



Full wwPDB X-ray Structure Validation Report ⓘ

May 17, 2020 – 02:41 am BST

PDB ID : 3IEL
Title : Crystal Structure of TTHA0252 from *Thermus thermophilus* HB8 complexed with UMP
Authors : Ishikawa, H.; Nakagawa, N.; Kuramitsu, S.; Yokoyama, S.; Masui, R.
Deposited on : 2009-07-23
Resolution : 2.35 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 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 : 2.11
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) : 2.11

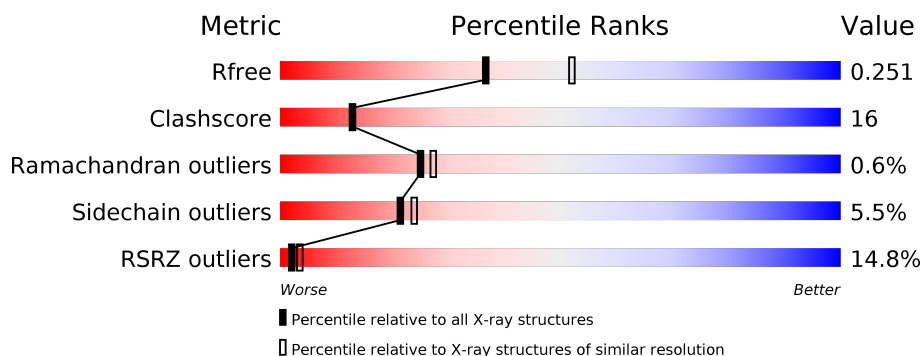
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1164 (2.36-2.36)
Clashscore	141614	1232 (2.36-2.36)
Ramachandran outliers	138981	1211 (2.36-2.36)
Sidechain outliers	138945	1212 (2.36-2.36)
RSRZ outliers	127900	1150 (2.36-2.36)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments on 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	431	<div> <div>3%</div> <div>73%</div> <div>24%</div> <div>.</div> </div>
1	B	431	<div> <div>2%</div> <div>74%</div> <div>23%</div> <div>.</div> </div>
1	C	431	<div> <div>26%</div> <div>62%</div> <div>36%</div> <div>.</div> </div>
1	D	431	<div> <div>30%</div> <div>57%</div> <div>41%</div> <div>.</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	SO4	A	433	-	-	X	X
2	SO4	A	442	-	-	-	X
2	SO4	A	443	-	-	X	-
2	SO4	A	444	-	-	-	X
2	SO4	A	446	-	-	-	X
2	SO4	A	451	-	-	-	X
2	SO4	B	440	-	-	-	X
2	SO4	C	447	-	-	-	X
2	SO4	C	453	-	-	X	-
2	SO4	D	437	-	-	-	X
2	SO4	D	442	-	-	-	X
2	SO4	D	443	-	-	-	X
3	FLC	A	464	-	-	-	X
3	FLC	B	455	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 14251 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 Ribonuclease TTHA0252.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			
1	B	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			
1	C	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			
1	D	431	Total	C	N	O	S	0	0	0
			3326	2127	597	594	8			

- Molecule 2 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

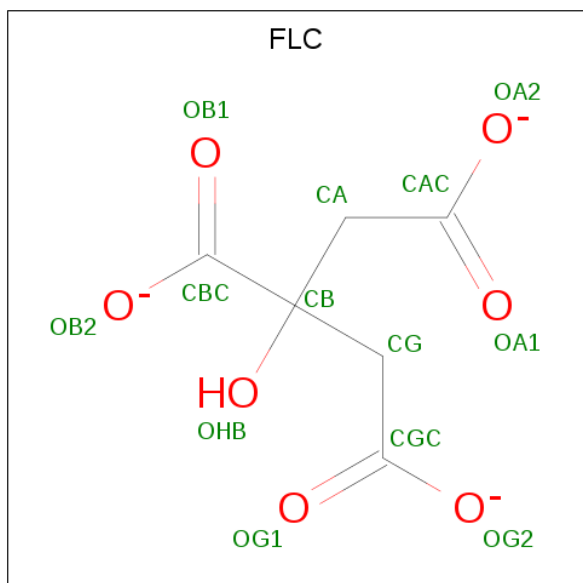
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is CITRATE ANION (three-letter code: FLC) (formula: $\text{C}_6\text{H}_5\text{O}_7$).



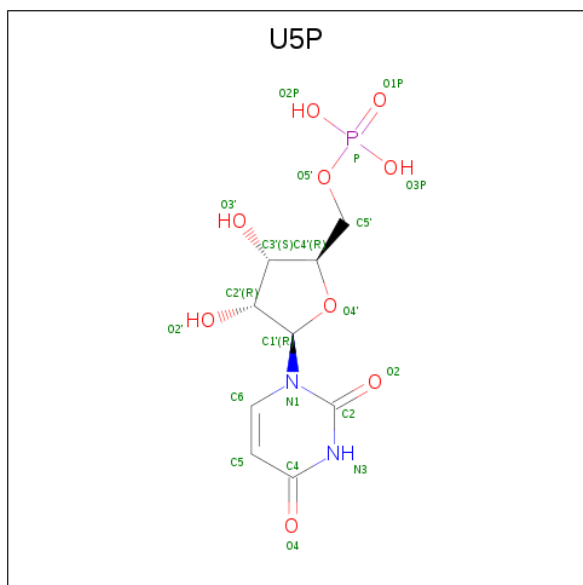
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	B	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is URIDINE-5'-MONOPHOSPHATE (three-letter code: U5P) (formula: $C_9H_{13}N_2O_9P$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
4	A	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
4	A	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
4	B	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
4	B	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
4	C	1	Total	C	N	O	P	0	0
			21	9	2	9	1		
4	D	1	Total	C	N	O	P	0	0
			21	9	2	9	1		

- Molecule 5 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	B	2	Total	Zn	0	0
			2	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total 2	Zn 2	0	0
5	D	2	Total 2	Zn 2	0	0
5	C	2	Total 2	Zn 2	0	0

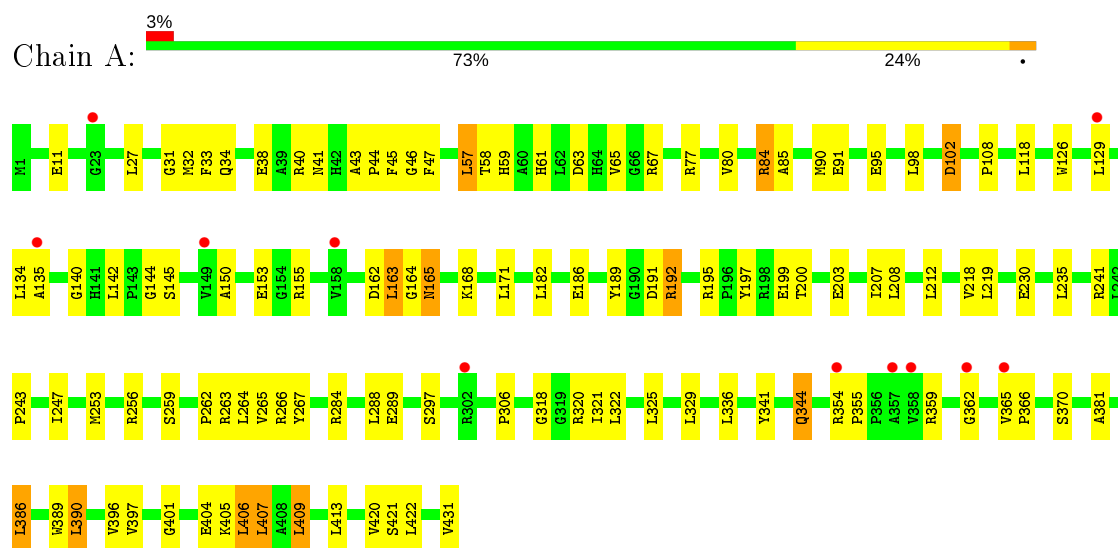
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	118	Total 118	O 118	0	0
6	B	95	Total 95	O 95	0	0
6	C	47	Total 47	O 47	0	0
6	D	26	Total 26	O 26	0	0

