



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 08:01 PM UTC

PDB ID : 8HWI / pdb_00008hwi
Title : Bacterial STING from Larkinella arboricola in complex with 3'3'-c-di-GMP
Authors : Wang, Y.-C.; Yang, C.-S.; Hou, M.-H.; Chen, Y.
Deposited on : 2022-12-30
Resolution : 2.73 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:

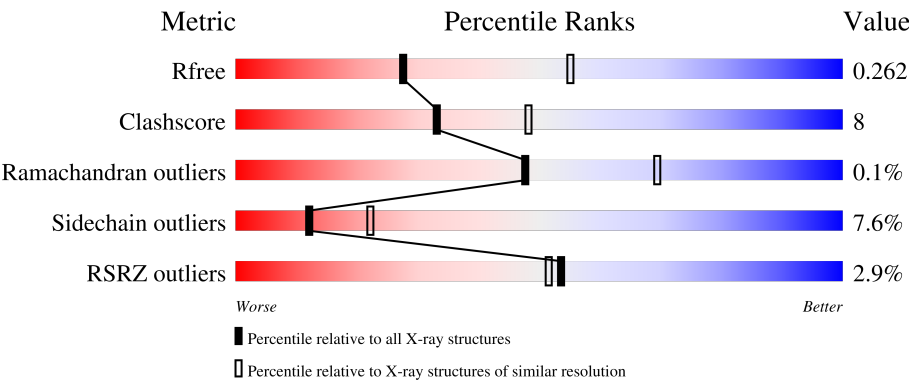
MolProbity : 4-5-2 with Phenix2.0
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0
EDS : 3.0
Buster-report : wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4 : 9.0.010 (Gargrove)
Density-Fitness : 1.0.12
Ideal 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 i

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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}	180053	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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	177	0% 71%23%5%
1	B	177	2% 76%21%
1	C	177	6% 75%21%
1	D	177	3% 73%23%
1	E	177	5% 74%23%

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Mol	Chain	Length	Quality of chain
1	F	177	% 76% 23%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 9190 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 CD-NTase-associated protein 12.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	173	Total	C	N	O	0	0	0
			1462	955	232	275			
1	B	177	Total	C	N	O	0	0	0
			1482	966	236	279			
1	C	173	Total	C	N	O	0	0	0
			1462	955	232	275			
1	D	173	Total	C	N	O	0	0	0
			1462	955	232	275			
1	E	173	Total	C	N	O	0	0	0
			1462	955	232	275			
1	F	177	Total	C	N	O	0	0	0
			1482	966	236	279			

There are 24 discrepancies between the modelled and reference sequences:

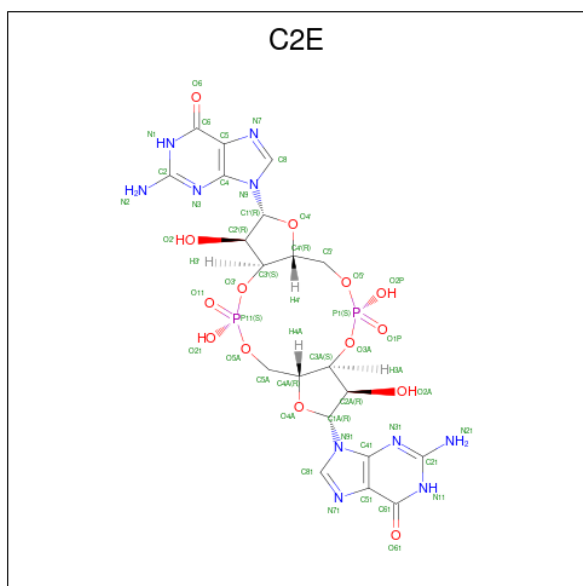
Chain	Residue	Modelled	Actual	Comment	Reference
A	155	GLY	-	expression tag	UNP A0A327WNX5
A	156	GLY	-	expression tag	UNP A0A327WNX5
A	157	GLY	-	expression tag	UNP A0A327WNX5
A	158	MET	-	expression tag	UNP A0A327WNX5
B	155	GLY	-	expression tag	UNP A0A327WNX5
B	156	GLY	-	expression tag	UNP A0A327WNX5
B	157	GLY	-	expression tag	UNP A0A327WNX5
B	158	MET	-	expression tag	UNP A0A327WNX5
C	155	GLY	-	expression tag	UNP A0A327WNX5
C	156	GLY	-	expression tag	UNP A0A327WNX5
C	157	GLY	-	expression tag	UNP A0A327WNX5
C	158	MET	-	expression tag	UNP A0A327WNX5
D	155	GLY	-	expression tag	UNP A0A327WNX5
D	156	GLY	-	expression tag	UNP A0A327WNX5
D	157	GLY	-	expression tag	UNP A0A327WNX5
D	158	MET	-	expression tag	UNP A0A327WNX5
E	155	GLY	-	expression tag	UNP A0A327WNX5

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Chain	Residue	Modelled	Actual	Comment	Reference
E	156	GLY	-	expression tag	UNP A0A327WNX5
E	157	GLY	-	expression tag	UNP A0A327WNX5
E	158	MET	-	expression tag	UNP A0A327WNX5
F	155	GLY	-	expression tag	UNP A0A327WNX5
F	156	GLY	-	expression tag	UNP A0A327WNX5
F	157	GLY	-	expression tag	UNP A0A327WNX5
F	158	MET	-	expression tag	UNP A0A327WNX5

- Molecule 2 is 9,9'-[(2R,3R,3aS,5S,7aR,9R,10R,10aS,12S,14aR)-3,5,10,12-tetrahydroxy-5,12-dioxidoctahydro-2H,7H-difuro[3,2-d:3',2'-j][1,3,7,9,2,8]tetraoxadiphosphacyclododecine-2,9-diyl]bis(2-amino-1,9-dihydro-6H-purin-6-one) (CCD ID: C2E) (formula: C₂₀H₂₄N₁₀O₁₄P₂) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	D	1	Total 46	C 20	N 10	O 14	P 2	0	0
2	F	1	Total 46	C 20	N 10	O 14	P 2	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	64	Total	O	0	0
			64	64		

