



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 9, 2026 – 11:32 AM UTC

PDB ID : 6XHS / pdb_00006xhs
Title : Crystal structure of S. aureus TarI in complex with CTP (space group P1211)
Authors : Li, F.K.K.; Strynadka, N.C.J.
Deposited on : 2020-06-19
Resolution : 2.90 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

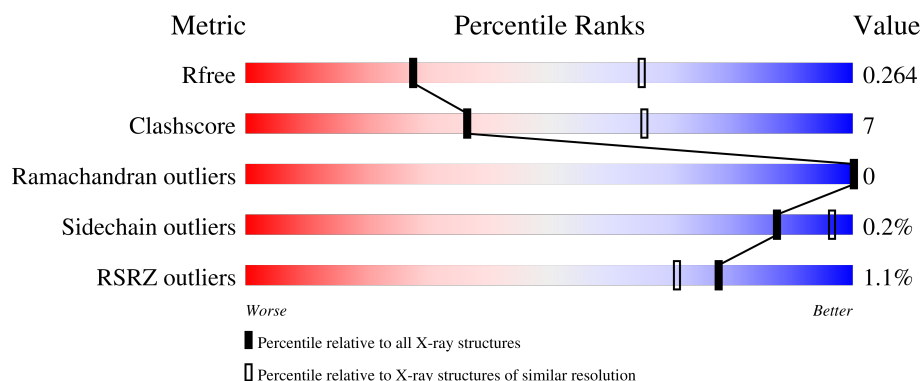
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

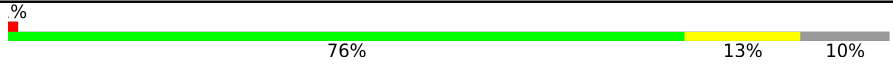
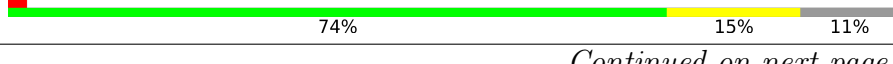
The reported resolution of this entry is 2.90 Å.

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	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	261	
1	B	261	
1	C	261	
1	D	261	
1	E	261	

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Mol	Chain	Length	Quality of chain
1	F	261	2% 76% 11% • 12%

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10567 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 Ribitol-5-phosphate cytidyltransferase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	234	Total	C	N	O	S	0	0	0
			1790	1135	301	348	6			
1	B	227	Total	C	N	O	S	0	0	0
			1711	1089	282	335	5			
1	C	236	Total	C	N	O	S	0	0	0
			1761	1118	289	348	6			
1	D	235	Total	C	N	O	S	0	0	0
			1769	1122	299	342	6			
1	E	232	Total	C	N	O	S	0	0	0
			1736	1107	288	335	6			
1	F	230	Total	C	N	O	S	0	0	0
			1696	1077	279	334	6			

There are 138 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	239	GLY	-	expression tag	UNP Q2G1C0
A	240	GLY	-	expression tag	UNP Q2G1C0
A	241	SER	-	expression tag	UNP Q2G1C0
A	242	LEU	-	expression tag	UNP Q2G1C0
A	243	VAL	-	expression tag	UNP Q2G1C0
A	244	PRO	-	expression tag	UNP Q2G1C0
A	245	ARG	-	expression tag	UNP Q2G1C0
A	246	GLY	-	expression tag	UNP Q2G1C0
A	247	SER	-	expression tag	UNP Q2G1C0
A	248	ALA	-	expression tag	UNP Q2G1C0
A	249	ALA	-	expression tag	UNP Q2G1C0
A	250	ALA	-	expression tag	UNP Q2G1C0
A	251	ALA	-	expression tag	UNP Q2G1C0
A	252	LEU	-	expression tag	UNP Q2G1C0
A	253	GLU	-	expression tag	UNP Q2G1C0
A	254	HIS	-	expression tag	UNP Q2G1C0
A	255	HIS	-	expression tag	UNP Q2G1C0

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Chain	Residue	Modelled	Actual	Comment	Reference
A	256	HIS	-	expression tag	UNP Q2G1C0
A	257	HIS	-	expression tag	UNP Q2G1C0
A	258	HIS	-	expression tag	UNP Q2G1C0
A	259	HIS	-	expression tag	UNP Q2G1C0
A	260	HIS	-	expression tag	UNP Q2G1C0
A	261	HIS	-	expression tag	UNP Q2G1C0
B	239	GLY	-	expression tag	UNP Q2G1C0
B	240	GLY	-	expression tag	UNP Q2G1C0
B	241	SER	-	expression tag	UNP Q2G1C0
B	242	LEU	-	expression tag	UNP Q2G1C0
B	243	VAL	-	expression tag	UNP Q2G1C0
B	244	PRO	-	expression tag	UNP Q2G1C0
B	245	ARG	-	expression tag	UNP Q2G1C0
B	246	GLY	-	expression tag	UNP Q2G1C0
B	247	SER	-	expression tag	UNP Q2G1C0
B	248	ALA	-	expression tag	UNP Q2G1C0
B	249	ALA	-	expression tag	UNP Q2G1C0
B	250	ALA	-	expression tag	UNP Q2G1C0
B	251	ALA	-	expression tag	UNP Q2G1C0
B	252	LEU	-	expression tag	UNP Q2G1C0
B	253	GLU	-	expression tag	UNP Q2G1C0
B	254	HIS	-	expression tag	UNP Q2G1C0
B	255	HIS	-	expression tag	UNP Q2G1C0
B	256	HIS	-	expression tag	UNP Q2G1C0
B	257	HIS	-	expression tag	UNP Q2G1C0
B	258	HIS	-	expression tag	UNP Q2G1C0
B	259	HIS	-	expression tag	UNP Q2G1C0
B	260	HIS	-	expression tag	UNP Q2G1C0
B	261	HIS	-	expression tag	UNP Q2G1C0
C	239	GLY	-	expression tag	UNP Q2G1C0
C	240	GLY	-	expression tag	UNP Q2G1C0
C	241	SER	-	expression tag	UNP Q2G1C0
C	242	LEU	-	expression tag	UNP Q2G1C0
C	243	VAL	-	expression tag	UNP Q2G1C0
C	244	PRO	-	expression tag	UNP Q2G1C0
C	245	ARG	-	expression tag	UNP Q2G1C0
C	246	GLY	-	expression tag	UNP Q2G1C0
C	247	SER	-	expression tag	UNP Q2G1C0
C	248	ALA	-	expression tag	UNP Q2G1C0
C	249	ALA	-	expression tag	UNP Q2G1C0
C	250	ALA	-	expression tag	UNP Q2G1C0
C	251	ALA	-	expression tag	UNP Q2G1C0

