



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 10, 2024 – 02:39 PM EST

PDB ID : 2RHL
Title : Synthetic Gene Encoded Bacillus Subtilis FtsZ NCS Dimer with Bound GDP
Authors : Lovell, S.; Halloran, Z.; Hjerrild, K.; Sheridan, D.; Burgin, A.; Stewart, L.;
Accelerated Technologies Center for Gene to 3D Structure (ATCG3D)
Deposited on : 2007-10-09
Resolution : 2.45 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 : 4.02b-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

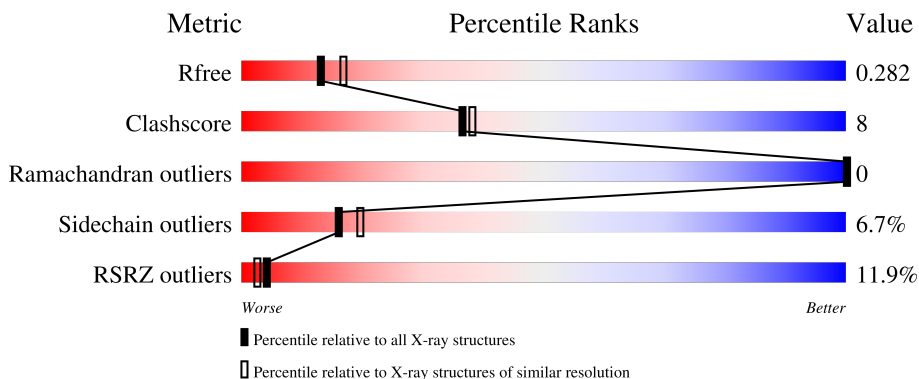
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.45 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	1544 (2.48-2.44)
Clashscore	141614	1613 (2.48-2.44)
Ramachandran outliers	138981	1598 (2.48-2.44)
Sidechain outliers	138945	1598 (2.48-2.44)
RSRZ outliers	127900	1523 (2.48-2.44)

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	325	
1	B	325	

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4642 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 Cell Division Protein ftsZ.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	305	2199	1369	379	441	10	0	0	0
1	B	315	2290	1427	397	456	10	0	0	0

There are 42 discrepancies between the modelled and reference sequences:

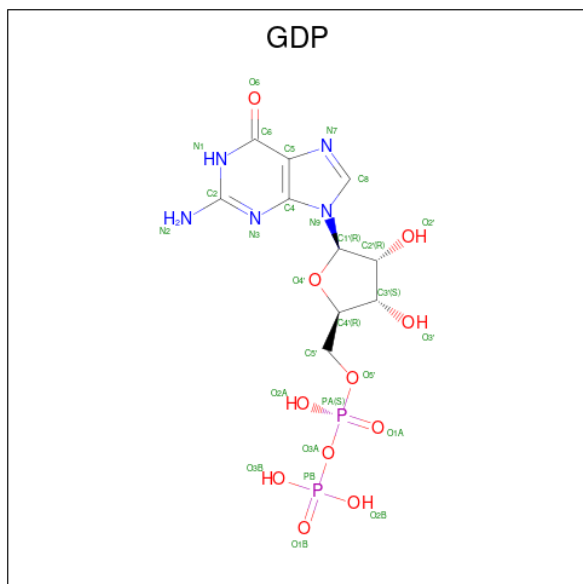
Chain	Residue	Modelled	Actual	Comment	Reference
A	11	MET	-	expression tag	UNP P17865
A	316	LEU	-	expression tag	UNP P17865
A	317	GLU	-	expression tag	UNP P17865
A	318	ASN	-	expression tag	UNP P17865
A	319	LEU	-	expression tag	UNP P17865
A	320	TYR	-	expression tag	UNP P17865
A	321	PHE	-	expression tag	UNP P17865
A	322	GLN	-	expression tag	UNP P17865
A	323	GLY	-	expression tag	UNP P17865
A	324	HIS	-	expression tag	UNP P17865
A	325	HIS	-	expression tag	UNP P17865
A	326	HIS	-	expression tag	UNP P17865
A	327	HIS	-	expression tag	UNP P17865
A	328	HIS	-	expression tag	UNP P17865
A	329	HIS	-	expression tag	UNP P17865
A	330	GLU	-	expression tag	UNP P17865
A	331	TYR	-	expression tag	UNP P17865
A	332	MET	-	expression tag	UNP P17865
A	333	PRO	-	expression tag	UNP P17865
A	334	MET	-	expression tag	UNP P17865
A	335	GLU	-	expression tag	UNP P17865
B	11	MET	-	expression tag	UNP P17865
B	316	LEU	-	expression tag	UNP P17865
B	317	GLU	-	expression tag	UNP P17865
B	318	ASN	-	expression tag	UNP P17865