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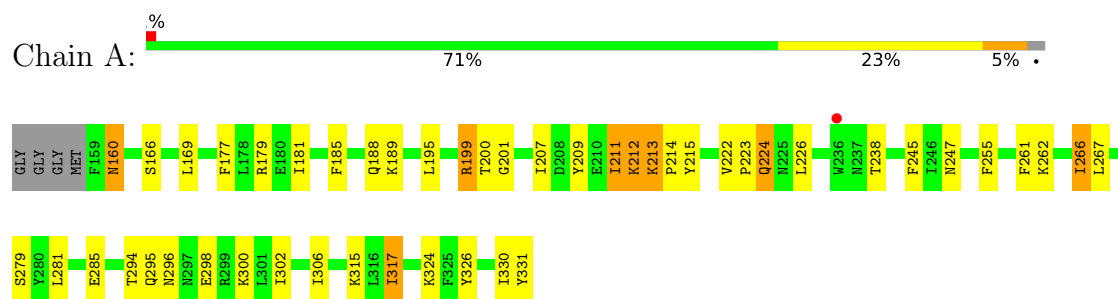
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	50	Total 50	O 50	0	0
3	C	21	Total 21	O 21	0	0
3	D	37	Total 37	O 37	0	0
3	E	34	Total 34	O 34	0	0
3	F	34	Total 34	O 34	0	0

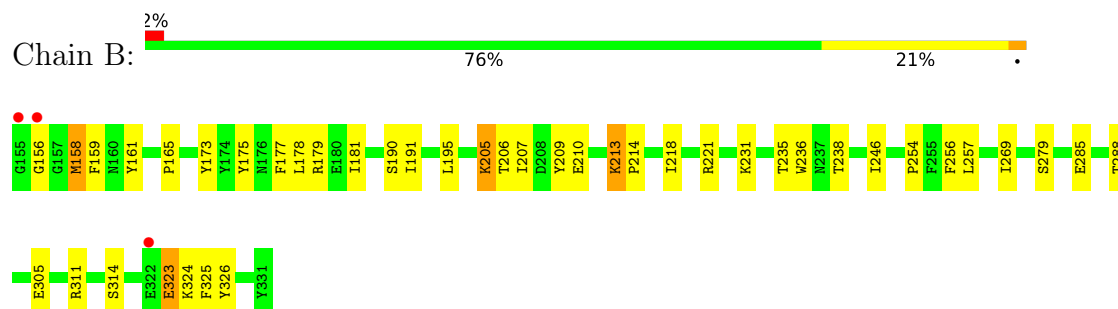
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

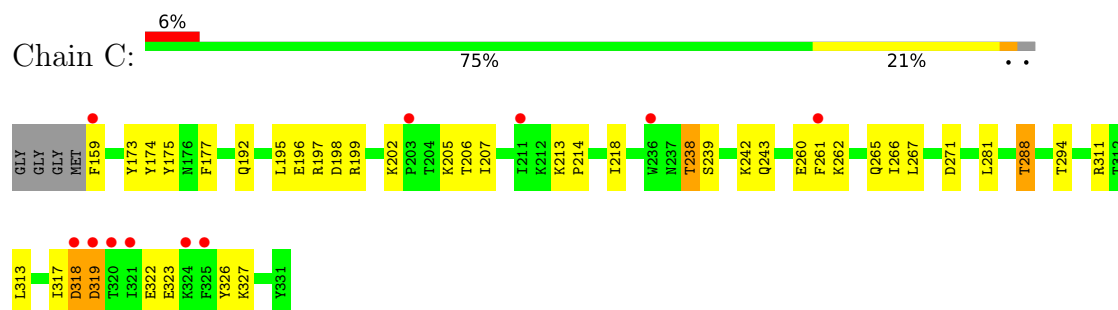
• Molecule 1: CD-NTase-associated protein 12



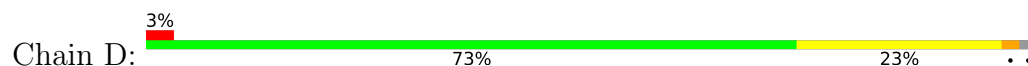
• Molecule 1: CD-NTase-associated protein 12

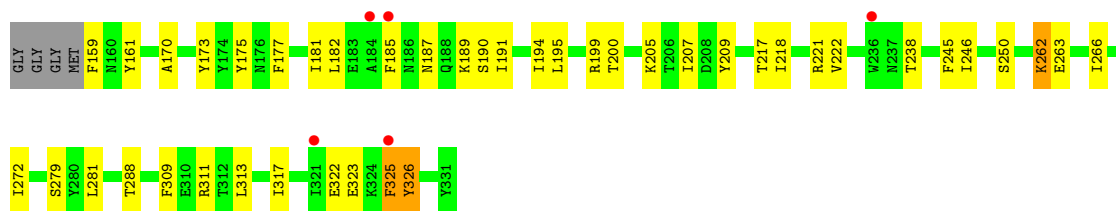


• Molecule 1: CD-NTase-associated protein 12

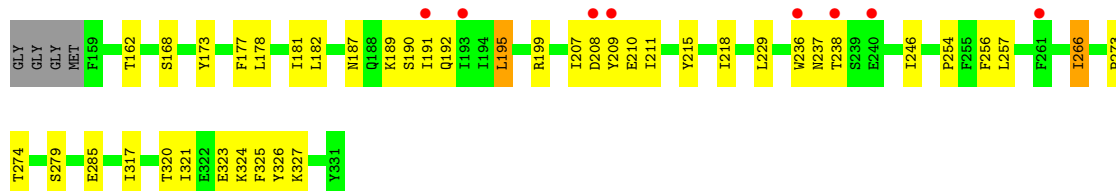
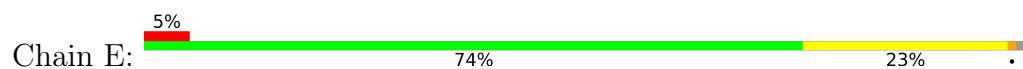