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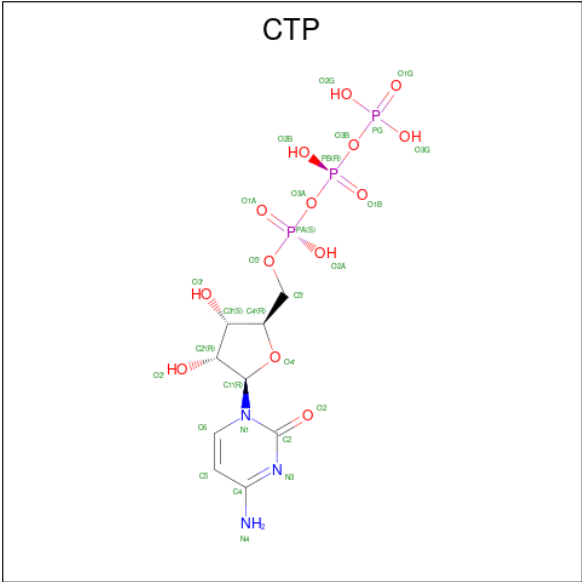
Chain	Residue	Modelled	Actual	Comment	Reference
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C	255	HIS	-	expression tag	UNP Q2G1C0
C	256	HIS	-	expression tag	UNP Q2G1C0
C	257	HIS	-	expression tag	UNP Q2G1C0
C	258	HIS	-	expression tag	UNP Q2G1C0
C	259	HIS	-	expression tag	UNP Q2G1C0
C	260	HIS	-	expression tag	UNP Q2G1C0
C	261	HIS	-	expression tag	UNP Q2G1C0
D	239	GLY	-	expression tag	UNP Q2G1C0
D	240	GLY	-	expression tag	UNP Q2G1C0
D	241	SER	-	expression tag	UNP Q2G1C0
D	242	LEU	-	expression tag	UNP Q2G1C0
D	243	VAL	-	expression tag	UNP Q2G1C0
D	244	PRO	-	expression tag	UNP Q2G1C0
D	245	ARG	-	expression tag	UNP Q2G1C0
D	246	GLY	-	expression tag	UNP Q2G1C0
D	247	SER	-	expression tag	UNP Q2G1C0
D	248	ALA	-	expression tag	UNP Q2G1C0
D	249	ALA	-	expression tag	UNP Q2G1C0
D	250	ALA	-	expression tag	UNP Q2G1C0
D	251	ALA	-	expression tag	UNP Q2G1C0
D	252	LEU	-	expression tag	UNP Q2G1C0
D	253	GLU	-	expression tag	UNP Q2G1C0
D	254	HIS	-	expression tag	UNP Q2G1C0
D	255	HIS	-	expression tag	UNP Q2G1C0
D	256	HIS	-	expression tag	UNP Q2G1C0
D	257	HIS	-	expression tag	UNP Q2G1C0
D	258	HIS	-	expression tag	UNP Q2G1C0
D	259	HIS	-	expression tag	UNP Q2G1C0
D	260	HIS	-	expression tag	UNP Q2G1C0
D	261	HIS	-	expression tag	UNP Q2G1C0
E	239	GLY	-	expression tag	UNP Q2G1C0
E	240	GLY	-	expression tag	UNP Q2G1C0
E	241	SER	-	expression tag	UNP Q2G1C0
E	242	LEU	-	expression tag	UNP Q2G1C0
E	243	VAL	-	expression tag	UNP Q2G1C0
E	244	PRO	-	expression tag	UNP Q2G1C0
E	245	ARG	-	expression tag	UNP Q2G1C0
E	246	GLY	-	expression tag	UNP Q2G1C0
E	247	SER	-	expression tag	UNP Q2G1C0

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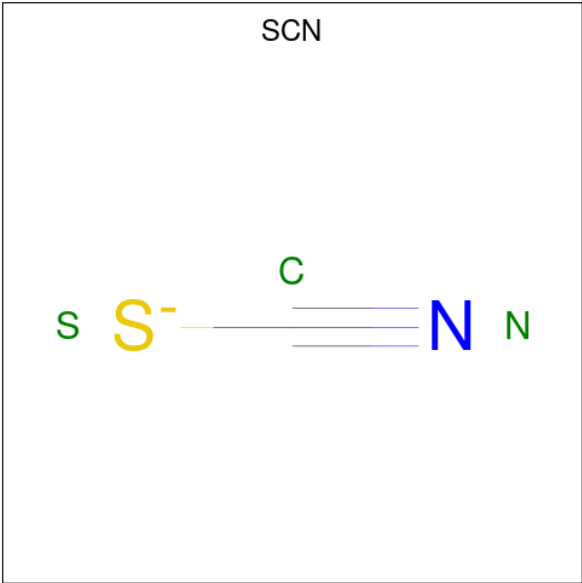
Chain	Residue	Modelled	Actual	Comment	Reference
E	248	ALA	-	expression tag	UNP Q2G1C0
E	249	ALA	-	expression tag	UNP Q2G1C0
E	250	ALA	-	expression tag	UNP Q2G1C0
E	251	ALA	-	expression tag	UNP Q2G1C0
E	252	LEU	-	expression tag	UNP Q2G1C0
E	253	GLU	-	expression tag	UNP Q2G1C0
E	254	HIS	-	expression tag	UNP Q2G1C0
E	255	HIS	-	expression tag	UNP Q2G1C0
E	256	HIS	-	expression tag	UNP Q2G1C0
E	257	HIS	-	expression tag	UNP Q2G1C0
E	258	HIS	-	expression tag	UNP Q2G1C0
E	259	HIS	-	expression tag	UNP Q2G1C0
E	260	HIS	-	expression tag	UNP Q2G1C0
E	261	HIS	-	expression tag	UNP Q2G1C0
F	239	GLY	-	expression tag	UNP Q2G1C0
F	240	GLY	-	expression tag	UNP Q2G1C0
F	241	SER	-	expression tag	UNP Q2G1C0
F	242	LEU	-	expression tag	UNP Q2G1C0
F	243	VAL	-	expression tag	UNP Q2G1C0
F	244	PRO	-	expression tag	UNP Q2G1C0
F	245	ARG	-	expression tag	UNP Q2G1C0
F	246	GLY	-	expression tag	UNP Q2G1C0
F	247	SER	-	expression tag	UNP Q2G1C0
F	248	ALA	-	expression tag	UNP Q2G1C0
F	249	ALA	-	expression tag	UNP Q2G1C0
F	250	ALA	-	expression tag	UNP Q2G1C0
F	251	ALA	-	expression tag	UNP Q2G1C0
F	252	LEU	-	expression tag	UNP Q2G1C0
F	253	GLU	-	expression tag	UNP Q2G1C0
F	254	HIS	-	expression tag	UNP Q2G1C0
F	255	HIS	-	expression tag	UNP Q2G1C0
F	256	HIS	-	expression tag	UNP Q2G1C0
F	257	HIS	-	expression tag	UNP Q2G1C0
F	258	HIS	-	expression tag	UNP Q2G1C0
F	259	HIS	-	expression tag	UNP Q2G1C0
F	260	HIS	-	expression tag	UNP Q2G1C0
F	261	HIS	-	expression tag	UNP Q2G1C0

- Molecule 2 is CYTIDINE-5'-TRIPHOSPHATE (CCD ID: CTP) (formula: $C_9H_{16}N_3O_{14}P_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	B	1	Total	C	N	O	P	0	1
			58	18	6	28	6		
2	E	1	Total	C	N	O	P	0	0
			29	9	3	14	3		

- Molecule 3 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	C	1	Total	C	N	S	0	0
			3	1	1	1		
3	F	1	Total	C	N	S	0	0
			3	1	1	1		

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg) (labeled as "Ligand of Interest" by depositor).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	E	1	Total 1	Mg 1	0	0

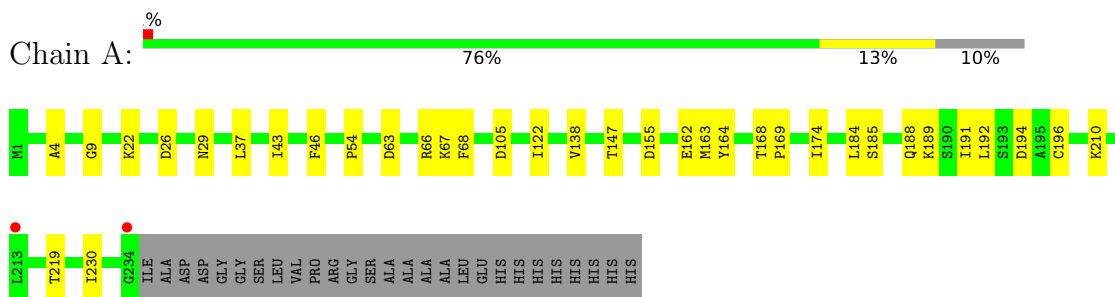
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total 2	O 2	0	0
5	B	2	Total 2	O 2	0	0
5	C	1	Total 1	O 1	0	0
5	D	2	Total 2	O 2	0	0
5	E	3	Total 3	O 3	0	0