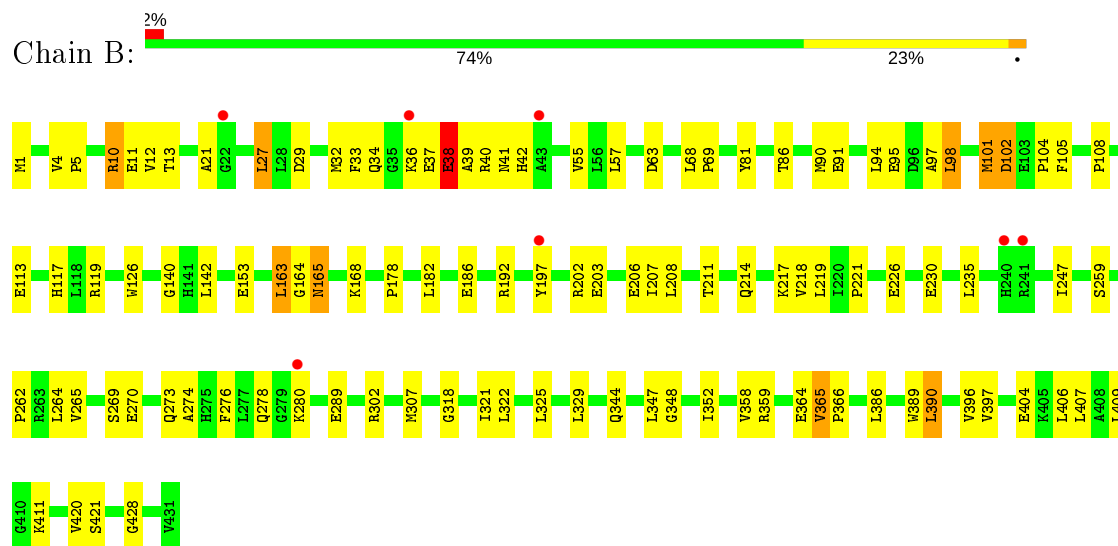
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Ribonuclease TTHA0252

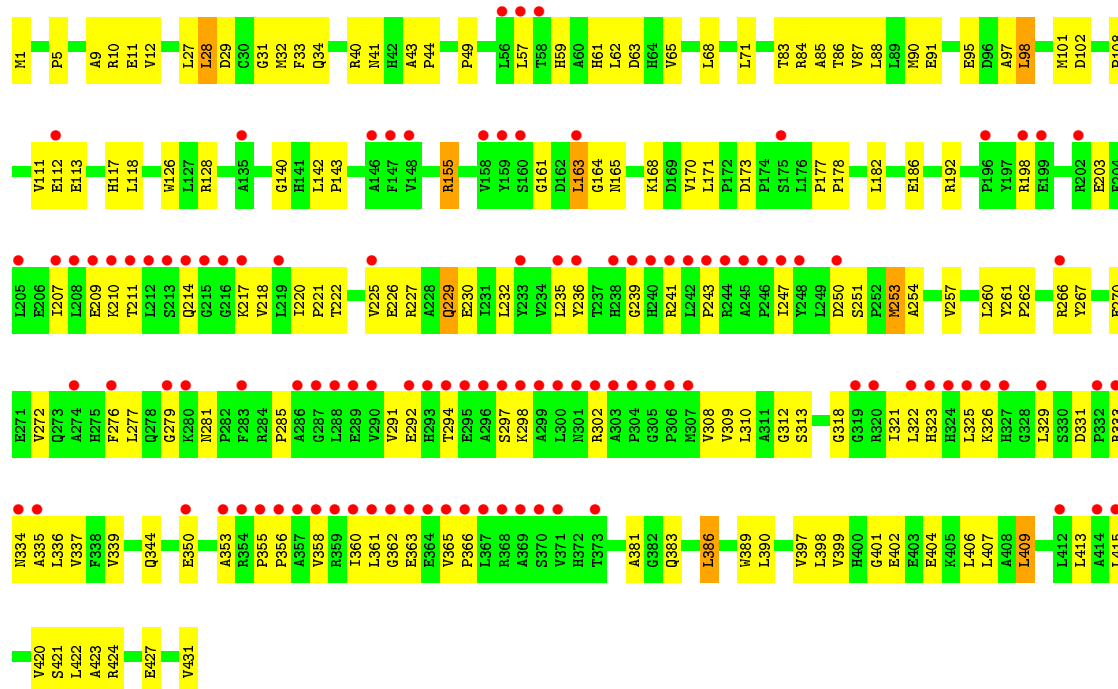


• Molecule 1: Ribonuclease TTHA0252

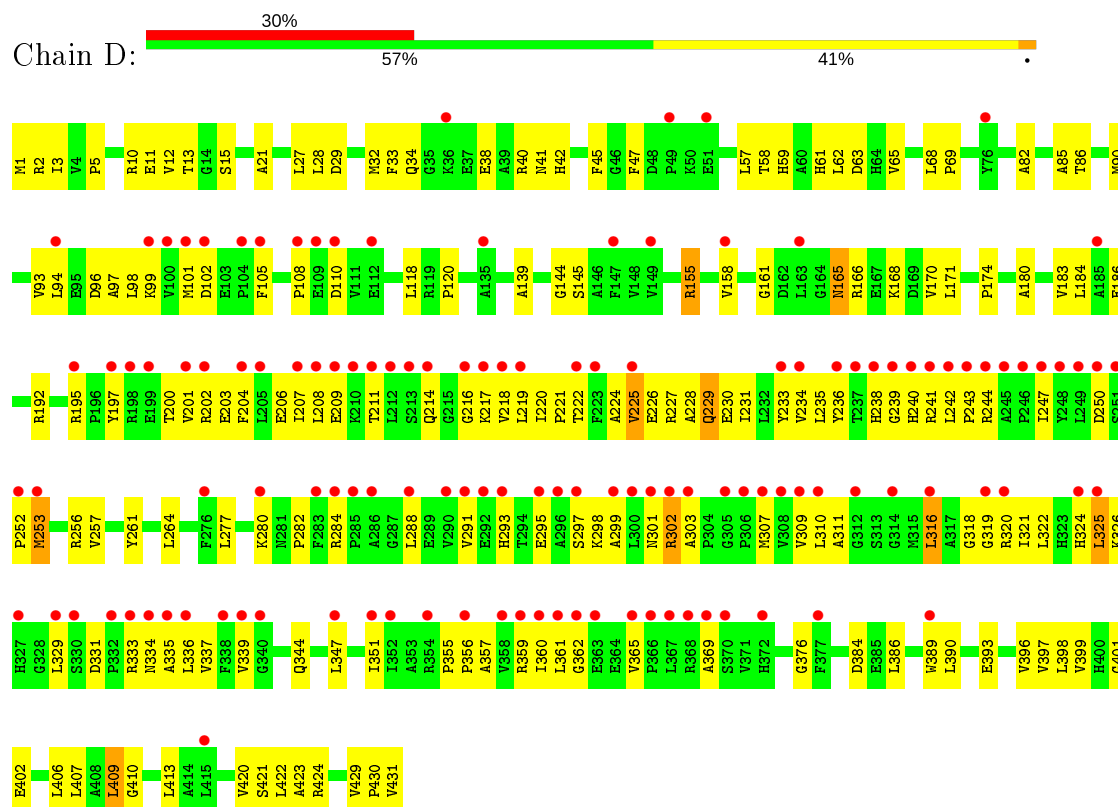


• Molecule 1: Ribonuclease TTHA0252





• Molecule 1: Ribonuclease TTHA0252



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	145.24Å 146.68Å 120.35Å 90.00° 110.11° 90.00°	Depositor
Resolution (Å)	50.00 – 2.35 44.60 – 2.35	Depositor EDS
% Data completeness (in resolution range)	95.3 (50.00-2.35) 95.4 (44.60-2.35)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	5.28 (at 2.34Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.222 , 0.259 0.215 , 0.251	Depositor DCC
R_{free} test set	9797 reflections (10.00%)	wwPDB-VP
Wilson B-factor (Å ²)	45.9	Xtriage
Anisotropy	0.257	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 50.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	14251	wwPDB-VP
Average B, all atoms (Å ²)	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.02% 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: SO4, FLC, ZN, U5P