• Molecule 1: CD-NTase-associated protein 12

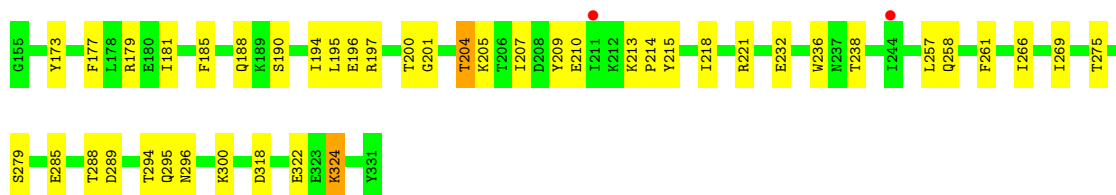
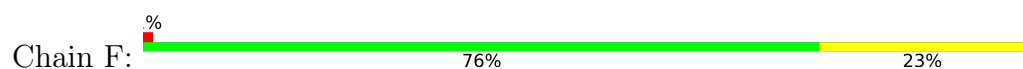




● Molecule 1: CD-NTase-associated protein 12



● Molecule 1: CD-NTase-associated protein 12



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	67.99Å 72.49Å 231.07Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.31 – 2.73 29.31 – 2.73	Depositor EDS
% Data completeness (in resolution range)	85.7 (29.31-2.73) 85.8 (29.31-2.73)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.43 (at 2.72Å)	Xtriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.209 , 0.266 0.208 , 0.262	Depositor DCC
R_{free} test set	1343 reflections (4.29%)	wwPDB-VP
Wilson B-factor (Å ²)	46.1	Xtriage
Anisotropy	0.237	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 58.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	9190	wwPDB-VP
Average B, all atoms (Å ²)	61.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.72% 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: C2E

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	0.90	0/1495	1.26	1/2021 (0.0%)
1	B	0.94	0/1515	1.28	0/2046
1	C	0.92	0/1495	1.27	1/2021 (0.0%)
1	D	0.94	0/1495	1.28	0/2021
1	E	0.95	0/1495	1.28	1/2021 (0.0%)
1	F	0.95	0/1515	1.30	2/2046 (0.1%)
All	All	0.93	0/9010	1.28	5/12176 (0.0%)

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	318	ASP	N-CA-C	-5.51	102.13	110.24
1	A	160	ASN	N-CA-C	-5.24	106.57	113.12
1	F	258	GLN	CA-C-N	5.14	125.15	121.65
1	F	258	GLN	C-N-CA	5.14	125.15	121.65
1	E	187	ASN	N-CA-C	-5.12	106.72	113.17

There are no chirality outliers.

There are no planarity outliers.