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Chain	Residue	Modelled	Actual	Comment	Reference
B	319	LEU	-	expression tag	UNP P17865
B	320	TYR	-	expression tag	UNP P17865
B	321	PHE	-	expression tag	UNP P17865
B	322	GLN	-	expression tag	UNP P17865
B	323	GLY	-	expression tag	UNP P17865
B	324	HIS	-	expression tag	UNP P17865
B	325	HIS	-	expression tag	UNP P17865
B	326	HIS	-	expression tag	UNP P17865
B	327	HIS	-	expression tag	UNP P17865
B	328	HIS	-	expression tag	UNP P17865
B	329	HIS	-	expression tag	UNP P17865
B	330	GLU	-	expression tag	UNP P17865
B	331	TYR	-	expression tag	UNP P17865
B	332	MET	-	expression tag	UNP P17865
B	333	PRO	-	expression tag	UNP P17865
B	334	MET	-	expression tag	UNP P17865
B	335	GLU	-	expression tag	UNP P17865

- Molecule 2 is GUANOSINE-5'-DIPHOSPHATE (three-letter code: GDP) (formula: $C_{10}H_{15}N_5O_{11}P_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	
2	A	1	Total	C	N	O	P	0	0
				28	10	5	11		
2	B	1	Total	C	N	O	P	0	0
				28	10	5	11		

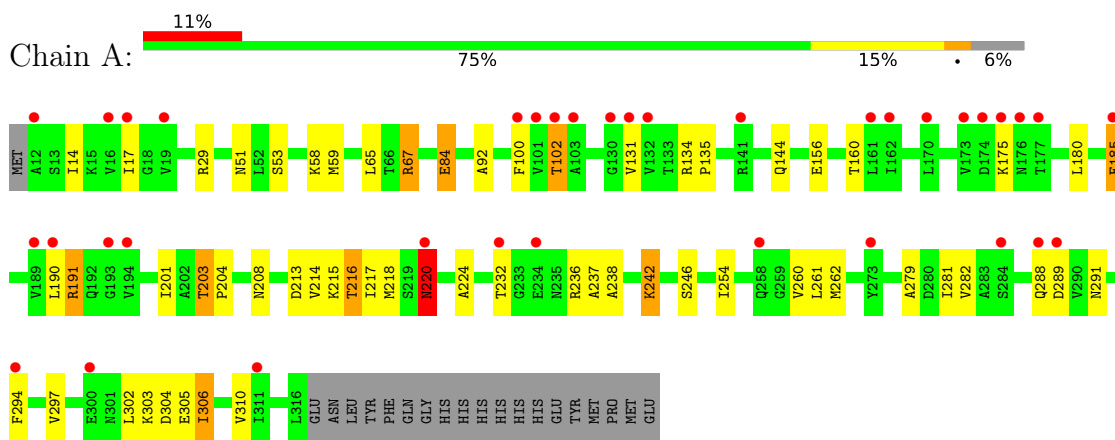
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	51	Total 51	O 51	0	0
3	B	46	Total 46	O 46	0	0