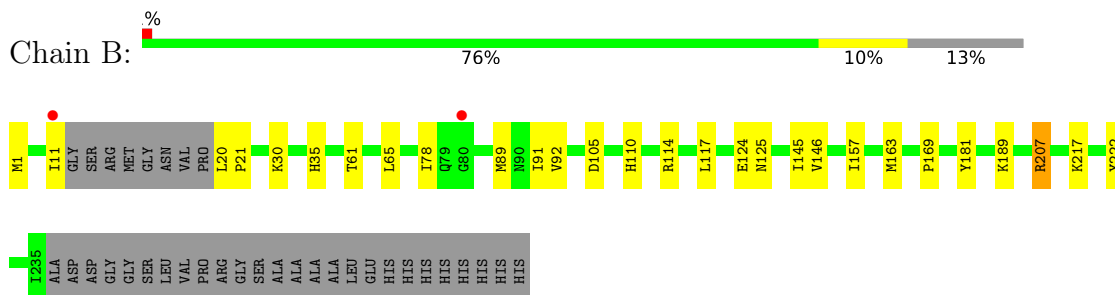
3 Residue-property plots

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.

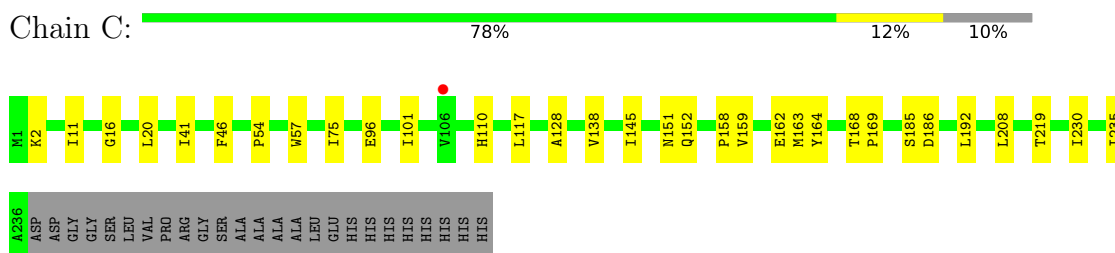
- Molecule 1: Ribitol-5-phosphate cytidyltransferase 1



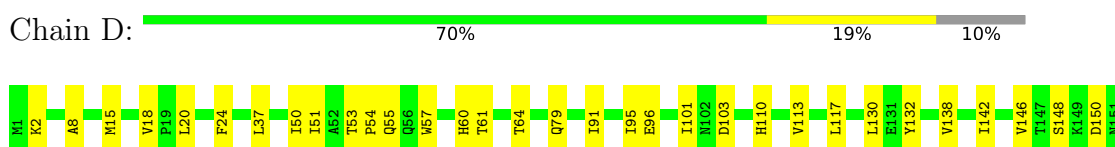
- Molecule 1: Ribitol-5-phosphate cytidyltransferase 1



- Molecule 1: Ribitol-5-phosphate cytidyltransferase 1

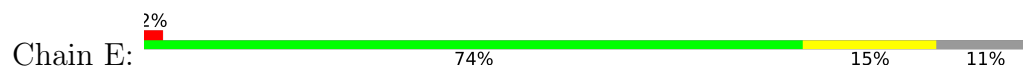


- Molecule 1: Ribitol-5-phosphate cytidyltransferase 1

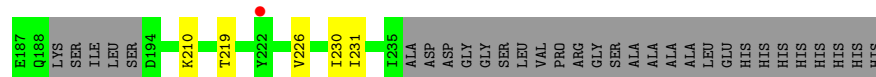
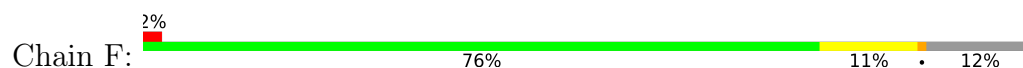




- Molecule 1: Ribitol-5-phosphate cytidyltransferase 1



- Molecule 1: Ribitol-5-phosphate cytidyltransferase 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.36Å 138.52Å 109.56Å 90.00° 96.46° 90.00°	Depositor
Resolution (Å)	49.04 – 2.90 49.04 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.04-2.90) 99.7 (49.04-2.90)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.57 (at 2.91Å)	Xtriage
Refinement program	PHENIX 1.16_3549	Depositor
R, R_{free}	0.210 , 0.267 0.210 , 0.264	Depositor DCC
R_{free} test set	1617 reflections (2.50%)	wwPDB-VP
Wilson B-factor (Å ²)	54.2	Xtriage
Anisotropy	0.601	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 49.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	10567	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.47% 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: SCN, CTP, MG

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	0.57	1/1817 (0.1%)	0.79	0/2473
1	B	0.53	0/1736	0.81	1/2369 (0.0%)
1	C	0.51	0/1788	0.80	0/2445
1	D	0.51	0/1796	0.79	1/2452 (0.0%)
1	E	0.46	0/1763	0.77	1/2408 (0.0%)
1	F	0.57	0/1722	0.86	1/2360 (0.0%)
All	All	0.53	1/10622 (0.0%)	0.81	4/14507 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	164	TYR	C-O	-5.18	1.17	1.23

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	200	VAL	CB-CA-C	-7.68	102.14	111.97
1	E	84	ARG	CD-NE-CZ	-5.48	116.73	124.40
1	F	186	ASP	N-CA-C	5.12	116.95	108.20
1	B	207	ARG	CA-CB-CG	-5.05	104.01	114.10

There are no chirality outliers.

There are no planarity outliers.

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	1790	0	1786	21	0
1	B	1711	0	1670	18	0
1	C	1761	0	1706	21	0
1	D	1769	0	1737	42	0
1	E	1736	0	1698	28	0
1	F	1696	0	1612	28	0
2	B	58	0	22	1	0
2	E	29	0	11	2	0
3	C	3	0	0	0	0
3	F	3	0	0	1	0
4	E	1	0	0	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	1	0	0	0	0
5	D	2	0	0	0	0
5	E	3	0	0	0	0
All	All	10567	0	10242	150	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 7.