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	1462	0	1475	29	0
1	B	1482	0	1493	26	0
1	C	1462	0	1475	26	0
1	D	1462	0	1475	29	0
1	E	1462	0	1475	21	0
1	F	1482	0	1493	20	0
2	A	46	0	22	0	0
2	D	46	0	22	1	0
2	F	46	0	22	1	0
3	A	64	0	0	0	0
3	B	50	0	0	1	0
3	C	21	0	0	1	0
3	D	37	0	0	0	0
3	E	34	0	0	0	0
3	F	34	0	0	1	0
All	All	9190	0	8952	139	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 (139) 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:B:221:ARG:HD3	1:B:236:TRP:HZ3	1.51	0.76
1:F:195:LEU:HD11	1:F:207:ILE:HD11	1.70	0.73
1:E:195:LEU:HD12	1:E:207:ILE:HD11	1.71	0.71
1:E:218:ILE:O	1:E:326:TYR:HA	1.92	0.69
1:A:195:LEU:HD11	1:A:207:ILE:HD11	1.76	0.68
1:C:197:ARG:NH2	1:C:243:GLN:OE1	2.28	0.65
1:F:196:GLU:OE1	1:F:204:THR:HB	1.97	0.65
1:E:191:ILE:HG22	1:E:246:ILE:HG12	1.79	0.64
1:B:195:LEU:HD12	1:B:205:LYS:HD2	1.80	0.64
1:C:192:GLN:HG3	1:D:200:THR:HG23	1.80	0.63
1:E:192:GLN:HA	1:E:207:ILE:O	2.00	0.61
1:B:323:GLU:HB3	1:B:325:PHE:HD1	1.66	0.61
1:A:317:ILE:HD12	1:A:326:TYR:HE1	1.67	0.60
1:B:221:ARG:HD3	1:B:236:TRP:CZ3	2.36	0.60
1:C:260:GLU:HG2	1:C:267:LEU:HD12	1.84	0.59
1:C:266:ILE:HG23	1:C:266:ILE:O	2.03	0.59
1:E:229:LEU:HD21	1:E:274:THR:HA	1.84	0.58
1:C:319:ASP:HB2	1:C:322:GLU:H	1.68	0.58
1:D:195:LEU:HD11	1:D:207:ILE:HG13	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:313:LEU:O	1:C:317:ILE:HG13	2.03	0.58
1:E:181:ILE:HD13	1:E:257:LEU:HD21	1.84	0.57
1:A:317:ILE:HD12	1:A:326:TYR:CE1	2.39	0.57
1:E:191:ILE:HG13	1:E:209:TYR:HB3	1.87	0.57
1:F:318:ASP:O	1:F:322:GLU:HB2	2.04	0.56
1:A:195:LEU:HD11	1:A:207:ILE:CD1	2.36	0.56
1:A:317:ILE:HD13	1:A:324:LYS:HA	1.87	0.56
1:A:189:LYS:HA	1:A:211:ILE:HG22	1.88	0.55
1:B:195:LEU:HD11	1:B:207:ILE:HD11	1.88	0.55
1:D:161:TYR:CG	1:D:161:TYR:O	2.59	0.55
1:E:195:LEU:CD1	1:E:207:ILE:HD11	2.37	0.55
1:D:182:LEU:O	1:D:185:PHE:HB2	2.06	0.54
1:E:317:ILE:HD12	1:E:326:TYR:CE2	2.42	0.54
1:D:191:ILE:HG22	1:D:246:ILE:HG12	1.90	0.53
1:A:212:LYS:HB2	1:A:214:PRO:HD2	1.90	0.53
1:C:175:TYR:CD2	1:D:281:LEU:HD13	2.43	0.53
1:C:218:ILE:O	1:C:326:TYR:HA	2.09	0.53
1:B:218:ILE:O	1:B:326:TYR:HA	2.09	0.52
1:A:199:ARG:C	1:A:201:GLY:H	2.16	0.52
1:A:266:ILE:O	1:A:266:ILE:HG23	2.10	0.52
1:F:195:LEU:HD11	1:F:207:ILE:CD1	2.39	0.52
1:C:196:GLU:HB2	1:C:205:LYS:HB2	1.92	0.52
1:E:211:ILE:HG22	1:E:215:TYR:HE1	1.75	0.51
1:C:174:TYR:CD1	1:C:317:ILE:HG12	2.45	0.51
1:C:271:ASP:OD1	2:D:400:C2E:N21	2.42	0.51
1:D:161:TYR:O	1:D:161:TYR:CD2	2.64	0.51
1:D:195:LEU:HD12	1:D:205:LYS:HB3	1.92	0.51
1:A:185:PHE:HB3	1:A:215:TYR:CE1	2.46	0.51
1:D:173:TYR:O	1:D:177:PHE:HB3	2.10	0.51
1:F:197:ARG:HD3	1:F:201:GLY:HA2	1.92	0.51
1:E:190:SER:HB2	1:E:209:TYR:O	2.11	0.51
1:C:319:ASP:HB2	1:C:322:GLU:N	2.26	0.50
1:F:213:LYS:N	1:F:214:PRO:HD2	2.26	0.50
1:D:182:LEU:HB2	1:D:325:PHE:CE2	2.46	0.50
1:B:165:PRO:HD2	1:B:305:GLU:OE2	2.12	0.49
1:E:317:ILE:HD12	1:E:326:TYR:HE2	1.75	0.49
1:C:242:LYS:HB2	1:C:261:PHE:CE1	2.47	0.49
1:B:195:LEU:HD11	1:B:207:ILE:CD1	2.42	0.49
1:C:317:ILE:O	1:C:318:ASP:C	2.55	0.48
1:D:325:PHE:H	1:D:325:PHE:HD1	1.61	0.48
1:F:261:PHE:CZ	1:F:266:ILE:HG12	2.48	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:257:LEU:HD22	1:B:269:ILE:HG21	1.94	0.48
1:A:262:LYS:HB2	1:A:267:LEU:HD11	1.96	0.48
1:B:191:ILE:HG22	1:B:246:ILE:HG12	1.95	0.48
1:B:288:THR:HG22	1:E:162:THR:HG22	1.95	0.48
1:C:197:ARG:HG2	1:C:202:LYS:O	2.13	0.48
1:A:213:LYS:N	1:A:214:PRO:HD2	2.28	0.48
1:F:173:TYR:O	1:F:177:PHE:HB3	2.14	0.47
1:A:188:GLN:NE2	1:A:247:ASN:O	2.40	0.47
1:B:213:LYS:N	1:B:214:PRO:HD2	2.30	0.47
1:B:311:ARG:CG	1:D:311:ARG:HG3	2.45	0.47
1:B:173:TYR:O	1:B:177:PHE:HB3	2.14	0.47
1:C:174:TYR:CE1	1:C:317:ILE:HG12	2.49	0.47
1:C:192:GLN:HG3	1:D:200:THR:CG2	2.44	0.47
1:B:158:MET:HE2	1:B:159:PHE:H	1.79	0.47
1:A:177:PHE:CE1	1:A:181:ILE:HD11	2.50	0.46
1:A:261:PHE:CZ	1:A:266:ILE:HD12	2.50	0.46
1:F:296:ASN:O	1:F:300:LYS:HG3	2.16	0.46
1:F:232:GLU:O	1:F:236:TRP:HD1	1.99	0.46
1:B:161:TYR:HB2	3:B:406:HOH:O	2.15	0.46
1:E:173:TYR:O	1:E:177:PHE:HB3	2.16	0.46
1:E:254:PRO:HG2	1:E:256:PHE:CE1	2.50	0.46
1:A:281:LEU:HD13	1:B:175:TYR:CD2	2.50	0.46
1:C:281:LEU:HD13	1:D:175:TYR:CD2	2.49	0.46
1:D:313:LEU:O	1:D:317:ILE:HG13	2.16	0.46
1:C:266:ILE:O	1:C:266:ILE:CG2	2.63	0.46
1:D:177:PHE:CE1	1:D:181:ILE:HD11	2.51	0.46
1:D:195:LEU:HB2	1:D:205:LYS:HB2	1.97	0.46
1:F:275:THR:HB	2:F:400:C2E:O3'	2.17	0.45
1:D:218:ILE:O	1:D:326:TYR:HA	2.17	0.45
1:F:194:ILE:HD13	1:F:197:ARG:HH21	1.81	0.45
1:A:294:THR:HG22	1:A:295:GLN:HG3	1.99	0.45
1:E:173:TYR:CE1	1:E:273:PRO:HB3	2.52	0.45
1:B:156:GLY:O	1:C:288:THR:HG23	2.17	0.45
1:B:231:LYS:O	1:B:235:THR:HG23	2.17	0.44
1:D:170:ALA:HB2	1:D:309:PHE:CD1	2.52	0.44
1:B:178:LEU:HB3	1:B:325:PHE:HE2	1.82	0.44
1:C:159:PHE:N	3:C:402:HOH:O	2.49	0.44
1:E:266:ILE:O	1:E:266:ILE:HG23	2.17	0.43
1:A:302:ILE:O	1:A:306:ILE:HG13	2.19	0.43
1:D:218:ILE:HD12	1:D:325:PHE:CD2	2.53	0.43
1:F:185:PHE:HB3	1:F:215:TYR:CE1	2.54	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:191:ILE:CG1	1:B:209:TYR:HB3	2.48	0.43
1:C:195:LEU:HD11	1:C:207:ILE:HD12	2.01	0.43
1:F:294:THR:HG22	1:F:295:GLN:HG3	2.00	0.43
1:B:305:GLU:OE1	1:B:305:GLU:HA	2.18	0.42
1:A:315:LYS:NZ	1:B:285:GLU:OE2	2.52	0.42
1:D:194:ILE:HD11	1:D:245:PHE:CE2	2.53	0.42
1:D:195:LEU:HB2	1:D:205:LYS:CB	2.50	0.42
1:F:181:ILE:HD13	1:F:257:LEU:HD21	2.02	0.42
1:E:236:TRP:O	1:E:238:THR:N	2.44	0.42
1:F:324:LYS:HB3	1:F:324:LYS:HE2	1.89	0.42
1:A:211:ILE:HD12	1:A:211:ILE:HA	1.90	0.42
1:B:254:PRO:HG2	1:B:256:PHE:CE1	2.55	0.42
1:F:210:GLU:CD	3:F:506:HOH:O	2.63	0.42
1:A:300:LYS:HD3	1:E:321:ILE:HG12	2.02	0.41
1:C:238:THR:HG22	1:C:239:SER:H	1.84	0.41
1:D:221:ARG:O	1:D:272:ILE:HG12	2.19	0.41
1:A:226:LEU:HD12	1:A:226:LEU:HA	1.88	0.41
1:C:173:TYR:O	1:C:177:PHE:HB3	2.20	0.41
1:D:262:LYS:O	1:D:263:GLU:HG2	2.20	0.41
1:A:209:TYR:OH	1:A:266:ILE:HG22	2.19	0.41
1:D:209:TYR:CZ	1:D:266:ILE:HG22	2.55	0.41
1:E:178:LEU:HB3	1:E:325:PHE:CE1	2.55	0.41
1:A:166:SER:HA	1:A:169:LEU:HD12	2.01	0.41
1:B:181:ILE:HD13	1:B:257:LEU:HD21	2.01	0.41
1:B:311:ARG:HG3	1:D:311:ARG:HG3	2.01	0.41
1:D:182:LEU:HD11	1:D:323:GLU:HG2	2.02	0.41
1:A:160:ASN:O	1:F:288:THR:HG23	2.21	0.41
1:A:224:GLN:HG2	1:A:330:ILE:HG22	2.03	0.41
1:A:245:PHE:HA	1:A:255:PHE:O	2.20	0.41
1:A:298:GLU:O	1:A:302:ILE:HG12	2.21	0.41
1:C:262:LYS:HB3	1:C:265:GLN:HB2	2.03	0.41
1:F:218:ILE:HG12	1:F:269:ILE:HD12	2.03	0.41
1:F:190:SER:HB3	1:F:209:TYR:O	2.20	0.41
1:C:213:LYS:N	1:C:214:PRO:CD	2.84	0.40
1:E:229:LEU:CD2	1:E:274:THR:HA	2.50	0.40
1:A:223:PRO:HA	1:A:331:TYR:OXT	2.21	0.40
1:D:190:SER:HB3	1:D:209:TYR:O	2.21	0.40
1:D:313:LEU:HD23	1:D:313:LEU:HA	1.94	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	171/177 (97%)	161 (94%)	10 (6%)	0	100	100
1	B	175/177 (99%)	167 (95%)	8 (5%)	0	100	100
1	C	171/177 (97%)	160 (94%)	11 (6%)	0	100	100
1	D	171/177 (97%)	162 (95%)	9 (5%)	0	100	100
1	E	171/177 (97%)	162 (95%)	8 (5%)	1 (1%)	21	36
1	F	175/177 (99%)	161 (92%)	14 (8%)	0	100	100
All	All	1034/1062 (97%)	973 (94%)	60 (6%)	1 (0%)	48	69