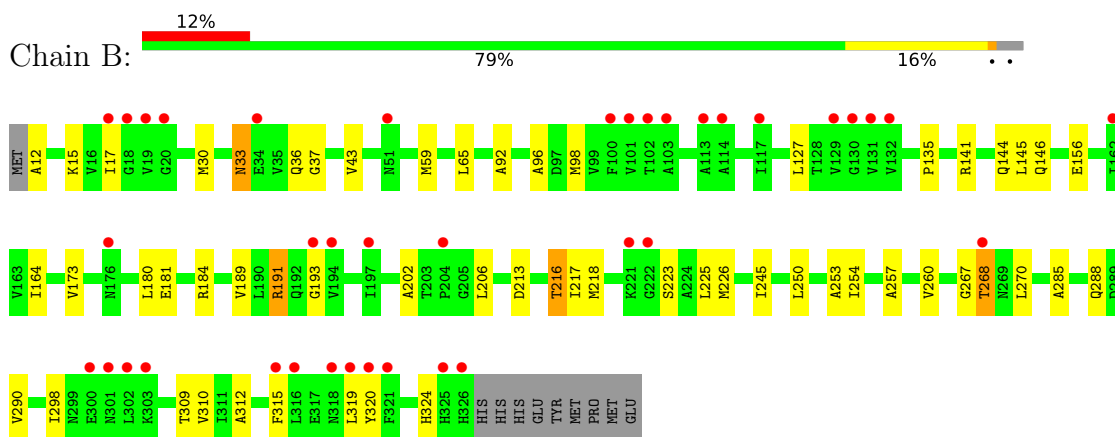
3 Residue-property plots

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 ($\text{RSRZ} > 2$). 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: Cell Division Protein ftsZ



- Molecule 1: Cell Division Protein ftsZ



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	82.29Å 97.58Å 135.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.45 29.52 – 2.45	Depositor EDS
% Data completeness (in resolution range)	99.0 (30.00-2.45) 99.0 (29.52-2.45)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.77 (at 2.45Å)	Xtrriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.227 , 0.270 0.233 , 0.282	Depositor DCC
R_{free} test set	2039 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtrriage
Anisotropy	0.071	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 50.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.35$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	4642	wwPDB-VP
Average B, all atoms (Å ²)	67.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.34% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GDP

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	0.75	3/2214 (0.1%)	0.75	2/2991 (0.1%)
1	B	0.72	0/2310	0.73	1/3121 (0.0%)
All	All	0.73	3/4524 (0.1%)	0.74	3/6112 (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	A	0	1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	185	GLU	CG-CD	5.57	1.60	1.51
1	A	84	GLU	CD-OE2	5.51	1.31	1.25
1	A	185	GLU	CB-CG	5.00	1.61	1.52

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	191	ARG	NE-CZ-NH2	-5.47	117.56	120.30
1	A	134	ARG	NE-CZ-NH1	5.42	123.01	120.30
1	A	191	ARG	NE-CZ-NH1	5.07	122.83	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	220	ASN	Peptide

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	2199	0	2257	35	0
1	B	2290	0	2330	40	0
2	A	28	0	12	0	0
2	B	28	0	12	0	0
3	A	51	0	0	2	0
3	B	46	0	0	3	0
All	All	4642	0	4611	72	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 8.