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	0.37	0/3407	0.65	0/4621
1	B	0.37	0/3407	0.66	1/4621 (0.0%)
1	C	0.32	0/3407	0.59	1/4621 (0.0%)
1	D	0.29	0/3407	0.57	1/4621 (0.0%)
All	All	0.34	0/13628	0.62	3/18484 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	390	LEU	CA-CB-CG	5.37	127.66	115.30
1	C	161	GLY	N-CA-C	-5.22	100.06	113.10
1	D	161	GLY	N-CA-C	-5.03	100.53	113.10

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	3326	0	3351	90	0
1	B	3326	0	3351	80	0
1	C	3326	0	3351	135	0
1	D	3326	0	3351	154	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	A	160	0	0	9	0
2	B	115	0	0	0	0
2	C	125	0	0	5	0
2	D	80	0	0	1	0
3	A	13	0	5	1	0
3	B	13	0	5	2	0
4	A	63	0	33	2	0
4	B	42	0	22	2	0
4	C	21	0	11	0	0
4	D	21	0	11	0	0
5	A	2	0	0	0	0
5	B	2	0	0	0	0
5	C	2	0	0	0	0
5	D	2	0	0	0	0
6	A	118	0	0	5	0
6	B	95	0	0	6	0
6	C	47	0	0	3	0
6	D	26	0	0	1	0
All	All	14251	0	13491	452	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 16.

All (452) 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:C:98:LEU:HD11	1:C:108:PRO:HA	1.40	1.03
1:D:235:LEU:HD23	1:D:247:ILE:HD13	1.37	1.03
1:B:33:PHE:H	1:B:41:ASN:HD21	1.05	1.01
1:D:33:PHE:H	1:D:41:ASN:HD21	1.10	0.99
1:B:153:GLU:HG2	6:B:519:HOH:O	1.65	0.97
1:A:153:GLU:HG2	2:A:433:SO4:O1	1.63	0.97
1:A:33:PHE:H	1:A:41:ASN:HD21	1.05	0.94
1:A:306:PRO:HD2	1:B:302:ARG:HH22	1.33	0.91
1:C:33:PHE:H	1:C:41:ASN:HD21	1.15	0.89
1:B:265:VAL:HG12	6:B:532:HOH:O	1.76	0.85
1:D:222:THR:HG22	1:D:339:VAL:HG21	1.58	0.83
1:D:284:ARG:HD3	1:D:288:LEU:HD23	1.59	0.83
1:D:1:MET:HG3	1:D:21:ALA:HB2	1.59	0.82
1:A:208:LEU:HD23	1:A:218:VAL:HG21	1.63	0.81
1:C:360:ILE:HG22	1:C:361:LEU:HD13	1.63	0.80

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:153:GLU:HA	2:A:433:SO4:O3	1.82	0.80
1:D:98:LEU:HD21	1:D:108:PRO:HB3	1.64	0.80
1:A:168:LYS:HE3	1:A:230:GLU:OE1	1.81	0.79
1:D:168:LYS:HE2	1:D:230:GLU:OE1	1.83	0.79
1:B:97:ALA:O	1:B:101:MET:HB2	1.81	0.78
1:D:322:LEU:HB3	1:D:361:LEU:HD11	1.64	0.78
1:D:211:THR:HG21	1:D:335:ALA:HB2	1.64	0.78
1:B:101:MET:HG2	1:B:104:PRO:HB3	1.68	0.75
1:C:168:LYS:HE3	1:C:230:GLU:OE1	1.87	0.75
1:B:33:PHE:N	1:B:41:ASN:HD21	1.83	0.75
1:A:404:GLU:CD	1:A:404:GLU:H	1.89	0.75
1:C:97:ALA:O	1:C:101:MET:HB2	1.87	0.74
1:C:10:ARG:HH12	1:C:424:ARG:HG2	1.52	0.73
1:A:155:ARG:HD3	1:A:431:VAL:O	1.88	0.73
1:A:34:GLN:HE21	1:A:63:ASP:HB3	1.54	0.73
1:C:10:ARG:HH22	1:C:424:ARG:NH1	1.86	0.73
1:D:407:LEU:HD22	1:D:422:LEU:HD21	1.70	0.73
1:D:360:ILE:HG22	1:D:361:LEU:HD13	1.70	0.72
1:B:208:LEU:HD23	1:B:218:VAL:HG21	1.71	0.72
1:D:309:VAL:HG11	1:D:324:HIS:CD2	2.25	0.71
1:C:43:ALA:HB1	1:C:44:PRO:HD2	1.72	0.71
1:C:229:GLN:CD	1:C:229:GLN:H	1.94	0.71
1:A:34:GLN:NE2	1:A:63:ASP:HB3	2.06	0.71
1:C:34:GLN:HE21	1:C:63:ASP:HB3	1.55	0.70
1:C:218:VAL:HB	1:C:308:VAL:HG12	1.74	0.70
1:D:318:GLY:HA2	1:D:322:LEU:HD11	1.74	0.69
1:B:33:PHE:H	1:B:41:ASN:ND2	1.86	0.69
1:B:278:GLN:HB2	1:B:280:LYS:HD3	1.74	0.69
1:C:33:PHE:N	1:C:41:ASN:HD21	1.91	0.68
1:C:404:GLU:CD	1:C:404:GLU:H	1.96	0.68
1:C:163:LEU:HD21	1:C:389:TRP:CD2	2.29	0.68
1:C:33:PHE:H	1:C:41:ASN:ND2	1.89	0.68
1:C:220:ILE:HG12	1:C:337:VAL:CG2	2.25	0.67
1:C:209:GLU:HG2	1:C:243:PRO:HD3	1.77	0.67
1:C:221:PRO:HB3	1:C:321:ILE:HG12	1.76	0.67
1:D:302:ARG:HG2	1:D:303:ALA:N	2.08	0.67
1:C:362:GLY:O	1:C:363:GLU:HG3	1.95	0.67
1:A:33:PHE:N	1:A:41:ASN:HD21	1.86	0.66
1:D:325:LEU:HD13	1:D:360:ILE:HD13	1.77	0.66
1:D:250:ASP:HA	1:D:291:VAL:HB	1.75	0.66
1:B:42:HIS:ND1	1:B:105:PHE:HB3	2.09	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:410:GLY:HA2	1:D:420:VAL:HG21	1.78	0.66
1:B:289:GLU:HG3	6:B:518:HOH:O	1.94	0.66
1:A:33:PHE:H	1:A:41:ASN:ND2	1.87	0.66
1:D:222:THR:HG22	1:D:339:VAL:CG2	2.26	0.66
1:C:247:ILE:HA	1:C:308:VAL:HG23	1.78	0.65
1:D:99:LYS:HE3	2:D:443:SO4:O2	1.97	0.65
1:C:229:GLN:NE2	1:C:229:GLN:H	1.95	0.64
1:C:322:LEU:HB3	1:C:361:LEU:HD11	1.78	0.64
1:C:235:LEU:HD13	1:C:247:ILE:HD13	1.78	0.64
1:D:401:GLY:HA3	1:D:406:LEU:HD11	1.79	0.64
1:C:83:THR:O	1:C:87:VAL:HG23	1.98	0.64
1:D:298:LYS:HA	1:D:301:ASN:HD22	1.62	0.64
1:D:200:THR:HG21	1:D:376:GLY:HA3	1.78	0.63
1:D:224:ALA:HB1	1:D:253:MET:HG2	1.80	0.63
1:D:325:LEU:O	1:D:329:LEU:HD13	1.97	0.63
1:D:239:GLY:HA2	1:D:242:LEU:HD12	1.80	0.63
1:A:362:GLY:HA2	2:A:443:SO4:O3	1.98	0.63
1:D:422:LEU:N	1:D:422:LEU:HD12	2.14	0.63
1:D:331:ASP:HB3	1:D:334:ASN:ND2	2.13	0.62
1:D:211:THR:HG21	1:D:335:ALA:CB	2.27	0.62
1:A:381:ALA:HB3	1:A:386:LEU:HD13	1.82	0.62
1:D:321:ILE:O	1:D:325:LEU:HG	2.00	0.62
1:C:358:VAL:O	1:C:365:VAL:HG22	2.00	0.62
1:A:321:ILE:O	1:A:325:LEU:HD13	2.00	0.62
1:D:253:MET:HA	1:D:256:ARG:HH21	1.65	0.62
1:D:209:GLU:HG3	1:D:243:PRO:HD3	1.81	0.61
1:D:97:ALA:O	1:D:101:MET:HB2	2.01	0.61
1:D:12:VAL:HG23	1:D:13:THR:HG23	1.83	0.60
1:D:309:VAL:C	1:D:310:LEU:HD12	2.22	0.60
1:C:1:MET:HG2	1:C:431:VAL:HG21	1.83	0.60
1:A:253:MET:HA	1:A:256:ARG:NH2	2.17	0.60
1:D:139:ALA:O	1:D:174:PRO:HG3	2.01	0.60
1:D:10:ARG:NH1	1:D:424:ARG:HG3	2.17	0.60
1:D:208:LEU:HD23	1:D:218:VAL:HG11	1.83	0.60
1:D:253:MET:HA	1:D:256:ARG:NH2	2.16	0.60
1:A:306:PRO:HD2	1:B:302:ARG:NH2	2.12	0.60
1:C:34:GLN:NE2	1:C:63:ASP:HB3	2.17	0.59
1:D:85:ALA:HB3	1:D:144:GLY:HA3	1.83	0.59
1:A:182:LEU:HD11	1:A:397:VAL:HG23	1.84	0.59
1:B:269:SER:O	1:B:273:GLN:HG3	2.01	0.59
1:A:259:SER:O	1:A:262:PRO:HD2	2.03	0.59