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	237	ASN

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	164/165 (99%)	150 (92%)	14 (8%)	10	18
1	B	165/165 (100%)	153 (93%)	12 (7%)	13	24
1	C	164/165 (99%)	154 (94%)	10 (6%)	17	30
1	D	164/165 (99%)	150 (92%)	14 (8%)	10	18
1	E	164/165 (99%)	150 (92%)	14 (8%)	10	18
1	F	165/165 (100%)	154 (93%)	11 (7%)	15	27

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	986/990 (100%)	911 (92%)	75 (8%)	12	22

All (75) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	179	ARG
1	A	199	ARG
1	A	200	THR
1	A	211	ILE
1	A	212	LYS
1	A	213	LYS
1	A	222	VAL
1	A	224	GLN
1	A	238	THR
1	A	266	ILE
1	A	279	SER
1	A	285	GLU
1	A	296	ASN
1	A	317	ILE
1	B	158	MET
1	B	179	ARG
1	B	190	SER
1	B	205	LYS
1	B	206	THR
1	B	210	GLU
1	B	213	LYS
1	B	238	THR
1	B	279	SER
1	B	314	SER
1	B	323	GLU
1	B	324	LYS
1	C	198	ASP
1	C	199	ARG
1	C	206	THR
1	C	238	THR
1	C	288	THR
1	C	294	THR
1	C	311	ARG
1	C	319	ASP
1	C	323	GLU
1	C	327	LYS
1	D	159	PHE

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Mol	Chain	Res	Type
1	D	187	ASN
1	D	189	LYS
1	D	199	ARG
1	D	217	THR
1	D	222	VAL
1	D	238	THR
1	D	250	SER
1	D	262	LYS
1	D	279	SER
1	D	288	THR
1	D	322	GLU
1	D	325	PHE
1	D	326	TYR
1	E	168	SER
1	E	182	LEU
1	E	189	LYS
1	E	195	LEU
1	E	199	ARG
1	E	208	ASP
1	E	210	GLU
1	E	266	ILE
1	E	279	SER
1	E	285	GLU
1	E	320	THR
1	E	323	GLU
1	E	324	LYS
1	E	327	LYS
1	F	179	ARG
1	F	188	GLN
1	F	200	THR
1	F	204	THR
1	F	205	LYS
1	F	221	ARG
1	F	238	THR
1	F	279	SER
1	F	285	GLU
1	F	289	ASP
1	F	324	LYS

