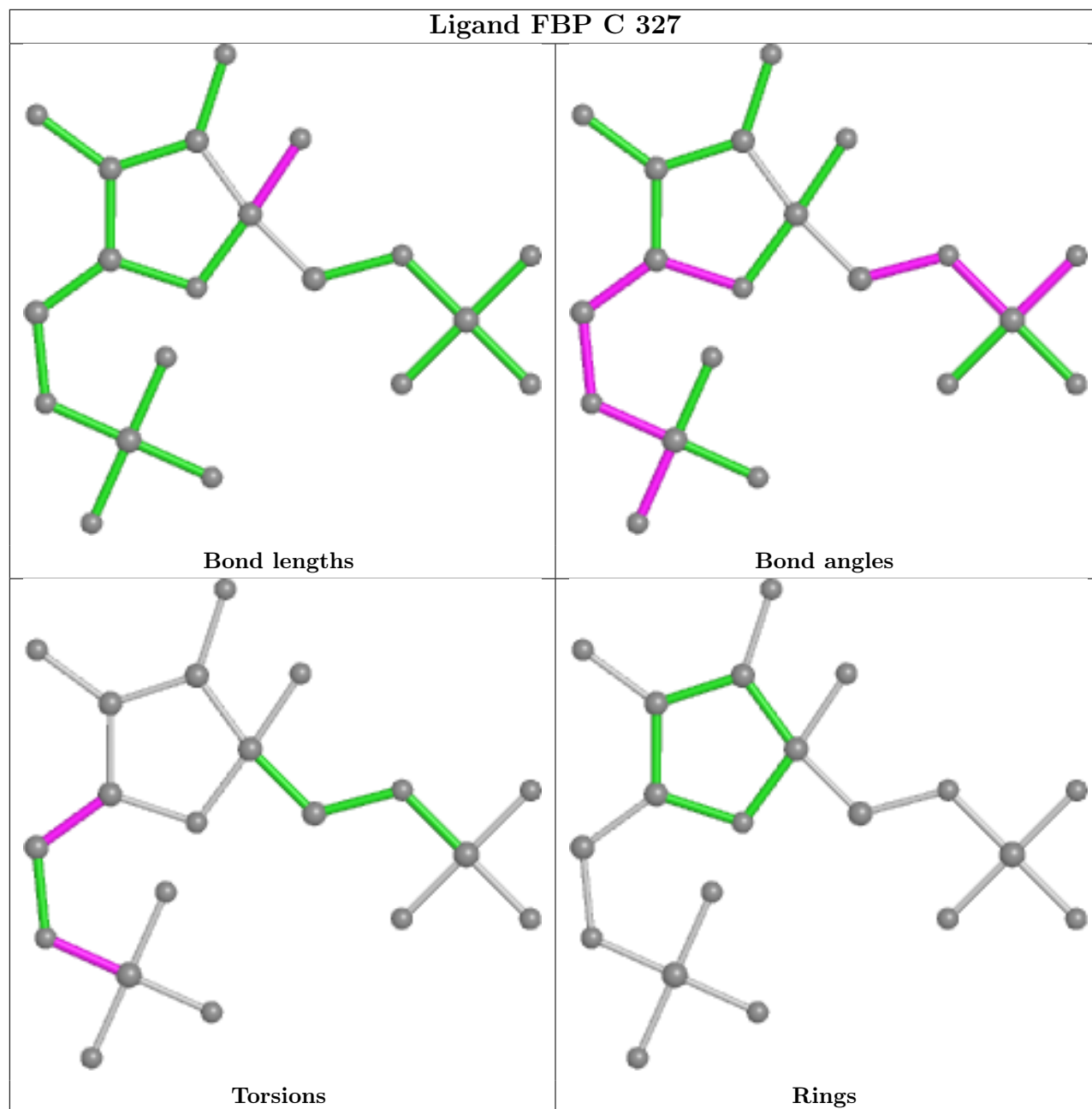