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:87:VAL:HG13	1:C:118:LEU:HD13	1.84	0.59
1:D:33:PHE:H	1:D:41:ASN:ND2	1.90	0.59
1:C:209:GLU:HG2	1:C:243:PRO:CD	2.33	0.58
1:C:424:ARG:HD3	1:C:427:GLU:OE2	2.02	0.58
1:B:289:GLU:CG	6:B:518:HOH:O	2.50	0.58
1:C:85:ALA:HB2	1:C:267:TYR:CD2	2.38	0.58
1:C:222:THR:HG22	1:C:339:VAL:HG21	1.86	0.58
1:C:170:VAL:HG13	1:C:171:LEU:HD13	1.86	0.58
1:D:45:PHE:HB3	1:D:47:PHE:CE1	2.39	0.58
1:B:235:LEU:HD13	1:B:247:ILE:HD13	1.86	0.57
1:B:359:ARG:HD2	1:B:364:GLU:OE2	2.04	0.57
1:D:229:GLN:H	1:D:229:GLN:NE2	2.02	0.57
1:D:59:HIS:CD2	1:D:61:HIS:HB2	2.39	0.57
1:A:57:LEU:HG	1:A:65:VAL:HG12	1.85	0.57
1:D:98:LEU:HD21	1:D:108:PRO:CB	2.34	0.57
1:B:1:MET:HG3	1:B:21:ALA:HB2	1.85	0.57
1:C:86:THR:HG22	1:C:90:MET:CE	2.34	0.57
1:D:34:GLN:HE21	1:D:63:ASP:HB3	1.70	0.57
1:B:12:VAL:HG21	4:B:456:U5P:O2	2.04	0.57
1:B:165:ASN:C	1:B:165:ASN:HD22	2.07	0.57
1:C:217:LYS:HB2	1:C:334:ASN:OD1	2.04	0.57
1:A:163:LEU:HD21	1:A:389:TRP:CD2	2.40	0.57
1:C:355:PRO:HB2	1:C:356:PRO:HD2	1.87	0.57
1:C:98:LEU:HD11	1:C:108:PRO:CA	2.26	0.57
1:C:10:ARG:NH2	1:C:424:ARG:NH1	2.53	0.56
1:C:220:ILE:HG23	1:C:337:VAL:HG23	1.87	0.56
1:C:40:ARG:HD2	6:C:467:HOH:O	2.05	0.56
1:D:355:PRO:HB2	1:D:356:PRO:HD2	1.86	0.56
1:A:129:LEU:HD21	6:A:575:HOH:O	2.05	0.56
1:A:189:TYR:CZ	4:A:465:U5P:H5	2.40	0.56
1:C:225:VAL:O	1:C:257:VAL:HG11	2.06	0.56
1:C:163:LEU:HD21	1:C:389:TRP:CE3	2.40	0.56
1:A:284:ARG:HD3	1:A:288:LEU:HD23	1.88	0.56
1:A:195:ARG:HD2	1:A:199:GLU:OE2	2.05	0.56
1:C:88:LEU:HB3	1:C:260:LEU:HD21	1.88	0.56
1:D:240:HIS:ND1	1:D:241:ARG:N	2.54	0.56
1:C:321:ILE:O	1:C:325:LEU:HD13	2.05	0.55
1:C:59:HIS:CD2	1:C:61:HIS:HB2	2.41	0.55
1:B:86:THR:HG22	1:B:90:MET:HE2	1.89	0.55
1:C:402:GLU:HB3	1:C:404:GLU:OE2	2.07	0.55
1:C:298:LYS:HD2	2:C:453:SO4:O3	2.06	0.55