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	160	ASN
1	A	224	GLN
1	A	265	GLN
1	A	296	ASN
1	A	303	ASN
1	B	265	GLN
1	C	265	GLN
1	D	265	GLN
1	D	303	ASN
1	E	160	ASN
1	E	258	GLN
1	F	258	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

3 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	C2E	D	400	-	52,52,52	0.50	0	78,82,82	0.61	0
2	C2E	F	400	-	52,52,52	0.42	0	78,82,82	0.57	0
2	C2E	A	400	-	52,52,52	0.53	0	78,82,82	0.64	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
2	C2E	D	400	-	-	0/30/62/62	0/6/7/7
2	C2E	F	400	-	-	1/30/62/62	0/6/7/7
2	C2E	A	400	-	-	0/30/62/62	0/6/7/7

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

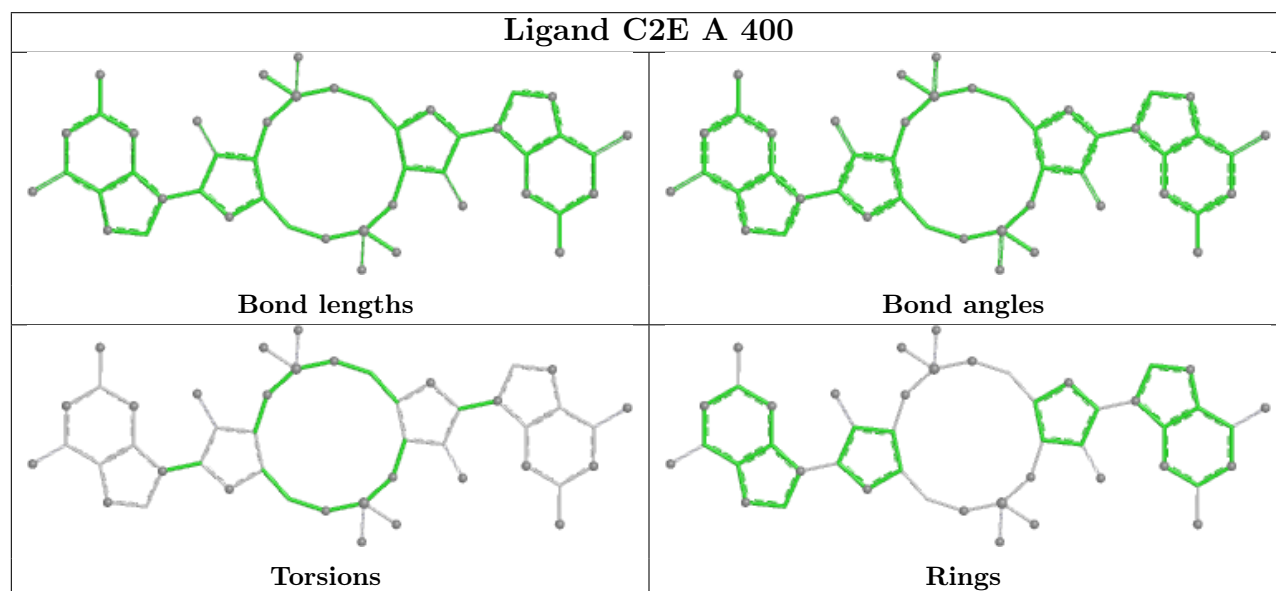
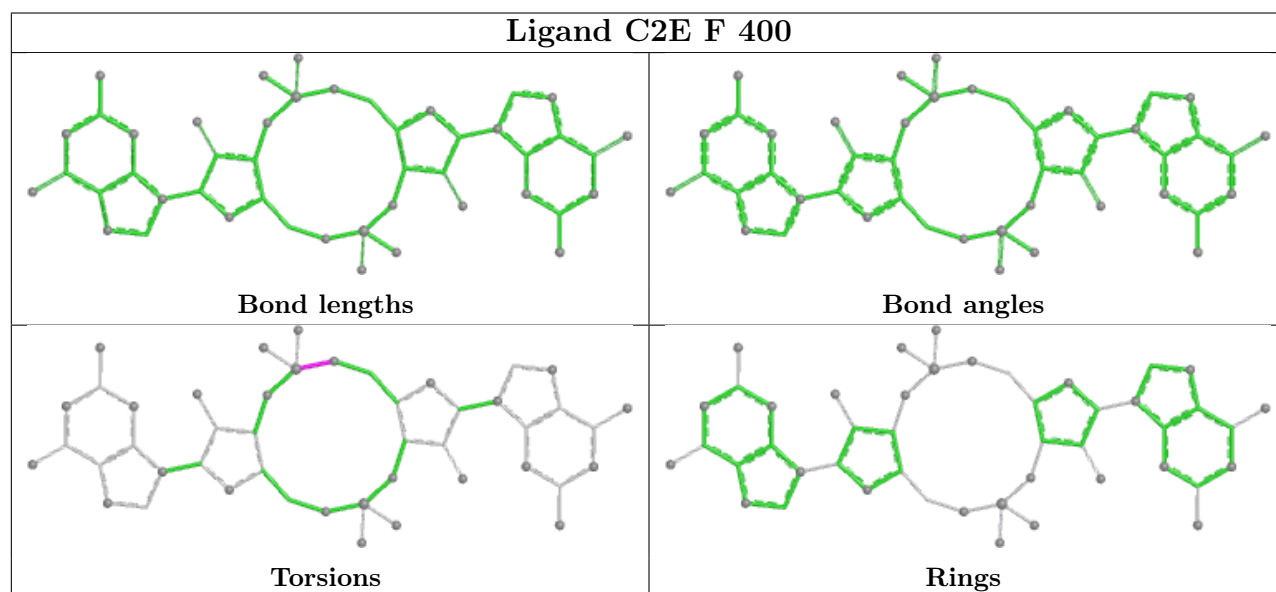
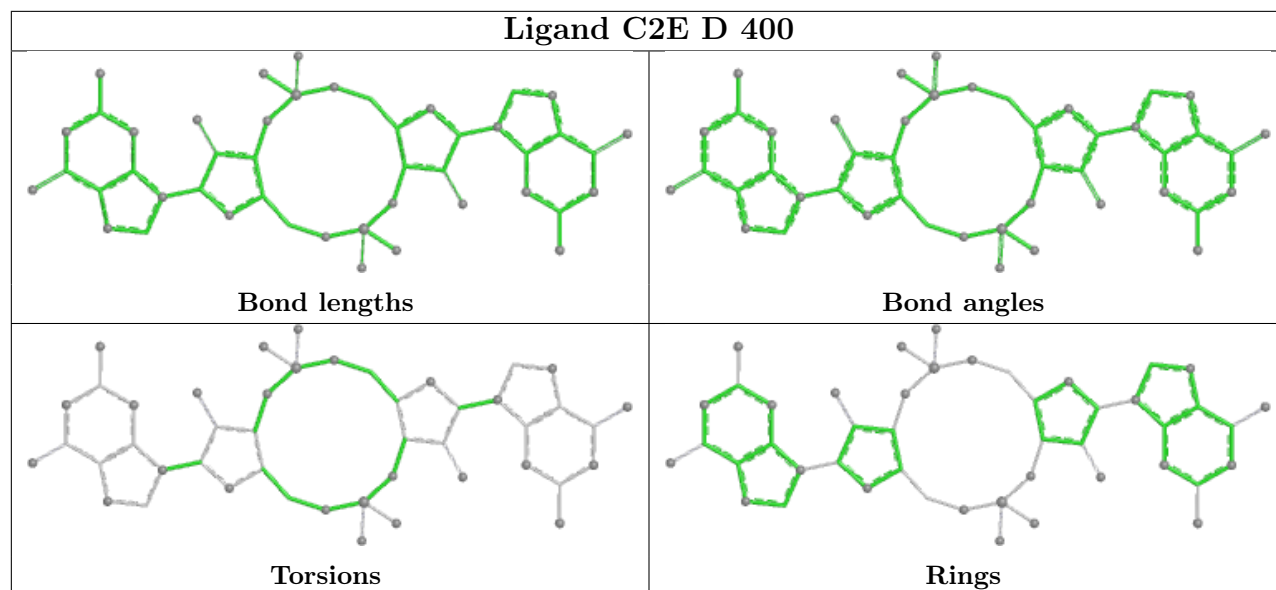
Mol	Chain	Res	Type	Atoms
2	F	400	C2E	C5A-O5A-P11-O11