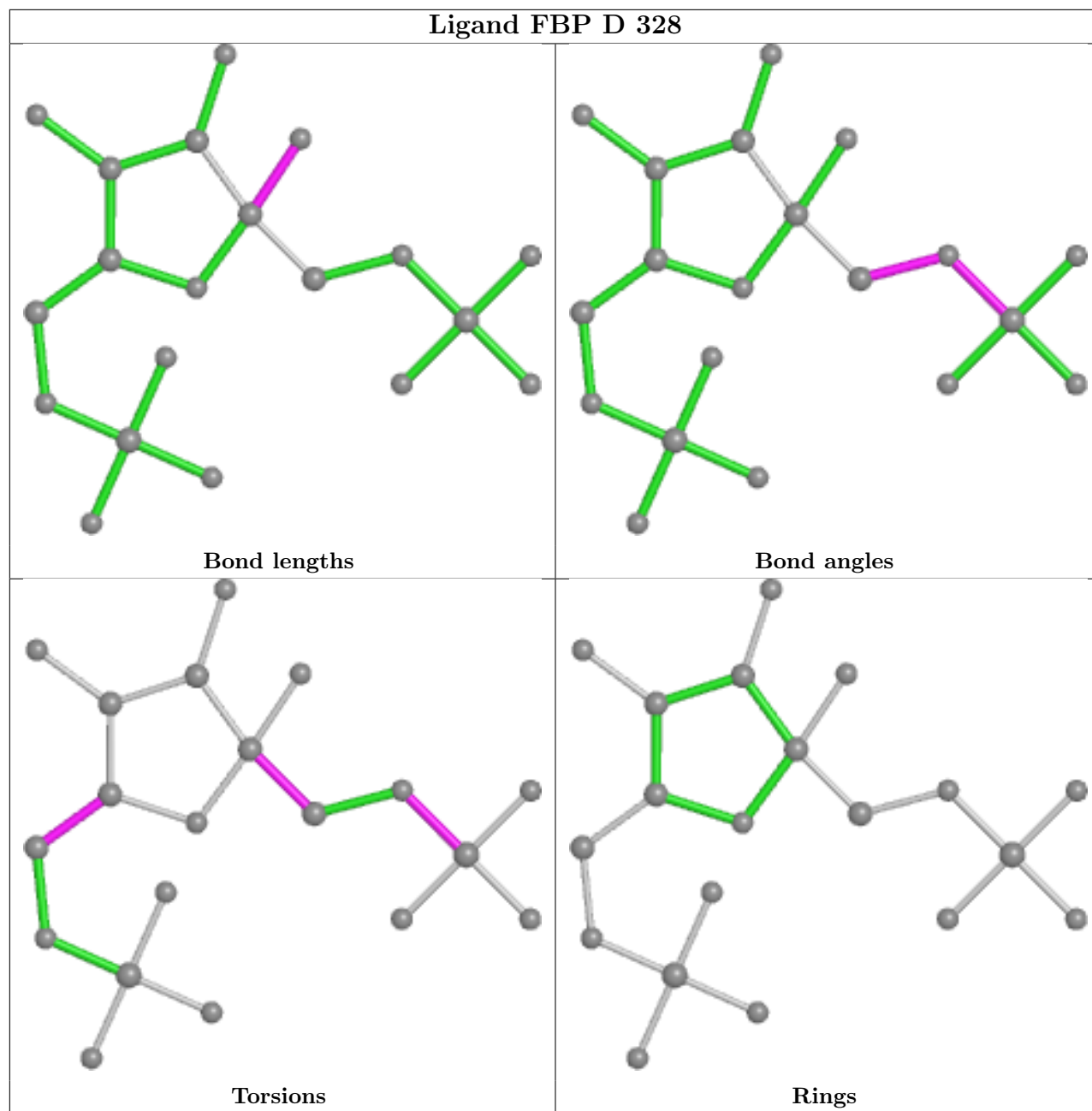
5.7 Other polymers ⓘ