All (150) 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:D:197:LYS:HA	1:D:200:VAL:CG2	1.82	1.10
1:D:197:LYS:HA	1:D:200:VAL:HG23	1.47	0.95
1:F:173:ASN:HB3	1:F:176:LEU:HD23	1.46	0.94
1:E:28:ASP:HB2	1:E:231:ILE:HD12	1.48	0.94
1:D:24:PHE:HZ	1:D:61:THR:HG22	1.44	0.80
1:F:133:GLY:O	1:F:176:LEU:HD21	1.82	0.80
1:D:197:LYS:CA	1:D:200:VAL:HG23	2.16	0.75
1:D:196:CYS:O	1:D:200:VAL:HG22	1.87	0.75
1:A:147:THR:HG22	1:A:155:ASP:HB3	1.68	0.74
1:C:128:ALA:HB2	1:F:18:VAL:HG11	1.70	0.73
1:D:146:VAL:HG13	1:D:157:ILE:HG12	1.70	0.72
1:D:57:TRP:O	1:D:61:THR:HG23	1.92	0.70
1:F:94:HIS:O	1:F:98:THR:HG22	1.91	0.70
1:B:61:THR:O	1:B:65:LEU:HD12	1.92	0.70
1:C:11:ILE:HG21	1:C:219:THR:HG23	1.73	0.70
1:B:124:GLU:HG2	1:C:20:LEU:HD11	1.75	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:197:LYS:HA	1:D:200:VAL:HG21	1.73	0.67
1:F:43:ILE:HD12	1:F:122:ILE:HG21	1.75	0.67
1:D:60:HIS:O	1:D:64:THR:HG23	1.94	0.66
1:D:197:LYS:C	1:D:200:VAL:HG23	2.21	0.66
1:B:207:ARG:NH1	1:C:16:GLY:O	2.27	0.66
1:C:41:ILE:HD11	1:C:75:ILE:HD11	1.77	0.65
1:C:138:VAL:HG21	1:C:208:LEU:HD23	1.79	0.65
1:B:89:MET:HA	1:B:92:VAL:HG22	1.79	0.64
1:D:24:PHE:CZ	1:D:61:THR:HG22	2.29	0.64
1:D:197:LYS:O	1:D:200:VAL:HG23	1.98	0.62
1:E:10:GLY:HA3	2:E:301:CTP:O1B	1.99	0.62
1:B:217:LYS:NZ	2:B:301[A]:CTP:O2A	2.33	0.61
1:D:37:LEU:HD11	1:D:51:ILE:HD11	1.83	0.60
1:D:20:LEU:HD21	1:E:124:GLU:HG3	1.84	0.59
1:F:48:LYS:NZ	1:F:98:THR:HG21	2.17	0.59
1:E:28:ASP:HB2	1:E:231:ILE:CD1	2.28	0.58
1:A:26:ASP:OD2	1:A:29:ASN:HA	2.03	0.58
1:D:103:ASP:OD1	1:D:103:ASP:N	2.38	0.56
1:D:53:THR:HG21	1:D:61:THR:HG21	1.86	0.56
1:D:2:LYS:HE2	1:D:130:LEU:HD11	1.88	0.55
1:D:110:HIS:CE1	1:D:117:LEU:HD13	2.42	0.55
1:A:9:GLY:HA2	1:A:54:PRO:HD3	1.87	0.55
1:F:11:ILE:HG21	1:F:219:THR:HG23	1.89	0.55
1:F:27:LEU:HD12	1:F:32:ILE:HG12	1.89	0.54
1:D:142:ILE:HG12	1:D:165:GLN:OE1	2.06	0.54
1:B:181:TYR:CZ	1:B:189:LYS:HD3	2.42	0.54
1:E:132:TYR:CG	1:E:207:ARG:HG3	2.43	0.53
1:E:227:ALA:O	1:E:231:ILE:HG12	2.09	0.53
1:A:22:LYS:NZ	1:A:219:THR:O	2.42	0.53
1:F:117:LEU:CD1	1:F:169:PRO:HD3	2.39	0.53
1:F:147:THR:HG22	1:F:155:ASP:HB3	1.90	0.53
1:F:138:VAL:CG1	1:F:164:TYR:HB3	2.39	0.52
1:B:110:HIS:CE1	1:B:117:LEU:HD13	2.45	0.52
1:E:110:HIS:CE1	1:E:117:LEU:HD13	2.45	0.52
1:D:54:PRO:HD2	1:D:57:TRP:CE3	2.46	0.51
1:C:110:HIS:CE1	1:C:117:LEU:HD13	2.46	0.51
1:D:188:GLN:O	1:D:192:LEU:HD13	2.11	0.51
2:E:301:CTP:H6	2:E:301:CTP:H5'2	1.76	0.50
1:E:113:VAL:HG23	1:E:217:LYS:HG3	1.94	0.50
1:E:179:GLU:O	1:E:183:GLN:HG3	2.12	0.50
1:F:138:VAL:HG13	1:F:164:TYR:HB3	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:114:ARG:NH1	1:B:217:LYS:HD3	2.27	0.49
1:F:116:PHE:HE1	1:F:231:ILE:HG12	1.78	0.49
1:B:1:MET:HB2	1:B:105:ASP:OD2	2.13	0.49
1:E:27:LEU:HD13	1:E:224:LEU:HD11	1.95	0.48
1:A:67:LYS:HD3	1:A:68:PHE:CE2	2.48	0.48
1:E:38:GLU:O	1:E:41:ILE:HG12	2.13	0.48
1:D:161:ASN:OD1	1:D:162:GLU:HG3	2.12	0.48
1:F:116:PHE:CE1	1:F:231:ILE:HG12	2.48	0.48
1:E:194:ASP:OD2	1:E:196:CYS:HB2	2.13	0.48
1:A:191:ILE:HD12	1:A:191:ILE:H	1.77	0.48
1:F:113:VAL:O	1:F:113:VAL:HG22	2.13	0.48
1:C:96:GLU:HB2	1:C:101:ILE:CD1	2.43	0.48
1:D:138:VAL:HG12	1:D:166:GLY:HA2	1.96	0.47
1:A:138:VAL:HG11	1:B:146:VAL:HG21	1.97	0.47
1:F:72:ASP:OD1	1:F:74:ARG:HB2	2.14	0.47
1:D:187:GLU:O	1:D:191:ILE:HG12	2.13	0.47
1:A:63:ASP:OD1	1:A:66:ARG:NH1	2.37	0.47
1:F:138:VAL:HG22	1:F:166:GLY:HA2	1.95	0.47
1:E:4:ALA:HB2	1:E:46:PHE:CE1	2.50	0.47
1:E:132:TYR:CD1	1:E:207:ARG:HG3	2.50	0.47
1:D:154:ILE:HD13	1:D:157:ILE:HD11	1.96	0.47
1:D:8:ALA:HB3	1:D:53:THR:CG2	2.45	0.46
1:A:185:SER:O	1:A:189:LYS:HG2	2.16	0.46
1:A:105:ASP:HB3	1:A:174:ILE:HD12	1.97	0.46
1:E:18:VAL:HG21	1:E:25:LEU:HD11	1.97	0.46
1:D:196:CYS:O	1:D:200:VAL:CG2	2.62	0.46
1:F:89:MET:HE1	1:F:178:LYS:HA	1.97	0.46
1:D:230:ILE:HG23	1:D:235:ILE:HG13	1.98	0.46
1:C:192:LEU:HD23	1:C:192:LEU:HA	1.76	0.46
1:E:224:LEU:HD12	1:E:227:ALA:HB3	1.98	0.45
1:F:226:VAL:O	1:F:230:ILE:HG13	2.16	0.45
1:D:150:ASP:OD1	1:D:152:GLN:HB2	2.16	0.45
1:A:230:ILE:HD11	1:B:222:TYR:OH	2.17	0.45
1:D:193:SER:O	1:D:193:SER:OG	2.34	0.45