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:170:VAL:HG12	1:D:171:LEU:HD12	1.87	0.55
1:D:396:VAL:HG12	1:D:398:LEU:HD12	1.89	0.55
1:D:229:GLN:H	1:D:229:GLN:CD	2.10	0.55
1:C:331:ASP:HB3	1:C:334:ASN:ND2	2.21	0.55
1:C:360:ILE:CG2	1:C:361:LEU:HD13	2.34	0.54
1:B:27:LEU:HD13	1:B:29:ASP:O	2.07	0.54
1:D:360:ILE:O	1:D:361:LEU:HB2	2.07	0.54
1:A:370:SER:HA	2:A:451:SO4:O2	2.07	0.54
1:B:202:ARG:O	1:B:206:GLU:HG3	2.07	0.54
1:C:401:GLY:HA3	1:C:406:LEU:HD11	1.89	0.54
1:D:284:ARG:HD3	1:D:288:LEU:CD2	2.33	0.54
1:C:236:TYR:HD1	1:C:285:PRO:HA	1.73	0.54
1:B:208:LEU:HD21	1:B:218:VAL:HG11	1.90	0.54
1:D:229:GLN:HG3	1:D:261:TYR:CZ	2.42	0.54
1:C:182:LEU:HD11	1:C:397:VAL:HG23	1.89	0.53
1:D:224:ALA:CB	1:D:253:MET:HG2	2.38	0.53
1:D:236:TYR:OH	1:D:280:LYS:HE2	2.08	0.53
1:A:359:ARG:NH1	2:A:443:SO4:O3	2.41	0.53
1:D:86:THR:HG22	1:D:90:MET:CE	2.39	0.53
1:D:225:VAL:O	1:D:257:VAL:HG11	2.08	0.53
1:D:69:PRO:O	1:D:110:ASP:HB3	2.09	0.53
1:C:214:GLN:NE2	1:C:333:ARG:HA	2.24	0.53
1:D:2:ARG:HG3	1:D:430:PRO:HA	1.90	0.53
1:D:1:MET:HG3	1:D:21:ALA:CB	2.35	0.53
1:D:360:ILE:CG2	1:D:361:LEU:HD13	2.38	0.53
1:C:270:GLU:HA	1:C:270:GLU:OE1	2.09	0.52
1:B:226:GLU:HG2	6:B:538:HOH:O	2.08	0.52
1:A:344:GLN:HA	1:A:344:GLN:NE2	2.24	0.52
1:C:236:TYR:CD1	1:C:285:PRO:HA	2.45	0.52
1:A:98:LEU:HD11	1:A:108:PRO:HA	1.91	0.52
1:C:86:THR:HG22	1:C:90:MET:HE2	1.92	0.52
1:A:263:ARG:HG2	1:D:277:LEU:HD21	1.91	0.52
1:C:57:LEU:HG	1:C:65:VAL:HG12	1.92	0.52
1:D:86:THR:HG22	1:D:90:MET:HE2	1.91	0.52
1:B:274:ALA:O	1:B:278:GLN:HG2	2.10	0.52
1:B:411:LYS:HB2	3:B:455:FLC:OHB	2.10	0.52
1:C:5:PRO:HG2	1:C:423:ALA:HB1	1.91	0.52
1:B:42:HIS:CE1	1:B:105:PHE:HB3	2.45	0.52
1:C:28:LEU:O	1:C:29:ASP:HB2	2.09	0.52
1:D:214:GLN:HE21	1:D:333:ARG:HA	1.75	0.52
1:D:183:VAL:HG21	1:D:393:GLU:HG3	1.92	0.51