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	310/326 (95%)	0.02	9 (2%)	51	53	30, 50, 71, 90	0
1	B	312/326 (95%)	0.10	8 (2%)	56	57	28, 46, 70, 80	0
1	C	301/326 (92%)	0.17	16 (5%)	26	29	30, 50, 72, 89	0
1	D	301/326 (92%)	0.58	35 (11%)	4	5	45, 67, 89, 103	0
1	E	311/326 (95%)	0.03	11 (3%)	44	47	33, 50, 69, 89	0
1	F	311/326 (95%)	0.12	9 (2%)	51	53	30, 50, 71, 90	0
1	G	302/326 (92%)	0.21	15 (4%)	28	31	31, 51, 73, 90	0
1	H	301/326 (92%)	0.53	30 (9%)	7	8	45, 65, 95, 116	0
All	All	2449/2608 (93%)	0.22	133 (5%)	25	28	28, 53, 81, 116	0

The worst 5 of 133 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	223	TYR	9.4
1	B	204	ASP	7.8
1	E	206	TYR	6.8
1	G	206	TYR	6.7
1	D	205	ALA	6.1

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 ⓘ

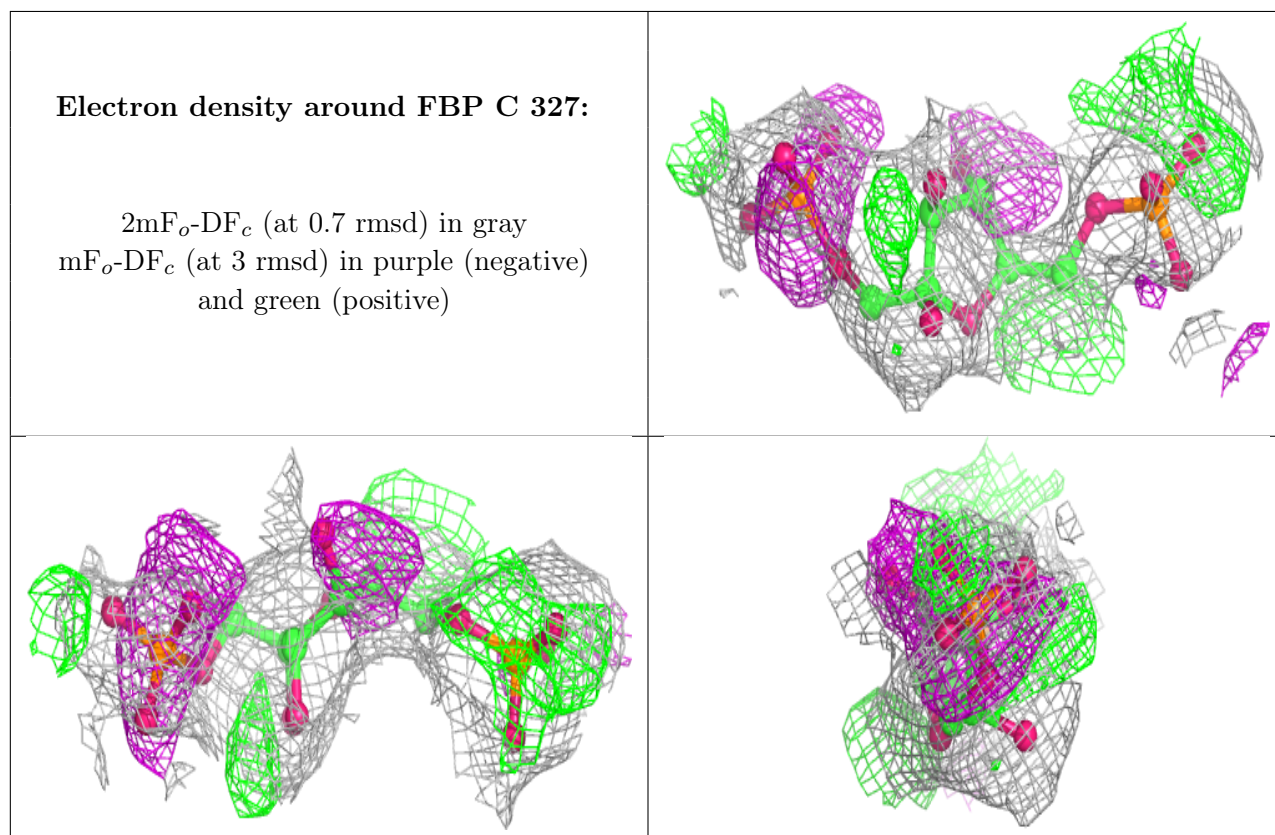There are no monosaccharides in this entry.