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	D	400	C2E	1	0
2	F	400	C2E	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.



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	173/177 (97%)	-0.11	1 (0%) 85 85	14, 44, 97, 163	0
1	B	177/177 (100%)	-0.00	3 (1%) 69 66	14, 42, 94, 118	0
1	C	173/177 (97%)	0.31	11 (6%) 25 25	16, 58, 139, 173	0
1	D	173/177 (97%)	0.25	5 (2%) 53 51	18, 59, 137, 156	0
1	E	173/177 (97%)	0.35	8 (4%) 37 36	20, 64, 119, 179	0
1	F	177/177 (100%)	0.28	2 (1%) 78 77	21, 60, 128, 162	0
All	All	1046/1062 (98%)	0.18	30 (2%) 53 51	14, 52, 125, 179	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	325	PHE	3.7
1	E	261	PHE	3.3
1	C	236	TRP	3.2
1	E	236	TRP	3.0
1	C	324	LYS	2.9
1	D	236	TRP	2.9
1	D	325	PHE	2.9
1	C	321	ILE	2.8
1	B	155	GLY	2.8
1	C	261	PHE	2.8
1	C	211	ILE	2.7
1	A	236	TRP	2.7
1	E	193	ILE	2.6
1	D	184	ALA	2.6
1	C	203	PRO	2.5
1	E	191	ILE	2.5
1	C	318	ASP	2.5
1	C	320	THR	2.5
1	F	244	ILE	2.4

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Mol	Chain	Res	Type	RSRZ
1	E	208	ASP	2.4
1	F	211	ILE	2.3
1	D	185	PHE	2.3
1	E	238	THR	2.3
1	B	322	GLU	2.3
1	E	240	GLU	2.2
1	C	159	PHE	2.2
1	D	321	ILE	2.2
1	B	156	GLY	2.2
1	E	209	TYR	2.1
1	C	319	ASP	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

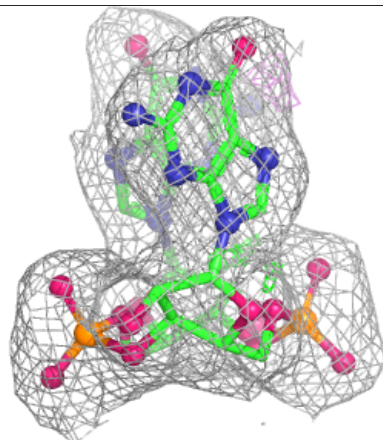
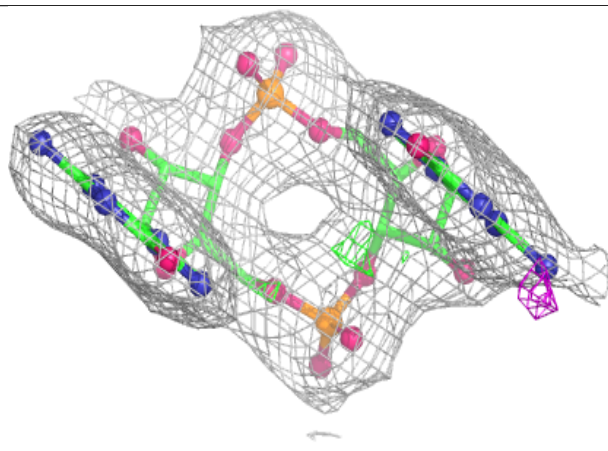
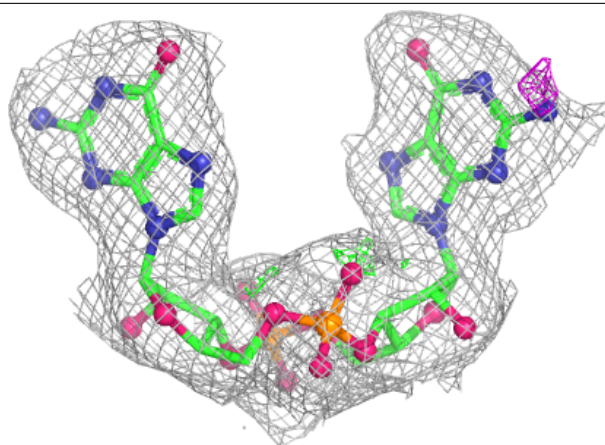
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	C2E	D	400	46/46	0.96	0.06	18,22,25,27	0
2	C2E	F	400	46/46	0.96	0.07	24,33,43,46	0
2	C2E	A	400	46/46	0.98	0.05	11,13,16,16	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.