1:C:168:THR:HB	1:C:169:PRO:HA	1.98	0.45
1:A:168:THR:HB	1:A:169:PRO:HA	1.98	0.45
1:C:145:ILE:HB	1:C:163:MET:HE2	1.99	0.44
1:C:159:VAL:HG13	1:C:162:GLU:HG3	1.99	0.44
1:F:117:LEU:HD11	1:F:169:PRO:HD3	1.98	0.44
1:C:151:ASN:C	1:C:152:GLN:HG2	2.43	0.44
1:D:110:HIS:NE2	1:D:117:LEU:HD13	2.33	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:19:PRO:C	1:E:20:LEU:HD23	2.43	0.44
1:C:164:TYR:CE1	1:D:148:SER:HB3	2.52	0.44
1:A:43:ILE:HG13	1:A:122:ILE:HG21	2.00	0.43
1:D:96:GLU:HB2	1:D:101:ILE:CD1	2.48	0.43
1:C:159:VAL:CG1	1:C:162:GLU:HG3	2.49	0.43
1:F:138:VAL:O	1:F:210:LYS:HA	2.19	0.43
1:E:184:LEU:HD23	1:E:184:LEU:HA	1.73	0.43
1:A:162:GLU:C	1:A:163:MET:HE2	2.44	0.43
1:A:194:ASP:OD1	1:A:196:CYS:N	2.52	0.43
1:C:54:PRO:HD2	1:C:57:TRP:CE3	2.53	0.43
1:C:159:VAL:O	1:C:163:MET:HG2	2.19	0.43
1:D:50:ILE:HG21	1:D:91:ILE:HG23	2.01	0.43
1:D:55:GLN:HB2	1:D:79:GLN:CD	2.44	0.42
1:E:15:MET:HG3	1:E:22:LYS:HG2	2.01	0.42
1:F:133:GLY:O	1:F:176:LEU:CD2	2.62	0.42
1:B:11:ILE:HA	1:B:21:PRO:HB3	2.01	0.42
1:C:2:LYS:O	1:C:46:PHE:HA	2.18	0.42
1:C:230:ILE:HG23	1:C:235:ILE:HB	2.02	0.42
1:D:91:ILE:O	1:D:95:ILE:HG13	2.20	0.42
1:E:224:LEU:HD12	1:E:224:LEU:HA	1.71	0.42
1:F:113:VAL:HG12	3:F:301:SCN:C	2.49	0.42
1:E:8:ALA:O	1:E:53:THR:HA	2.20	0.42
1:E:121:ILE:HD11	1:E:212:GLU:HG2	2.00	0.42
1:D:18:VAL:HG21	1:E:128:ALA:HB2	2.01	0.41
1:D:113:VAL:CG2	1:D:218:VAL:O	2.68	0.41
1:F:186:ASP:OD2	1:F:186:ASP:N	2.51	0.41
1:B:20:LEU:HA	1:B:21:PRO:HD3	1.81	0.41
1:B:30:LYS:HB3	1:B:35:HIS:HE2	1.85	0.41
1:F:27:LEU:CD2	1:F:231:ILE:HG13	2.50	0.41
1:A:184:LEU:HB2	1:A:189:LYS:HE3	2.00	0.41
1:B:146:VAL:HG12	1:B:157:ILE:HG12	2.02	0.41
1:F:98:THR:HG23	1:F:99:ASN:H	1.84	0.41
1:A:37:LEU:HD23	1:A:37:LEU:HA	1.77	0.41
1:F:133:GLY:C	1:F:176:LEU:HD21	2.45	0.41
1:B:145:ILE:HG21	1:B:163:MET:HE2	2.03	0.41
1:F:98:THR:HG23	1:F:99:ASN:N	2.36	0.41
1:C:145:ILE:O	1:C:158:PRO:HD2	2.20	0.41
1:E:22:LYS:H	1:E:22:LYS:HG3	1.61	0.41
1:E:49:ILE:O	1:E:75:ILE:HA	2.20	0.41
1:A:138:VAL:O	1:A:210:LYS:HA	2.21	0.41
1:B:78:ILE:HD11	1:B:91:ILE:HG12	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:125:ASN:OD1	1:B:169:PRO:HB2	2.21	0.41
1:D:8:ALA:HB3	1:D:53:THR:HG22	2.01	0.41
1:D:197:LYS:CA	1:D:200:VAL:CG2	2.71	0.41
1:A:184:LEU:HD13	1:A:192:LEU:HD12	2.03	0.41
1:A:185:SER:OG	1:A:188:GLN:HG3	2.21	0.41
1:E:38:GLU:HA	1:E:41:ILE:HG12	2.02	0.41
1:C:185:SER:OG	1:C:186:ASP:N	2.54	0.40
1:D:15:MET:HE2	1:E:164:TYR:HE2	1.86	0.40
1:E:89:MET:HG3	1:E:181:TYR:CE2	2.56	0.40
1:A:4:ALA:HB2	1:A:46:PHE:CE1	2.56	0.40
1:D:132:TYR:CG	1:D:207:ARG:HD3	2.57	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	232/261 (89%)	224 (97%)	8 (3%)	0	100	100
1	B	223/261 (85%)	218 (98%)	5 (2%)	0	100	100
1	C	234/261 (90%)	228 (97%)	6 (3%)	0	100	100
1	D	233/261 (89%)	226 (97%)	7 (3%)	0	100	100
1	E	230/261 (88%)	222 (96%)	8 (4%)	0	100	100
1	F	226/261 (87%)	218 (96%)	8 (4%)	0	100	100
All	All	1378/1566 (88%)	1336 (97%)	42 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	196/227 (86%)	196 (100%)	0	100	100
1	B	182/227 (80%)	182 (100%)	0	100	100
1	C	187/227 (82%)	187 (100%)	0	100	100
1	D	189/227 (83%)	188 (100%)	1 (0%)	81	93
1	E	183/227 (81%)	183 (100%)	0	100	100
1	F	176/227 (78%)	175 (99%)	1 (1%)	78	93
All	All	1113/1362 (82%)	1111 (100%)	2 (0%)	87	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	200	VAL
1	F	176	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	60	HIS
1	A	125	ASN
1	A	151	ASN
1	A	188	GLN
1	B	102	ASN
1	B	183	GLN
1	C	167	GLN
1	C	215	ASN
1	D	151	ASN
1	D	165	GLN
1	E	165	GLN
1	F	44	ASN
1	F	119	HIS
1	F	228	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 6 ligands modelled in this entry, 1 is monoatomic - leaving 5 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	$\# Z > 2$
3	SCN	F	301	-	1,2,2	0.29	0	0,1,1	-	-
2	CTP	B	301[A]	-	29,30,30	4.38	16 (55%)	43,47,47	1.06	3 (6%)
2	CTP	B	301[B]	-	29,30,30	4.40	16 (55%)	43,47,47	1.01	1 (2%)
2	CTP	E	301	4	29,30,30	4.04	16 (55%)	43,47,47	0.97	2 (4%)
3	SCN	C	301	-	1,2,2	0.01	0	0,1,1	-	-