All (72) 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:84:GLU:OE1	3:A:354:HOH:O	1.67	1.12
1:B:225:LEU:HD12	1:B:315:PHE:CE2	2.13	0.83
1:B:193:GLY:HA2	1:B:226:MET:HE3	1.62	0.82
1:B:225:LEU:CD1	1:B:315:PHE:CE2	2.69	0.76
1:A:201:ILE:HD11	1:A:214:VAL:HG21	1.69	0.74
1:A:67:ARG:HH22	1:B:146:GLN:HE22	1.40	0.68
1:B:223:SER:HA	3:B:339:HOH:O	1.94	0.67
1:A:237:ALA:HA	1:A:306:ILE:HD11	1.76	0.67
1:B:30:MET:HG2	1:B:191:ARG:HG3	1.79	0.65
1:A:213:ASP:O	1:A:216:THR:HB	1.98	0.64
1:B:135:PRO:O	1:B:144:GLN:NE2	2.31	0.64
1:B:193:GLY:HA2	1:B:226:MET:CE	2.28	0.63
1:B:181:GLU:OE1	1:B:184:ARG:HD3	1.98	0.62
1:B:206:LEU:HD11	1:B:270:LEU:O	1.99	0.62
1:B:17:ILE:HD11	1:B:43:VAL:HG21	1.83	0.60
1:A:254:ILE:HD12	1:A:310:VAL:HG11	1.84	0.60
1:B:268:THR:HA	1:B:298:ILE:HD12	1.84	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:254:ILE:HD12	1:B:310:VAL:HG11	1.85	0.58
1:A:254:ILE:CD1	1:A:310:VAL:HG11	2.32	0.58
1:A:215:LYS:NZ	3:A:366:HOH:O	2.37	0.57
1:A:59:MET:HE2	1:A:92:ALA:HB2	1.85	0.57
1:B:17:ILE:HD11	1:B:43:VAL:CG2	2.36	0.56
1:B:257:ALA:HB2	1:B:312:ALA:HB1	1.87	0.56
1:B:15:LYS:HD2	1:B:96:ALA:HB2	1.88	0.55
1:A:216:THR:HG22	1:A:217:ILE:HG23	1.89	0.53
1:B:253:ALA:O	1:B:315:PHE:HZ	1.92	0.53
1:A:302:LEU:HD22	1:A:305:GLU:HB3	1.90	0.53
1:A:238:ALA:HA	1:A:281:ILE:CD1	2.39	0.52
1:B:12:ALA:O	3:B:358:HOH:O	2.19	0.52
1:A:160:THR:HG23	1:A:220:ASN:HB2	1.92	0.52
1:A:53:SER:O	1:A:58:LYS:NZ	2.37	0.51
1:B:254:ILE:HG22	3:B:363:HOH:O	2.11	0.51
1:A:203:THR:HG22	1:A:204:PRO:HD2	1.93	0.51
1:B:245:ILE:HD12	1:B:285:ALA:HB2	1.92	0.51
1:B:37:GLY:HA3	1:B:202:ALA:HB1	1.93	0.50
1:B:59:MET:HE1	1:B:92:ALA:HB2	1.94	0.50
1:A:262:MET:SD	1:A:282:VAL:HG21	2.51	0.50
1:A:14:ILE:HD11	1:A:201:ILE:HG22	1.94	0.49
1:B:141:ARG:NH1	1:B:145:LEU:HD21	2.28	0.49
1:A:102:THR:HG22	1:A:190:LEU:HD22	1.94	0.48
1:A:59:MET:HE3	1:A:59:MET:HB2	1.67	0.47
1:B:225:LEU:CD1	1:B:315:PHE:CZ	2.96	0.47
1:B:217:ILE:HD11	1:B:218:MET:HE1	1.96	0.47
1:A:236:ARG:HD2	1:A:306:ILE:HG23	1.95	0.47
1:A:261:LEU:C	1:A:261:LEU:HD23	2.35	0.47
1:A:67:ARG:HH22	1:B:146:GLN:NE2	2.10	0.46
1:A:238:ALA:O	1:A:242:LYS:HB2	2.17	0.45
1:B:260:VAL:HG23	1:B:290:VAL:HG21	2.00	0.44
1:B:225:LEU:HD11	1:B:315:PHE:CE2	2.52	0.44
1:A:220:ASN:OD1	1:A:224:ALA:HB2	2.17	0.43
1:B:225:LEU:HD12	1:B:315:PHE:CZ	2.52	0.43
1:A:237:ALA:HA	1:A:306:ILE:CD1	2.45	0.43
1:A:216:THR:HG23	1:A:291:ASN:ND2	2.33	0.43
1:A:279:ALA:HB1	1:A:294:PHE:CZ	2.54	0.43
1:A:135:PRO:O	1:A:144:GLN:NE2	2.51	0.43
1:B:226:MET:HE2	1:B:309:THR:HG23	2.00	0.43
1:A:232:THR:HG22	1:A:304:ASP:C	2.39	0.43
1:B:213:ASP:HA	1:B:216:THR:HG23	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:225:LEU:HD11	1:B:315:PHE:CZ	2.53	0.43
1:B:267:GLY:C	1:B:298:ILE:HG23	2.39	0.42
1:B:33:ASN:HD22	1:B:33:ASN:N	2.16	0.42
1:B:217:ILE:HD11	1:B:218:MET:CE	2.49	0.42
1:A:17:ILE:HG22	1:A:100:PHE:O	2.20	0.42
1:A:59:MET:HE2	1:A:92:ALA:CB	2.50	0.41
1:A:102:THR:HG22	1:A:131:VAL:O	2.21	0.41
1:A:260:VAL:HG13	1:A:310:VAL:HG13	2.03	0.41
1:B:98:MET:HG3	1:B:127:LEU:HB3	2.02	0.41
1:B:164:ILE:HD13	1:B:189:VAL:HG12	2.03	0.41
1:B:320:TYR:CE1	1:B:324:HIS:CD2	3.08	0.41
1:A:65:LEU:HD11	1:B:65:LEU:HD11	2.01	0.41
1:B:141:ARG:HH12	1:B:145:LEU:HD21	1.85	0.41
1:A:238:ALA:HA	1:A:281:ILE:HD13	2.03	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	303/325 (93%)	292 (96%)	11 (4%)	0	100	100
1	B	313/325 (96%)	307 (98%)	6 (2%)	0	100	100
All	All	616/650 (95%)	599 (97%)	17 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	227/246 (92%)	206 (91%)	21 (9%)	9	9
1	B	236/246 (96%)	226 (96%)	10 (4%)	30	39
All	All	463/492 (94%)	432 (93%)	31 (7%)	16	20