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:68:LEU:N	1:D:69:PRO:HD2	2.25	0.51
1:B:102:ASP:HA	6:B:524:HOH:O	2.09	0.51
1:C:294:THR:O	1:C:298:LYS:HG2	2.11	0.51
1:C:309:VAL:C	1:C:310:LEU:HD12	2.30	0.51
1:D:155:ARG:HD3	1:D:431:VAL:O	2.11	0.51
1:D:11:GLU:CD	1:D:40:ARG:HH12	2.14	0.51
1:A:11:GLU:OE2	1:A:40:ARG:NH1	2.42	0.51
1:C:155:ARG:HD3	1:C:431:VAL:O	2.11	0.51
1:C:292:GLU:HB2	2:C:433:SO4:O2	2.11	0.51
1:A:297:SER:OG	1:A:320:ARG:HG2	2.11	0.51
1:C:84:ARG:NH1	2:C:451:SO4:O3	2.36	0.51
1:A:32:MET:HA	1:A:67:ARG:HG3	1.93	0.50
1:C:409:LEU:HD22	1:C:413:LEU:HG	1.92	0.50
1:C:59:HIS:HD2	1:C:61:HIS:H	1.58	0.50
1:D:214:GLN:NE2	1:D:333:ARG:HA	2.27	0.50
1:D:218:VAL:O	1:D:220:ILE:HG13	2.11	0.50
1:A:134:LEU:HD23	1:A:150:ALA:HA	1.92	0.50
1:B:208:LEU:CD2	1:B:218:VAL:HG11	2.41	0.50
1:C:247:ILE:HG12	1:C:308:VAL:CG2	2.41	0.50
1:B:211:THR:HA	1:B:214:GLN:HG2	1.93	0.50
1:C:9:ALA:O	1:C:11:GLU:HG2	2.11	0.50
1:C:170:VAL:HG13	1:C:171:LEU:CD1	2.41	0.50
1:C:170:VAL:HG22	1:C:171:LEU:HD12	1.93	0.50
1:D:208:LEU:CD2	1:D:218:VAL:HG11	2.41	0.50
1:A:344:GLN:CA	1:A:344:GLN:HE21	2.25	0.50
1:B:12:VAL:HG23	1:B:13:THR:HG23	1.93	0.50
1:C:10:ARG:HH22	1:C:424:ARG:HH11	1.59	0.50
1:D:42:HIS:CE1	1:D:105:PHE:HB3	2.47	0.50
1:D:228:ALA:HB3	1:D:229:GLN:NE2	2.27	0.50
1:A:359:ARG:NH2	2:A:444:SO4:O2	2.45	0.49
1:C:365:VAL:HG23	1:C:365:VAL:O	2.12	0.49
1:C:381:ALA:HB3	1:C:386:LEU:HD13	1.94	0.49
1:D:298:LYS:HA	1:D:301:ASN:ND2	2.25	0.49
1:D:226:GLU:N	6:D:476:HOH:O	2.44	0.49
1:D:299:ALA:HA	1:D:302:ARG:HD2	1.94	0.49
1:B:208:LEU:CD2	1:B:218:VAL:HG21	2.41	0.49
1:A:165:ASN:C	1:A:165:ASN:HD22	2.15	0.49
1:A:59:HIS:CD2	1:A:61:HIS:HB2	2.47	0.49
1:B:34:GLN:HA	1:B:38:GLU:HG3	1.94	0.49
1:D:219:LEU:HD21	1:D:324:HIS:O	2.12	0.49
1:A:396:VAL:O	1:A:420:VAL:HA	2.11	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:33:PHE:N	1:D:41:ASN:HD21	1.93	0.49
1:D:326:LYS:HD2	1:D:361:LEU:HD22	1.93	0.49
1:A:90:MET:HE1	1:A:118:LEU:HD22	1.94	0.49
1:A:306:PRO:CD	1:B:302:ARG:HH22	2.15	0.49
1:C:250:ASP:HA	1:C:291:VAL:HB	1.94	0.49
1:D:322:LEU:HA	1:D:325:LEU:HD11	1.94	0.49
1:A:168:LYS:HE3	1:A:230:GLU:CD	2.33	0.49
1:C:128:ARG:NH2	6:C:471:HOH:O	2.45	0.49
1:B:163:LEU:HD21	1:B:389:TRP:CE3	2.48	0.49
1:B:34:GLN:HE21	1:B:63:ASP:HB3	1.78	0.49
1:D:240:HIS:CE1	1:D:241:ARG:HB3	2.48	0.49
1:D:65:VAL:CG1	1:D:94:LEU:HD11	2.43	0.49
1:B:11:GLU:OE1	1:B:40:ARG:NH1	2.45	0.48
1:A:389:TRP:HE3	1:A:390:LEU:HD13	1.78	0.48
1:D:12:VAL:HG12	1:D:401:GLY:HA2	1.95	0.48
1:D:203:GLU:O	1:D:207:ILE:HG13	2.13	0.48
1:D:239:GLY:HA2	1:D:242:LEU:CD1	2.43	0.48
1:D:329:LEU:HA	1:D:369:ALA:CB	2.43	0.48
1:C:366:PRO:HG2	2:C:454:SO4:O2	2.14	0.48
1:D:197:TYR:O	1:D:201:VAL:HG23	2.14	0.48
1:D:402:GLU:O	1:D:406:LEU:HD13	2.14	0.48
1:D:221:PRO:HD2	1:D:337:VAL:O	2.13	0.48
1:C:84:ARG:HB3	1:C:267:TYR:OH	2.13	0.48
1:C:323:HIS:ND1	2:C:453:SO4:O2	2.47	0.48
1:D:384:ASP:N	1:D:384:ASP:OD2	2.46	0.48
1:D:62:LEU:HD13	1:D:93:VAL:HG12	1.95	0.48
1:C:113:GLU:OE2	1:C:117:HIS:HE1	1.96	0.48
1:C:325:LEU:HG	1:C:329:LEU:HD11	1.96	0.48
1:C:57:LEU:HD23	1:C:90:MET:CE	2.44	0.48
1:D:280:LYS:O	1:D:282:PRO:HD3	2.14	0.48
1:D:3:ILE:HG12	1:D:184:LEU:HD22	1.95	0.48
1:D:34:GLN:NE2	1:D:63:ASP:HB3	2.29	0.48
1:A:43:ALA:HB1	1:A:44:PRO:HD2	1.95	0.48
1:B:168:LYS:HG2	1:B:197:TYR:CE2	2.48	0.48
1:C:142:LEU:HG	1:C:143:PRO:HD2	1.96	0.48
1:B:11:GLU:OE2	1:B:37:GLU:HG3	2.13	0.47
1:D:165:ASN:C	1:D:165:ASN:HD22	2.16	0.47
1:D:227:ARG:HG2	1:D:227:ARG:HH11	1.79	0.47
1:B:168:LYS:HE2	1:B:230:GLU:OE1	2.14	0.47
1:C:247:ILE:HG12	1:C:308:VAL:HG21	1.96	0.47
1:D:211:THR:OG1	1:D:218:VAL:HG22	2.15	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:142:LEU:HD22	1:B:226:GLU:HB2	1.96	0.47
1:A:163:LEU:HD21	1:A:389:TRP:CE3	2.48	0.47
1:C:226:GLU:HG2	1:C:261:TYR:OH	2.13	0.47
1:B:165:ASN:C	1:B:165:ASN:ND2	2.66	0.47
1:B:221:PRO:HB3	1:B:321:ILE:HG12	1.96	0.47
1:D:329:LEU:HA	1:D:369:ALA:HB2	1.97	0.47
1:A:389:TRP:CE3	1:A:390:LEU:HD13	2.50	0.47
1:D:360:ILE:HD12	1:D:365:VAL:HG11	1.97	0.47
1:D:399:VAL:HG12	1:D:423:ALA:HB3	1.97	0.47
1:C:211:THR:HG21	1:C:335:ALA:CB	2.45	0.47
1:C:262:PRO:HG3	1:C:281:ASN:ND2	2.30	0.47
1:D:359:ARG:HD3	1:D:362:GLY:HA2	1.97	0.47
1:C:253:MET:O	1:C:257:VAL:HG23	2.15	0.46
1:D:202:ARG:O	1:D:206:GLU:HG3	2.15	0.46
1:D:231:ILE:O	1:D:235:LEU:HD13	2.14	0.46
1:B:420:VAL:HG22	1:B:421:SER:N	2.30	0.46
1:B:404:GLU:HA	1:B:404:GLU:OE2	2.16	0.46
1:D:347:LEU:HD12	1:D:347:LEU:H	1.81	0.46
1:D:65:VAL:HG11	1:D:94:LEU:HD11	1.97	0.46
1:B:68:LEU:N	1:B:69:PRO:HD2	2.30	0.46
1:D:336:LEU:C	1:D:336:LEU:HD23	2.35	0.46
1:A:401:GLY:HA3	1:A:406:LEU:HD13	1.97	0.46
1:A:45:PHE:HB3	1:A:47:PHE:CE1	2.51	0.46
1:A:85:ALA:HB3	1:A:144:GLY:HA3	1.97	0.46
1:D:204:PHE:O	1:D:208:LEU:HG	2.15	0.46
1:D:318:GLY:HA2	1:D:322:LEU:CD1	2.43	0.46
1:A:153:GLU:CG	2:A:433:SO4:O1	2.50	0.46
1:B:36:LYS:C	1:B:37:GLU:HG2	2.37	0.46
1:C:192:ARG:HA	1:C:383:GLN:NE2	2.31	0.46
1:C:214:GLN:HE21	1:C:333:ARG:HA	1.81	0.46
1:C:57:LEU:HD21	1:C:68:LEU:HD22	1.98	0.46
1:D:319:GLY:C	1:D:321:ILE:H	2.20	0.46
1:D:347:LEU:N	1:D:347:LEU:HD12	2.30	0.46
1:B:98:LEU:HD11	1:B:108:PRO:HA	1.97	0.46
1:D:28:LEU:O	1:D:29:ASP:HB2	2.14	0.46
1:C:85:ALA:HB2	1:C:267:TYR:CE2	2.51	0.45
1:C:420:VAL:HG22	1:C:421:SER:N	2.31	0.45
1:B:217:LYS:HG2	1:B:307:MET:HG2	1.97	0.45
1:B:411:LYS:HD2	3:B:455:FLC:OHB	2.15	0.45
1:B:348:GLY:O	1:B:352:ILE:HG13	2.16	0.45
1:C:177:PRO:HD3	1:C:389:TRP:CE2	2.51	0.45