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	CTP	B	301[A]	-	-	7/22/38/38	0/2/2/2
2	CTP	E	301	4	-	9/22/38/38	0/2/2/2
2	CTP	B	301[B]	-	-	8/22/38/38	0/2/2/2

All (48) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	301[B]	CTP	O4'-C1'	9.07	1.63	1.42
2	E	301	CTP	O4'-C1'	9.07	1.63	1.42
2	B	301[A]	CTP	O4'-C1'	9.05	1.62	1.42
2	B	301[A]	CTP	PA-O3A	8.46	1.68	1.59
2	E	301	CTP	O4'-C4'	-7.79	1.27	1.45
2	B	301[A]	CTP	PB-O3A	7.65	1.67	1.59
2	B	301[B]	CTP	O4'-C4'	-7.43	1.28	1.45
2	B	301[B]	CTP	PB-O3A	7.37	1.67	1.59
2	B	301[B]	CTP	PA-O3A	7.36	1.67	1.59
2	B	301[A]	CTP	O4'-C4'	-7.35	1.28	1.45
2	B	301[A]	CTP	C2'-C1'	-7.33	1.30	1.53
2	B	301[B]	CTP	PB-O3B	7.32	1.67	1.59
2	B	301[B]	CTP	C2'-C1'	-7.31	1.30	1.53
2	E	301	CTP	C2'-C1'	-7.22	1.30	1.53
2	E	301	CTP	C2-N3	6.49	1.49	1.36
2	B	301[A]	CTP	C2-N3	6.44	1.49	1.36
2	B	301[B]	CTP	C2-N3	6.41	1.49	1.36
2	B	301[A]	CTP	C6-C5	6.39	1.49	1.35
2	B	301[B]	CTP	C6-C5	6.37	1.49	1.35
2	E	301	CTP	PB-O3A	6.28	1.66	1.59
2	E	301	CTP	C6-C5	5.99	1.49	1.35
2	E	301	CTP	C4-N3	5.60	1.45	1.34
2	B	301[B]	CTP	C4-N3	5.34	1.45	1.34
2	B	301[A]	CTP	C4-N3	5.34	1.45	1.34
2	E	301	CTP	PA-O3A	4.99	1.64	1.59
2	B	301[A]	CTP	PB-O3B	4.96	1.64	1.59
2	E	301	CTP	C4-N4	4.83	1.45	1.33
2	B	301[A]	CTP	C2-N1	4.68	1.49	1.40
2	B	301[B]	CTP	C2-N1	4.48	1.49	1.40
2	B	301[A]	CTP	C4-N4	4.48	1.44	1.33
2	B	301[B]	CTP	C4-N4	4.43	1.44	1.33
2	E	301	CTP	C2-N1	4.37	1.49	1.40
2	B	301[A]	CTP	O2'-C2'	3.56	1.51	1.43
2	E	301	CTP	O2'-C2'	3.54	1.51	1.43
2	B	301[B]	CTP	O2'-C2'	3.49	1.51	1.43
2	B	301[A]	CTP	C6-N1	3.47	1.46	1.38
2	B	301[B]	CTP	C6-N1	3.42	1.46	1.38
2	E	301	CTP	PB-O3B	3.33	1.63	1.59
2	E	301	CTP	C6-N1	3.09	1.45	1.38
2	B	301[A]	CTP	C5-C4	2.74	1.49	1.42
2	B	301[B]	CTP	C5-C4	2.71	1.49	1.42
2	B	301[B]	CTP	O3'-C3'	-2.67	1.36	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	301	CTP	O2-C2	-2.61	1.18	1.23
2	B	301[A]	CTP	O3'-C3'	-2.61	1.36	1.43
2	E	301	CTP	O3'-C3'	-2.59	1.36	1.43
2	B	301[A]	CTP	O2-C2	-2.52	1.19	1.23
2	B	301[B]	CTP	O2-C2	-2.51	1.19	1.23
2	E	301	CTP	C5-C4	2.26	1.48	1.42

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	301[A]	CTP	O4'-C1'-N1	2.57	114.18	108.36
2	B	301[B]	CTP	O4'-C1'-N1	2.48	113.98	108.36
2	E	301	CTP	C3'-C2'-C1'	2.37	105.94	101.46
2	B	301[A]	CTP	C2'-C1'-N1	-2.35	106.71	113.25
2	E	301	CTP	N4-C4-N3	2.34	122.10	117.91
2	B	301[A]	CTP	C3'-C2'-C1'	2.04	105.32	101.46

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	301[A]	CTP	C5'-O5'-PA-O1A
2	B	301[A]	CTP	C5'-O5'-PA-O2A
2	B	301[A]	CTP	C5'-O5'-PA-O3A
2	B	301[A]	CTP	PB-O3A-PA-O5'
2	B	301[B]	CTP	C5'-O5'-PA-O2A
2	B	301[B]	CTP	C5'-O5'-PA-O3A
2	B	301[B]	CTP	PB-O3B-PG-O2G
2	B	301[A]	CTP	C3'-C4'-C5'-O5'
2	B	301[A]	CTP	O4'-C4'-C5'-O5'
2	E	301	CTP	PA-O3A-PB-O1B
2	B	301[B]	CTP	O4'-C4'-C5'-O5'
2	B	301[B]	CTP	PB-O3A-PA-O5'
2	B	301[A]	CTP	PB-O3B-PG-O1G
2	E	301	CTP	PB-O3A-PA-O2A
2	E	301	CTP	PB-O3B-PG-O1G
2	B	301[B]	CTP	PB-O3B-PG-O3G
2	E	301	CTP	PB-O3B-PG-O2G
2	E	301	CTP	PB-O3B-PG-O3G
2	E	301	CTP	PB-O3A-PA-O1A
2	E	301	CTP	PA-O3A-PB-O2B
2	B	301[B]	CTP	PB-O3B-PG-O1G

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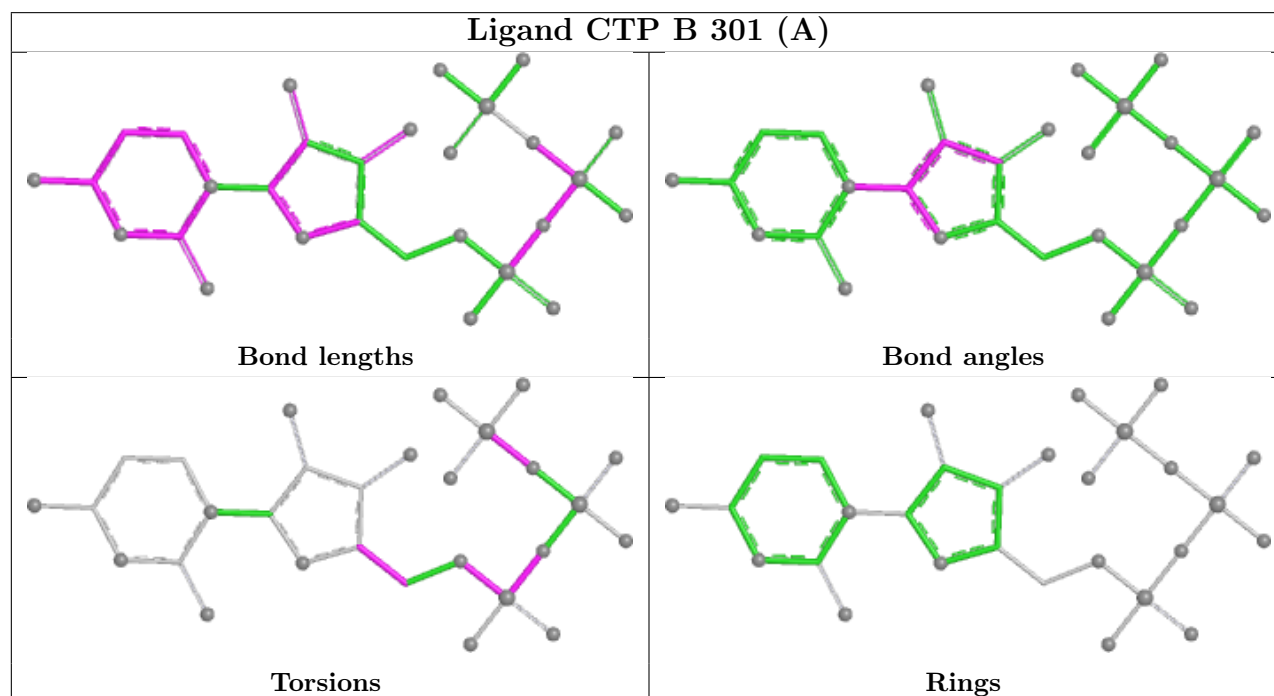
Mol	Chain	Res	Type	Atoms
2	E	301	CTP	O4'-C4'-C5'-O5'
2	E	301	CTP	C3'-C4'-C5'-O5'
2	B	301[B]	CTP	PA-O3A-PB-O2B