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

Mol	Chain	Res	Type
1	A	29	ARG
1	A	51	ASN
1	A	67	ARG
1	A	102	THR
1	A	156	GLU
1	A	175	LYS
1	A	180	LEU
1	A	185	GLU
1	A	191	ARG
1	A	203	THR
1	A	208	ASN
1	A	216	THR
1	A	218	MET
1	A	220	ASN
1	A	242	LYS
1	A	246	SER
1	A	288	GLN
1	A	289	ASP
1	A	297	VAL
1	A	303	LYS
1	A	306	ILE
1	B	33	ASN
1	B	36	GLN
1	B	156	GLU
1	B	173	VAL
1	B	180	LEU
1	B	216	THR
1	B	250	LEU
1	B	268	THR
1	B	288	GLN
1	B	319	LEU

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	33	ASN
1	A	176	ASN
1	A	208	ASN
1	A	301	ASN
1	B	33	ASN
1	B	51	ASN
1	B	88	GLN
1	B	146	GLN
1	B	208	ASN
1	B	276	GLN
1	B	318	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](#)

2 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	GDP	A	1	-	24,30,30	1.08	1 (4%)	30,47,47	1.30	5 (16%)
2	GDP	B	1	-	24,30,30	1.18	1 (4%)	30,47,47	1.37	5 (16%)

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	GDP	A	1	-	-	0/12/32/32	0/3/3/3
2	GDP	B	1	-	-	0/12/32/32	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	GDP	O4'-C1'	3.09	1.45	1.41
2	B	1	GDP	O4'-C1'	3.06	1.45	1.41

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1	GDP	C8-N7-C5	3.44	109.54	102.99
2	A	1	GDP	PA-O3A-PB	-3.22	121.78	132.83
2	A	1	GDP	O3B-PB-O3A	3.11	115.07	104.64
2	B	1	GDP	PA-O3A-PB	-3.10	122.17	132.83
2	B	1	GDP	C5-C6-N1	2.64	118.61	113.95
2	A	1	GDP	C5-C6-N1	2.44	118.26	113.95
2	B	1	GDP	O3B-PB-O3A	2.41	112.70	104.64
2	B	1	GDP	O6-C6-N1	-2.27	117.97	120.65
2	A	1	GDP	C8-N7-C5	2.10	106.99	102.99
2	A	1	GDP	O4'-C1'-C2'	2.02	109.88	106.93

There are no chirality outliers.