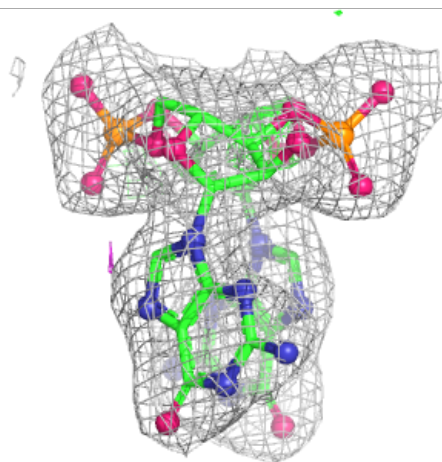
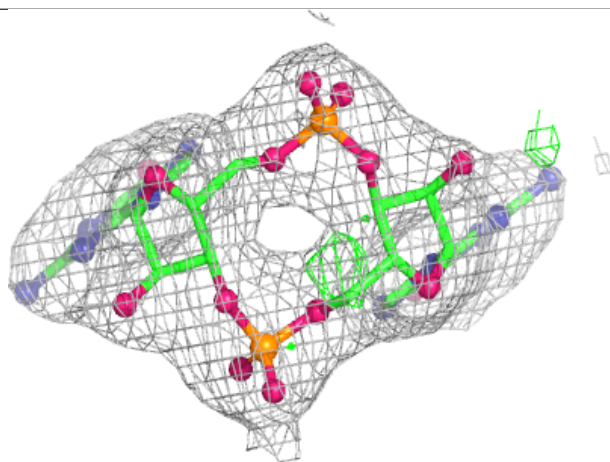
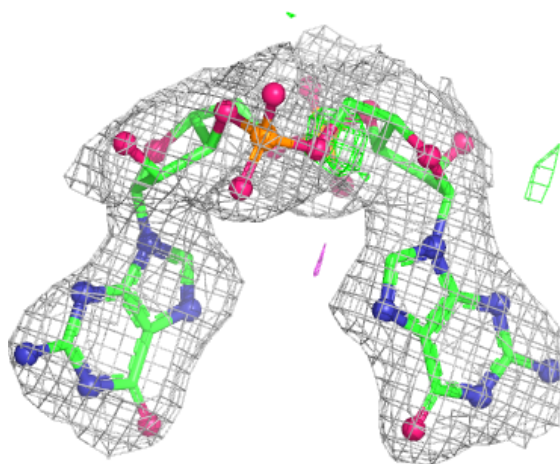
Electron density around C2E D 400:

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



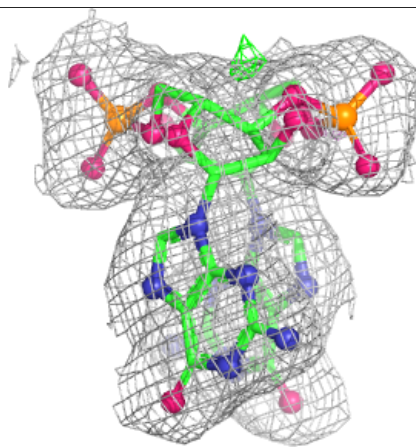
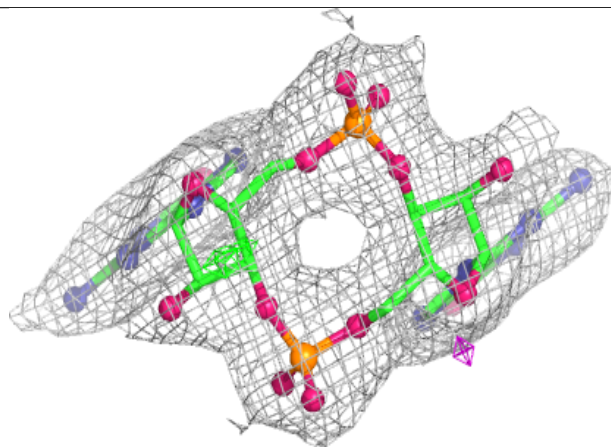
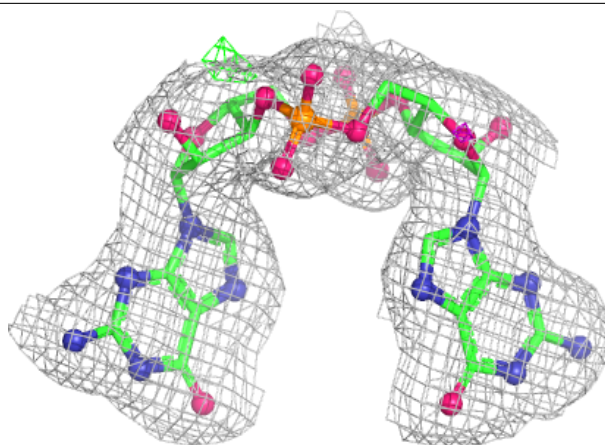
Electron density around C2E F 400:

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



Electron density around C2E A 400:

$2mF_o-DF_c$ (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.