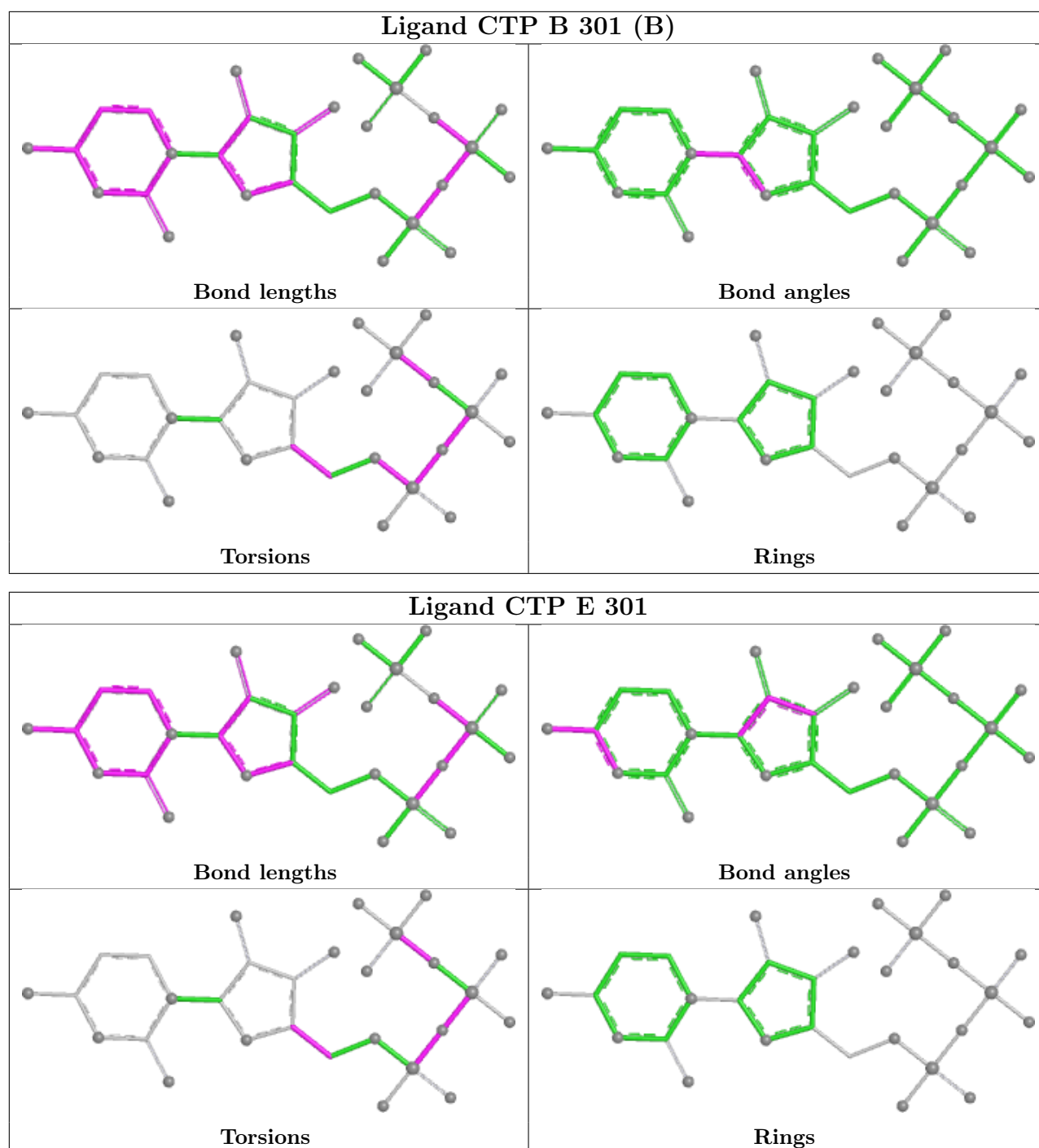
There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	301	SCN	1	0
2	B	301[A]	CTP	1	0
2	E	301	CTP	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 than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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	234/261 (89%)	-0.22	2 (0%) 81 75	28, 47, 75, 94	0
1	B	227/261 (86%)	-0.05	2 (0%) 81 75	32, 52, 83, 106	0
1	C	236/261 (90%)	-0.09	1 (0%) 88 85	33, 57, 95, 123	0
1	D	235/261 (90%)	-0.05	0 100 100	37, 56, 95, 129	0
1	E	232/261 (88%)	0.18	6 (2%) 57 48	39, 65, 119, 148	0
1	F	230/261 (88%)	0.31	5 (2%) 62 53	50, 71, 102, 117	0
All	All	1394/1566 (89%)	0.01	16 (1%) 78 71	28, 58, 100, 148	0

All (16) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	F	222	TYR	2.9
1	E	187	GLU	2.9
1	B	80	GLY	2.7
1	E	153	THR	2.6
1	E	150	ASP	2.4
1	A	234	GLY	2.4
1	C	106	VAL	2.4
1	A	213	LEU	2.4
1	E	184	LEU	2.4
1	E	191	ILE	2.4
1	E	133	GLY	2.3
1	F	136	ASP	2.1
1	F	26	ASP	2.1
1	F	180	SER	2.0
1	B	11	ILE	2.0
1	F	104	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](#)

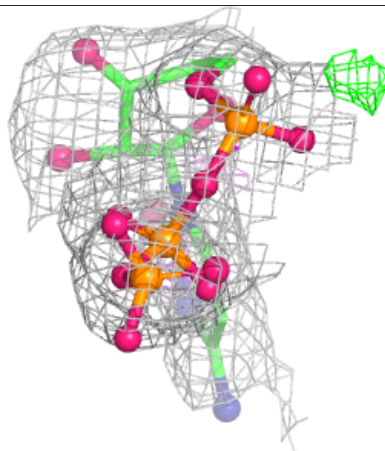
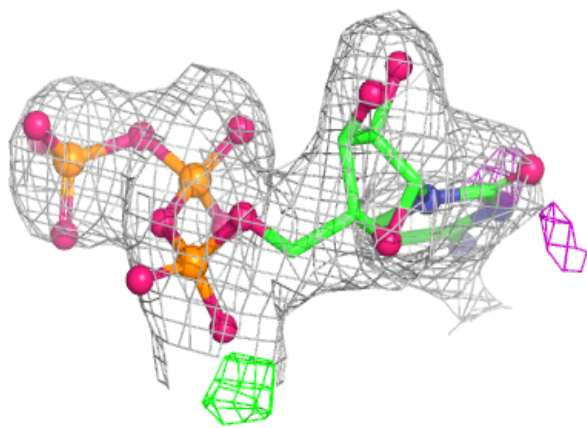
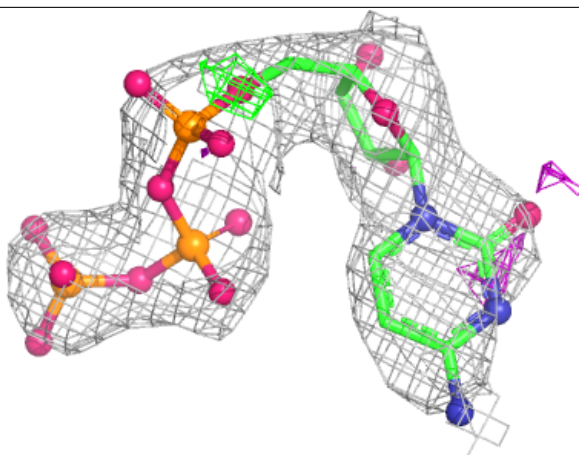
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	CTP	B	301[A]	29/29	0.85	0.11	51,53,54,55	29
2	CTP	B	301[B]	29/29	0.85	0.11	49,53,54,55	29
3	SCN	F	301	3/3	0.90	0.11	64,64,65,65	0
2	CTP	E	301	29/29	0.91	0.08	63,67,75,75	0
3	SCN	C	301	3/3	0.94	0.10	54,54,55,55	0
4	MG	E	302	1/1	0.97	0.05	62,62,62,62	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.