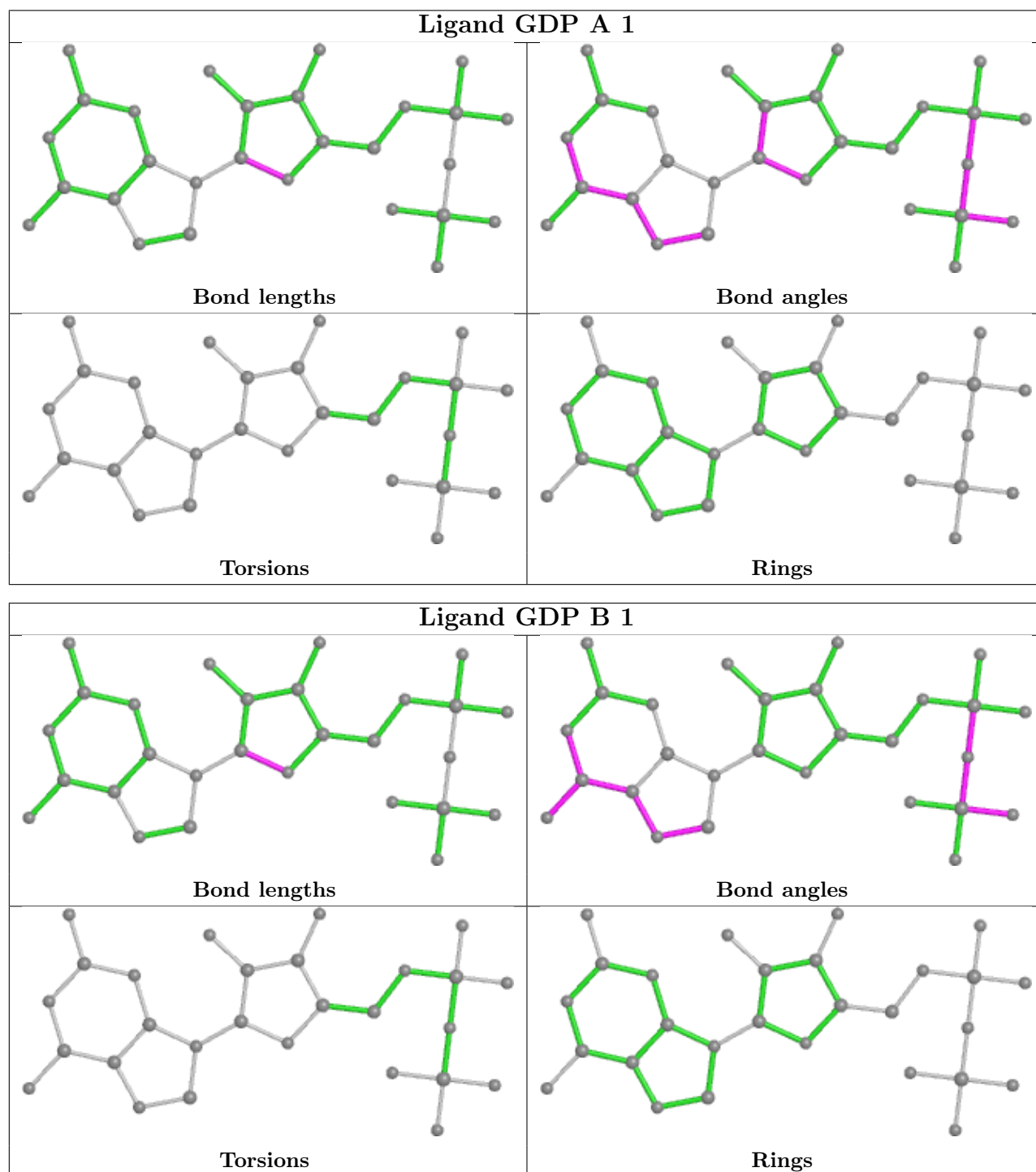
There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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

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	305/325 (93%)	0.47	36 (11%) 4 3	50, 67, 84, 96	0
1	B	315/325 (96%)	0.42	38 (12%) 4 2	51, 65, 85, 100	0
All	All	620/650 (95%)	0.44	74 (11%) 4 2	50, 66, 85, 100	0

All (74) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	176	ASN	5.8
1	A	175	LYS	5.8
1	A	131	VAL	5.2
1	B	221	LYS	4.9
1	B	222	GLY	4.7
1	A	174	ASP	4.7
1	A	102	THR	4.6
1	B	320	TYR	4.5
1	B	131	VAL	4.3
1	B	318	ASN	4.2
1	B	319	LEU	4.1
1	B	301	ASN	4.1
1	B	19	VAL	3.8
1	B	101	VAL	3.8
1	A	288	GLN	3.6
1	A	193	GLY	3.5
1	A	12	ALA	3.4
1	A	190	LEU	3.3
1	A	220	ASN	3.2
1	A	132	VAL	3.2
1	A	101	VAL	3.2
1	B	194	VAL	3.1
1	A	19	VAL	3.1
1	A	103	ALA	3.1