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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
2	FBP	C	327	20/20	0.76	0.26	38,67,79,87	0
3	NAD	D	327	44/44	0.92	0.14	66,74,81,83	0
2	FBP	D	328	20/20	0.93	0.13	46,59,65,79	0
2	FBP	F	327	20/20	0.96	0.12	43,53,60,65	0
2	FBP	G	327	20/20	0.97	0.16	36,42,52,60	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.
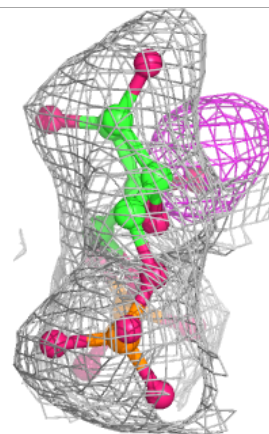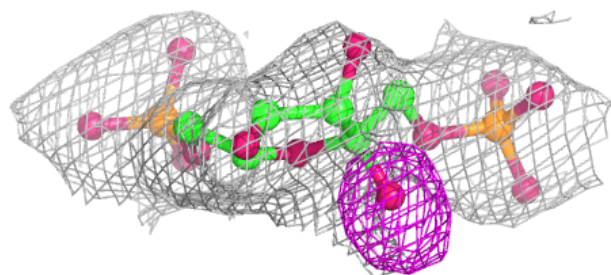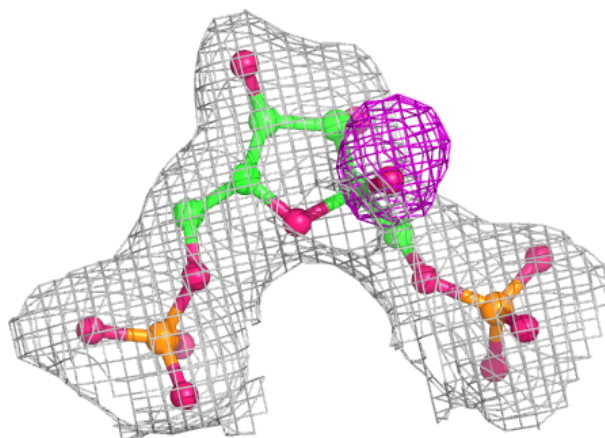

Electron density around FBP C 327:

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

Electron density around NAD D 327:

$2mF_o$-DF_c (at 0.7 rmsd) in gray
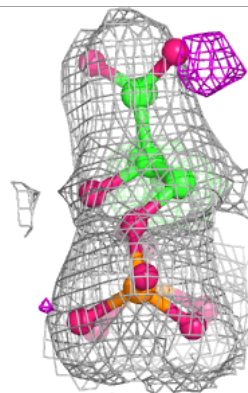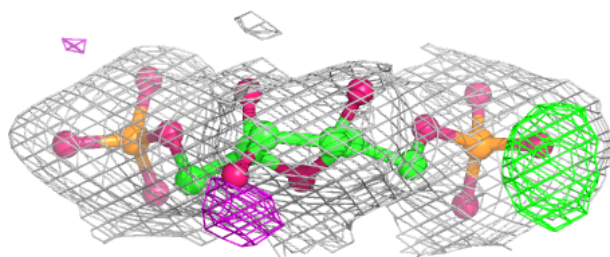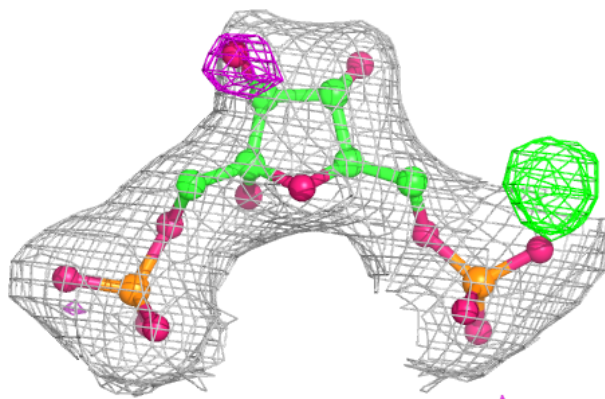mF_o-DF_c (at 3 rmsd) in purple (negative)
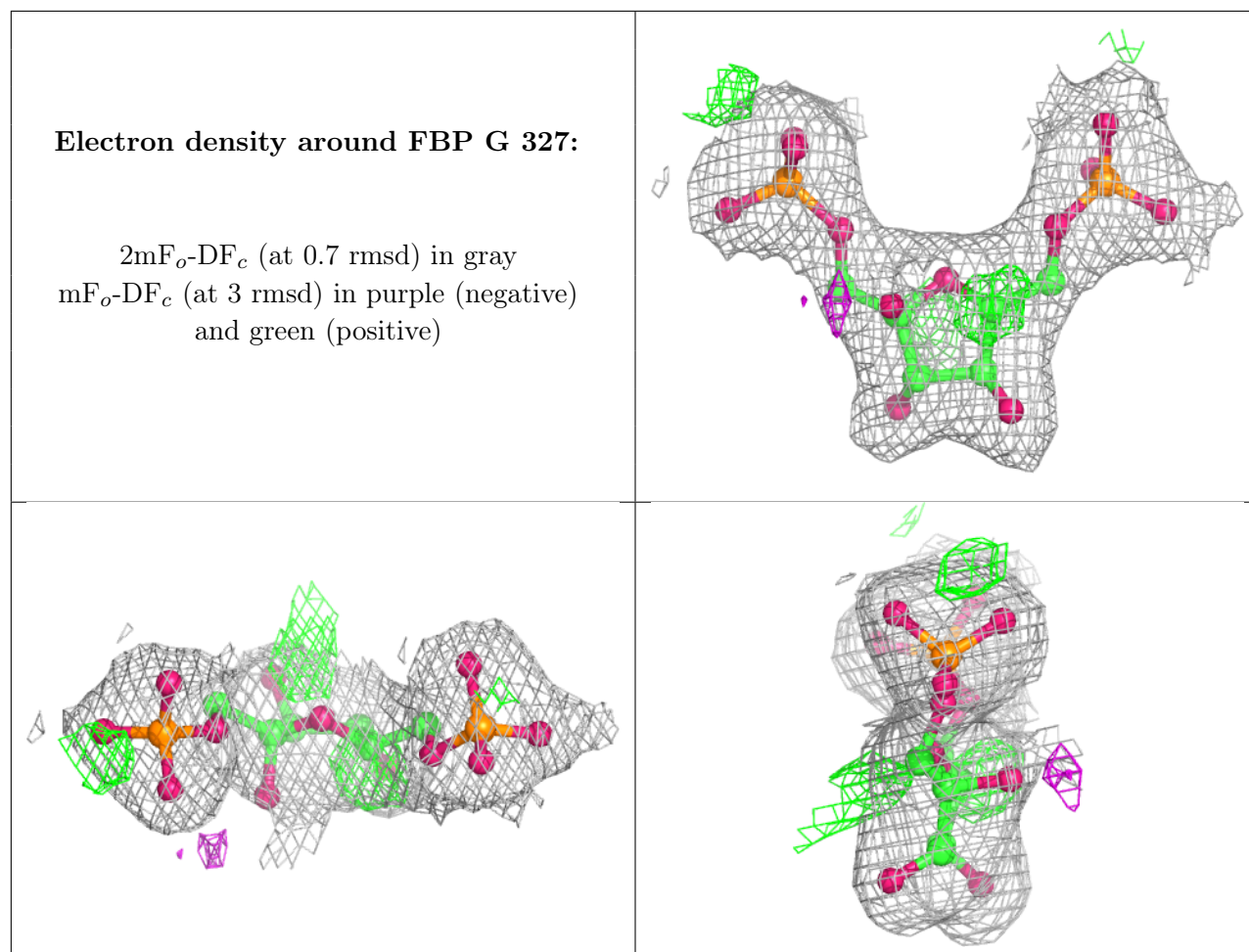and green (positive)
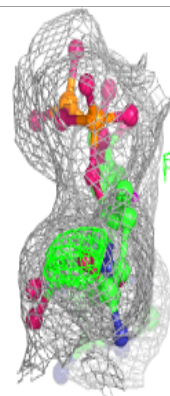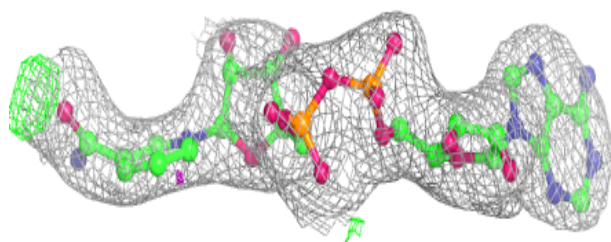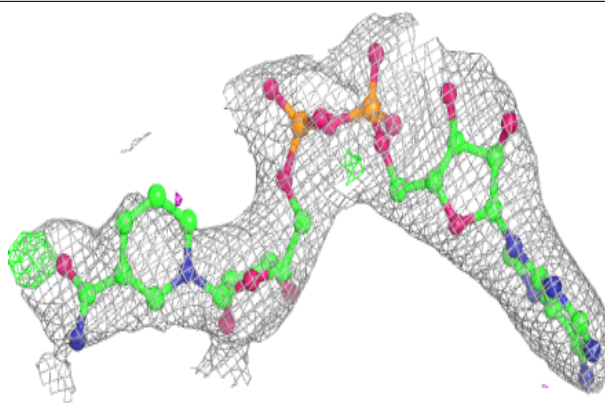
Electron density around FBP D 328:

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

Electron density around FBP F 327:

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

Electron density around FBP G 327:

$2mF_o$-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.