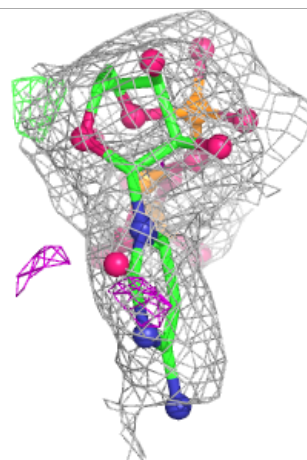
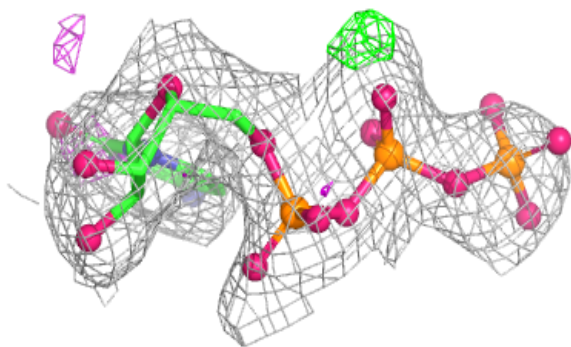
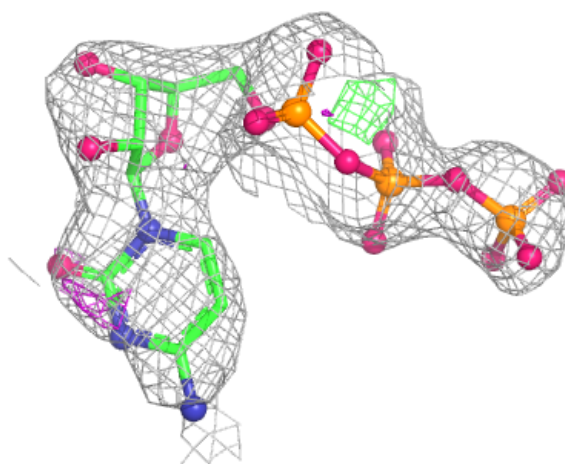
Electron density around CTP B 301 (A):

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



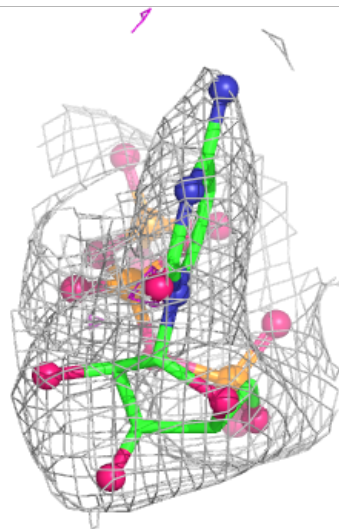
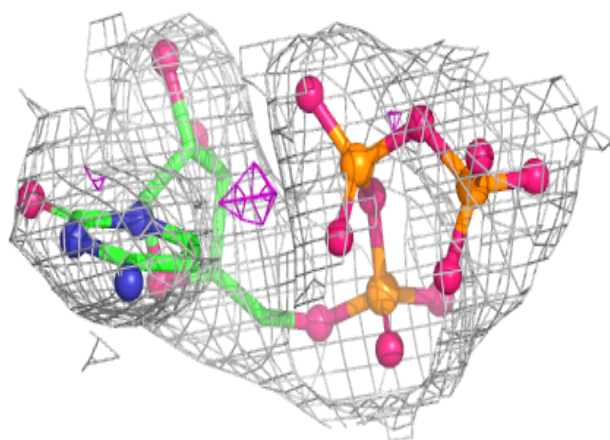
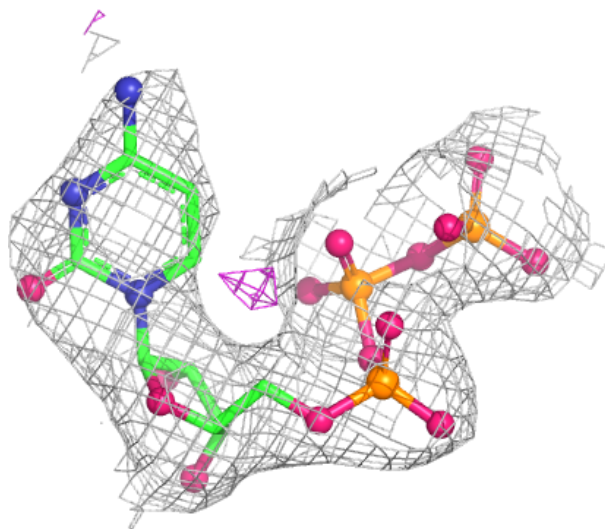
Electron density around CTP B 301 (B):

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



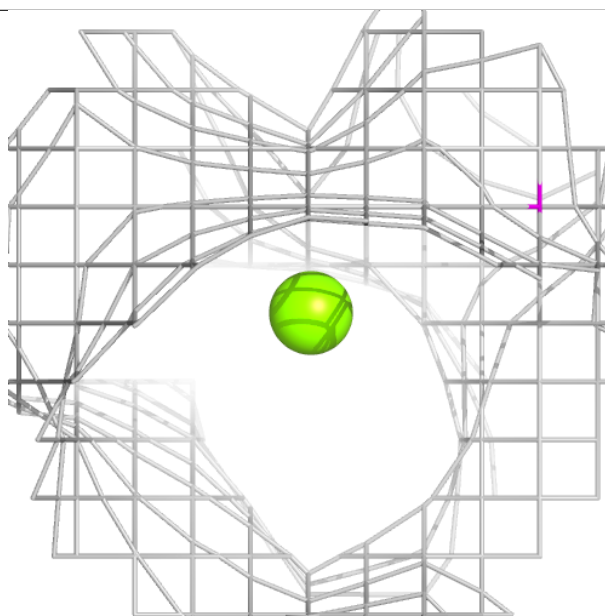
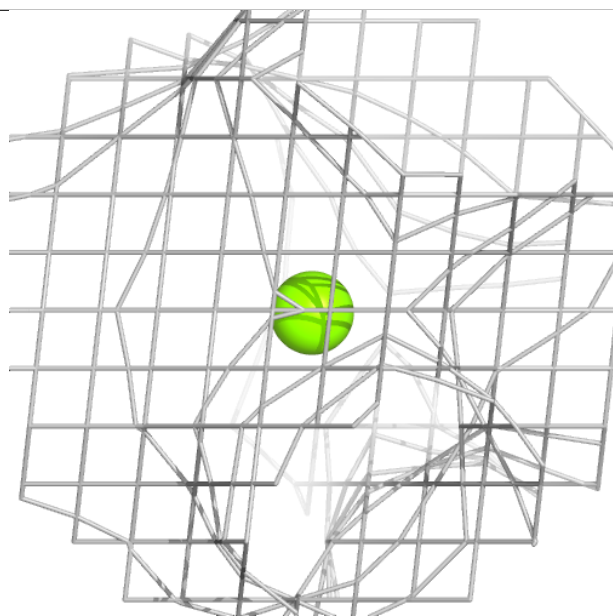
Electron density around CTP E 301:

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



Electron density around MG E 302:

$2mF_o-DF_c$ (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.