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:GLU:HG3	6:A:502:HOH:O	2.17	0.45
1:D:234:VAL:O	1:D:238:HIS:HB2	2.17	0.45
1:D:217:LYS:HG2	1:D:307:MET:HG2	1.99	0.45
1:D:347:LEU:O	1:D:351:ILE:HG13	2.16	0.45
1:B:163:LEU:HD21	1:B:389:TRP:CD2	2.51	0.45
1:B:140:GLY:O	1:B:164:GLY:HA3	2.17	0.45
1:C:214:GLN:O	1:C:333:ARG:HD2	2.17	0.45
1:B:276:PHE:HA	1:B:280:LYS:O	2.17	0.45
1:A:31:GLY:HA3	1:A:63:ASP:O	2.16	0.45
1:B:178:PRO:HB3	1:C:126:TRP:CE3	2.52	0.45
1:C:140:GLY:O	1:C:164:GLY:HA3	2.17	0.45
1:C:399:VAL:HG12	1:C:423:ALA:HB3	1.98	0.45
1:A:192:ARG:NH2	2:A:463:SO4:O2	2.47	0.45
1:A:407:LEU:HD13	1:A:422:LEU:CD2	2.47	0.45
1:B:182:LEU:HD11	1:B:397:VAL:HG23	1.99	0.45
1:C:143:PRO:HD3	1:C:226:GLU:HG3	1.99	0.45
1:C:229:GLN:HG3	1:C:261:TYR:CZ	2.53	0.45
1:C:267:TYR:HA	6:C:500:HOH:O	2.16	0.45
1:D:326:LYS:HG2	1:D:326:LYS:O	2.17	0.45
1:D:397:VAL:HG21	1:D:429:VAL:HG11	1.98	0.45
1:D:90:MET:HE1	1:D:118:LEU:HD22	1.99	0.45
1:A:235:LEU:HD13	1:A:247:ILE:HD13	1.99	0.44
1:B:428:GLY:H	4:B:457:U5P:C5	2.30	0.44
1:D:386:LEU:O	1:D:390:LEU:HD22	2.17	0.44
1:A:262:PRO:O	1:A:265:VAL:HG23	2.18	0.44
1:A:318:GLY:HA2	1:A:322:LEU:CD1	2.47	0.44
1:A:341:TYR:HB3	4:A:465:U5P:H5'2	2.00	0.44
1:C:211:THR:HG21	1:C:335:ALA:HB3	1.98	0.44
1:B:318:GLY:HA2	1:B:322:LEU:CD1	2.48	0.44
1:C:331:ASP:HB3	1:C:334:ASN:HD22	1.83	0.44
1:B:37:GLU:O	1:B:39:ALA:N	2.50	0.44
1:C:312:GLY:HA2	1:C:313:SER:C	2.38	0.44
1:C:1:MET:HG2	1:C:431:VAL:CG2	2.47	0.44
1:C:302:ARG:HG2	1:C:302:ARG:HH21	1.83	0.44
1:B:32:MET:HE2	1:B:105:PHE:HZ	1.82	0.44
1:B:259:SER:O	1:B:262:PRO:HD2	2.17	0.44
1:C:294:THR:O	1:C:297:SER:HB3	2.17	0.44
1:B:91:GLU:O	1:B:95:GLU:HG2	2.18	0.44
1:C:251:SER:HB3	1:C:254:ALA:HB3	2.00	0.44
1:D:235:LEU:O	1:D:239:GLY:HA3	2.17	0.44
1:D:359:ARG:HD2	1:D:359:ARG:C	2.38	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:239:GLY:C	1:C:241:ARG:H	2.20	0.44
1:D:220:ILE:HG22	1:D:222:THR:HG23	2.00	0.44
1:D:359:ARG:HD3	1:D:362:GLY:CA	2.48	0.44
1:A:102:ASP:HB2	6:A:580:HOH:O	2.17	0.43
1:D:422:LEU:CD1	1:D:422:LEU:N	2.80	0.43
1:A:57:LEU:HD23	1:A:90:MET:HE2	1.98	0.43
1:A:85:ALA:HB2	1:A:267:TYR:CD2	2.53	0.43
1:B:344:GLN:H	1:B:344:GLN:NE2	2.17	0.43
1:D:233:TYR:CE1	1:D:282:PRO:HB2	2.53	0.43
1:D:3:ILE:HG23	1:D:3:ILE:O	2.18	0.43
1:A:266:ARG:HG2	6:A:501:HOH:O	2.17	0.43
1:A:344:GLN:HE21	1:A:344:GLN:HA	1.79	0.43
1:C:10:ARG:NH2	1:C:424:ARG:HH12	2.15	0.43
1:D:158:VAL:HG23	1:D:180:ALA:HB2	2.01	0.43
1:D:252:PRO:O	1:D:256:ARG:HG3	2.18	0.43
1:A:289:GLU:CG	6:A:502:HOH:O	2.67	0.43
1:A:84:ARG:HB2	1:A:84:ARG:HE	1.40	0.43
1:B:101:MET:HG2	1:B:104:PRO:CB	2.41	0.43
1:B:113:GLU:OE2	1:B:117:HIS:HE1	2.01	0.43
1:D:235:LEU:HD23	1:D:247:ILE:HG21	2.00	0.43
1:D:325:LEU:HD12	1:D:326:LYS:N	2.34	0.43
1:D:65:VAL:HG12	1:D:65:VAL:O	2.19	0.43
1:A:212:LEU:CB	1:A:243:PRO:HG2	2.49	0.43
1:A:58:THR:O	1:A:145:SER:HA	2.18	0.43
1:C:229:GLN:HA	1:C:232:LEU:HD12	2.01	0.43
1:D:250:ASP:HB3	1:D:311:ALA:HB2	1.99	0.43
1:B:270:GLU:OE1	1:C:266:ARG:NH2	2.51	0.43
1:D:356:PRO:HG2	1:D:357:ALA:H	1.84	0.43
1:D:389:TRP:HE3	1:D:390:LEU:HD13	1.84	0.43
1:A:61:HIS:CD2	1:A:142:LEU:HD11	2.53	0.43
1:B:396:VAL:O	1:B:420:VAL:HA	2.19	0.43
1:D:316:LEU:HD22	1:D:325:LEU:HD21	2.01	0.43
1:D:216:GLY:HA3	1:D:333:ARG:O	2.19	0.43
1:A:197:TYR:O	1:A:200:THR:HB	2.19	0.43
1:A:203:GLU:O	1:A:207:ILE:HG13	2.19	0.43
1:A:98:LEU:HD11	1:A:108:PRO:CA	2.49	0.43
1:C:386:LEU:O	1:C:390:LEU:HD23	2.18	0.43
1:B:81:TYR:HA	1:B:119:ARG:O	2.19	0.42
1:C:272:VAL:O	1:C:276:PHE:HD2	2.00	0.42
1:B:33:PHE:HB3	1:B:37:GLU:HB2	2.00	0.42
1:D:396:VAL:HG12	1:D:398:LEU:CD1	2.49	0.42

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:80:VAL:HB	1:A:118:LEU:HD23	2.01	0.42
1:B:344:GLN:H	1:B:344:GLN:CD	2.21	0.42
1:D:309:VAL:HG12	1:D:310:LEU:N	2.32	0.42
1:D:401:GLY:CA	1:D:406:LEU:HD11	2.45	0.42
1:D:5:PRO:HG2	1:D:423:ALA:HB1	2.00	0.42
1:A:409:LEU:HD22	1:A:413:LEU:HG	2.01	0.42
1:A:59:HIS:CE1	1:A:162:ASP:OD1	2.73	0.42
1:C:12:VAL:HG12	1:C:401:GLY:HA2	2.02	0.42
1:D:32:MET:HB2	1:D:41:ASN:OD1	2.20	0.42
1:A:77:ARG:HD2	2:A:459:SO4:O4	2.20	0.42
1:B:126:TRP:CE3	1:C:178:PRO:HB3	2.54	0.42
1:B:318:GLY:HA2	1:B:322:LEU:HD11	2.02	0.42
1:B:347:LEU:HD11	1:B:358:VAL:HG11	2.01	0.42
1:D:220:ILE:HG22	1:D:222:THR:CG2	2.49	0.42
1:A:46:GLY:HA2	3:A:464:FLC:HG2	2.00	0.42
1:D:238:HIS:C	1:D:240:HIS:H	2.23	0.42
1:A:212:LEU:HB2	1:A:243:PRO:HG2	2.01	0.42
1:A:365:VAL:HA	1:A:366:PRO:HD3	1.87	0.42
1:C:386:LEU:O	1:C:390:LEU:CD2	2.68	0.42
1:C:59:HIS:NE2	1:C:61:HIS:HB2	2.35	0.42
1:D:82:ALA:O	1:D:120:PRO:HA	2.20	0.42
1:A:321:ILE:HG23	1:A:322:LEU:N	2.34	0.42
1:A:191:ASP:CG	1:A:405:LYS:HD2	2.40	0.42
1:A:11:GLU:CD	1:A:40:ARG:HH12	2.23	0.42
1:C:326:LYS:HD2	1:C:361:LEU:HD22	2.02	0.42
1:A:140:GLY:O	1:A:164:GLY:HA3	2.19	0.41
1:B:4:VAL:HA	1:B:5:PRO:HD3	1.85	0.41
1:B:203:GLU:O	1:B:207:ILE:HG13	2.20	0.41
1:D:58:THR:O	1:D:145:SER:HA	2.19	0.41
1:D:302:ARG:HG2	1:D:303:ALA:H	1.81	0.41
1:D:297:SER:CB	1:D:320:ARG:HD2	2.50	0.41
1:A:407:LEU:HD13	1:A:422:LEU:HD21	2.02	0.41
1:C:10:ARG:CD	1:C:422:LEU:HD23	2.51	0.41
1:A:354:ARG:N	1:A:355:PRO:CD	2.83	0.41
1:C:203:GLU:O	1:C:207:ILE:HG13	2.21	0.41
1:A:57:LEU:HD23	1:A:90:MET:CE	2.51	0.41
1:D:170:VAL:HG12	1:D:171:LEU:CD1	2.51	0.41
1:C:350:GLU:O	1:C:353:ALA:HB3	2.21	0.41
1:C:31:GLY:HA3	1:C:63:ASP:C	2.41	0.41
1:D:347:LEU:CD1	1:D:347:LEU:H	2.34	0.41
1:A:318:GLY:HA2	1:A:322:LEU:HD11	2.02	0.41