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Mol	Chain	Res	Type	RSRZ
1	B	316	LEU	3.0
1	A	194	VAL	3.0
1	B	51	ASN	3.0
1	B	17	ILE	3.0
1	B	100	PHE	2.9
1	B	130	GLY	2.9
1	B	103	ALA	2.9
1	B	102	THR	2.9
1	A	273	TYR	2.9
1	A	16	VAL	2.8
1	A	294	PHE	2.8
1	A	234	GLU	2.7
1	A	289	ASP	2.7
1	A	162	ILE	2.7
1	A	311	ILE	2.7
1	B	300	GLU	2.7
1	A	17	ILE	2.7
1	A	170	LEU	2.6
1	B	321	PHE	2.6
1	B	268	THR	2.6
1	B	315	PHE	2.5
1	A	284	SER	2.5
1	B	114	ALA	2.5
1	B	117	ILE	2.5
1	B	18	GLY	2.5
1	B	302	LEU	2.4
1	B	326	HIS	2.4
1	B	197	ILE	2.4
1	A	258	GLN	2.4
1	A	300	GLU	2.4
1	A	177	THR	2.3
1	A	130	GLY	2.3
1	A	161	LEU	2.3
1	A	232	THR	2.3
1	B	303	LYS	2.2
1	B	132	VAL	2.2
1	A	185	GLU	2.2
1	A	141	ARG	2.2
1	B	176	ASN	2.2
1	B	204	PRO	2.2
1	B	193	GLY	2.2
1	B	325	HIS	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	113	ALA	2.2
1	A	189	VAL	2.2
1	B	162	ILE	2.1
1	B	34	GLU	2.1
1	A	173	VAL	2.1
1	B	129	VAL	2.1
1	B	20	GLY	2.1
1	A	100	PHE	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](#)

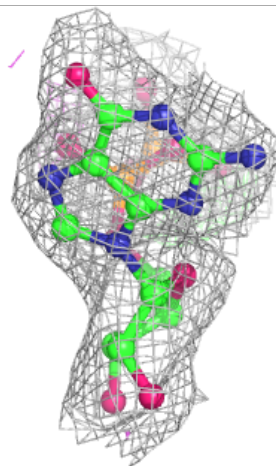
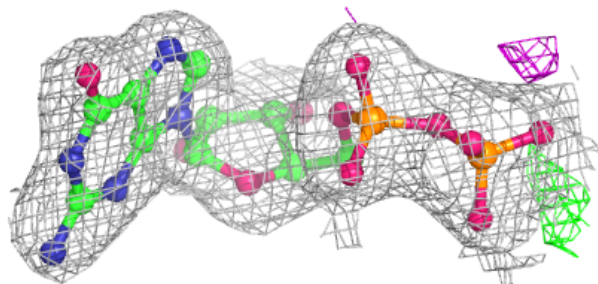
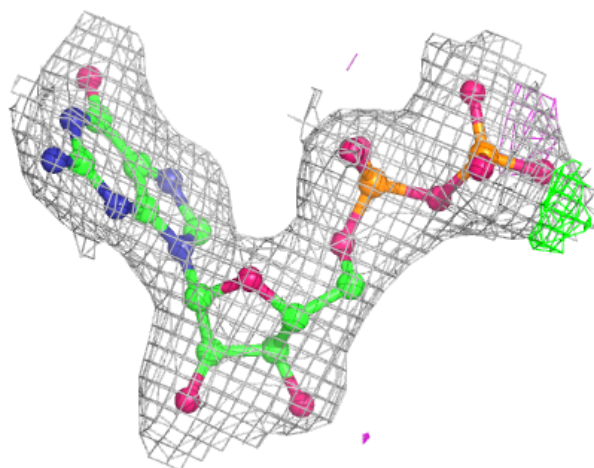
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

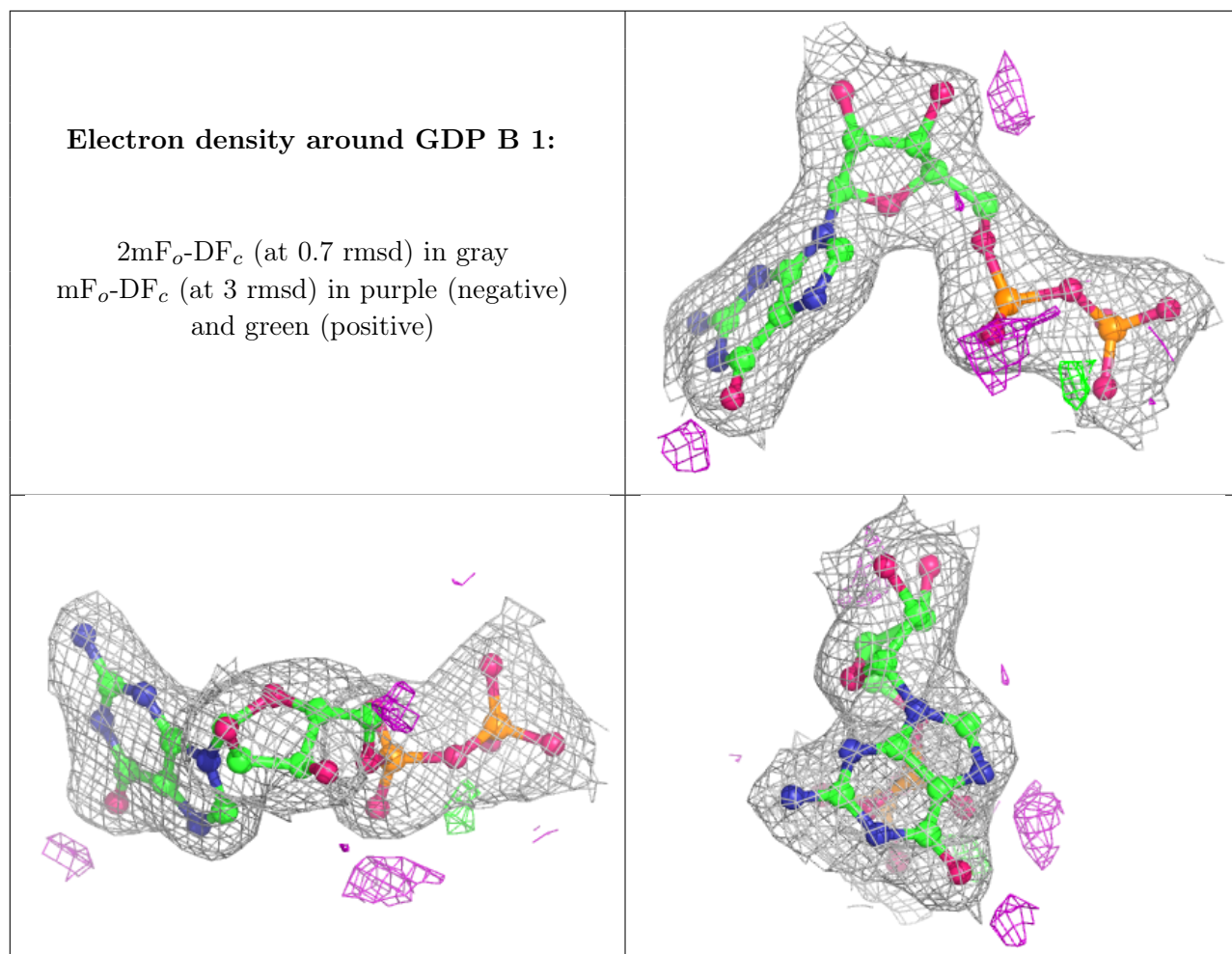
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	GDP	A	1	28/28	0.98	0.10	49,59,62,63	0
2	GDP	B	1	28/28	0.98	0.12	50,52,55,56	0

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 GDP A 1:

$2mF_o-DF_c$ (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.