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:GLU:O	1:A:95:GLU:HG2	2.21	0.41
1:B:10:ARG:HH11	1:B:10:ARG:HG2	1.86	0.41
1:B:55:VAL:HG12	1:B:57:LEU:HD13	2.02	0.41
1:C:98:LEU:HD12	1:C:111:VAL:HG21	2.03	0.41
1:C:49:PRO:HB3	1:C:71:LEU:HD12	2.02	0.41
1:D:295:GLU:H	1:D:295:GLU:CD	2.22	0.41
1:A:90:MET:HE1	1:A:118:LEU:CD2	2.50	0.41
1:B:365:VAL:HA	1:B:366:PRO:HD3	1.80	0.41
1:D:397:VAL:HA	1:D:421:SER:O	2.20	0.41
1:D:409:LEU:HD22	1:D:413:LEU:HD11	2.02	0.41
1:D:98:LEU:CD2	1:D:108:PRO:HA	2.51	0.41
1:C:247:ILE:HG23	1:C:308:VAL:HG23	2.04	0.41
1:C:277:LEU:C	1:C:279:GLY:H	2.24	0.41
1:C:318:GLY:HA2	1:C:322:LEU:HD11	2.01	0.41
1:C:326:LYS:HE3	1:C:363:GLU:OE1	2.21	0.41
1:D:33:PHE:HD2	1:D:41:ASN:ND2	2.19	0.41
1:C:209:GLU:O	1:C:210:LYS:C	2.59	0.40
1:C:32:MET:HE3	1:C:62:LEU:HD22	2.03	0.40
1:A:420:VAL:HG22	1:A:421:SER:N	2.36	0.40
1:C:227:ARG:HG2	1:C:227:ARG:HH21	1.86	0.40
1:C:91:GLU:O	1:C:95:GLU:HG2	2.21	0.40
1:D:409:LEU:O	1:D:413:LEU:HG	2.21	0.40
1:A:126:TRP:CE3	1:A:135:ALA:HB2	2.56	0.40
1:B:32:MET:CE	1:B:105:PHE:HZ	2.34	0.40
1:C:170:VAL:C	1:C:171:LEU:HD12	2.42	0.40
1:C:360:ILE:HD12	1:C:365:VAL:HG21	2.03	0.40
1:C:95:GLU:HA	1:C:95:GLU:OE2	2.21	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	429/431 (100%)	411 (96%)	17 (4%)	1 (0%)	47	56
1	B	429/431 (100%)	413 (96%)	15 (4%)	1 (0%)	47	56
1	C	429/431 (100%)	395 (92%)	32 (8%)	2 (0%)	29	32
1	D	429/431 (100%)	378 (88%)	44 (10%)	7 (2%)	9	8
All	All	1716/1724 (100%)	1597 (93%)	108 (6%)	11 (1%)	25	27

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	38	GLU
1	D	102	ASP
1	A	102	ASP
1	C	102	ASP
1	C	198	ARG
1	D	166	ARG
1	D	244	ARG
1	D	38	GLU
1	D	316	LEU
1	D	15	SER
1	D	225	VAL

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	342/342 (100%)	322 (94%)	20 (6%)	20	22
1	B	342/342 (100%)	321 (94%)	21 (6%)	18	20
1	C	342/342 (100%)	324 (95%)	18 (5%)	22	26
1	D	342/342 (100%)	326 (95%)	16 (5%)	26	31
All	All	1368/1368 (100%)	1293 (94%)	75 (6%)	21	24

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

Mol	Chain	Res	Type
1	A	27	LEU
1	A	38	GLU
1	A	57	LEU
1	A	84	ARG
1	A	163	LEU
1	A	165	ASN
1	A	171	LEU
1	A	186	GLU
1	A	192	ARG
1	A	219	LEU
1	A	241	ARG
1	A	264	LEU
1	A	329	LEU
1	A	336	LEU
1	A	344	GLN
1	A	386	LEU
1	A	390	LEU
1	A	406	LEU
1	A	407	LEU
1	A	409	LEU
1	B	10	ARG
1	B	27	LEU
1	B	38	GLU
1	B	94	LEU
1	B	98	LEU
1	B	101	MET
1	B	102	ASP
1	B	163	LEU
1	B	165	ASN
1	B	186	GLU
1	B	192	ARG
1	B	219	LEU
1	B	264	LEU
1	B	325	LEU
1	B	329	LEU
1	B	365	VAL
1	B	386	LEU
1	B	390	LEU
1	B	406	LEU
1	B	407	LEU
1	B	409	LEU
1	C	27	LEU
1	C	28	LEU

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	98	LEU
1	C	112	GLU
1	C	155	ARG
1	C	163	LEU
1	C	165	ASN
1	C	173	ASP
1	C	186	GLU
1	C	229	GLN
1	C	253	MET
1	C	336	LEU
1	C	344	GLN
1	C	386	LEU
1	C	398	LEU
1	C	407	LEU
1	C	409	LEU
1	C	415	LEU
1	D	27	LEU
1	D	57	LEU
1	D	96	ASP
1	D	155	ARG
1	D	165	ASN
1	D	186	GLU
1	D	192	ARG
1	D	195	ARG
1	D	229	GLN
1	D	253	MET
1	D	264	LEU
1	D	293	HIS
1	D	302	ARG
1	D	325	LEU
1	D	344	GLN
1	D	409	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	34	GLN
1	A	41	ASN
1	A	59	HIS
1	A	165	ASN
1	A	344	GLN
1	A	383	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	34	GLN
1	B	41	ASN
1	B	59	HIS
1	B	61	HIS
1	B	165	ASN
1	B	275	HIS
1	B	383	GLN
1	C	34	GLN
1	C	41	ASN
1	C	59	HIS
1	C	165	ASN
1	C	214	GLN
1	C	229	GLN
1	C	275	HIS
1	C	383	GLN
1	D	34	GLN
1	D	41	ASN
1	D	165	ASN
1	D	194	HIS
1	D	214	GLN
1	D	229	GLN
1	D	301	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 113 ligands modelled in this entry, 8 are monoatomic - leaving 105 for Mogul analysis.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and

the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	SO4	A	449	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	445	-	4,4,4	1.02	0	6,6,6	0.68	0
2	SO4	C	441	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	443	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	438	-	4,4,4	1.02	0	6,6,6	0.64	0
2	SO4	A	453	-	4,4,4	1.02	0	6,6,6	0.68	0
2	SO4	A	461	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	B	438	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	B	449	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	455	-	4,4,4	0.99	0	6,6,6	0.66	0
2	SO4	B	445	-	4,4,4	1.04	0	6,6,6	0.60	0
2	SO4	B	433	-	4,4,4	1.02	0	6,6,6	0.64	0
2	SO4	A	437	-	4,4,4	1.02	0	6,6,6	0.64	0
2	SO4	A	458	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	D	438	-	4,4,4	0.99	0	6,6,6	0.66	0
2	SO4	B	432	-	4,4,4	1.00	0	6,6,6	0.64	0
2	SO4	B	446	-	4,4,4	1.00	0	6,6,6	0.68	0
2	SO4	D	442	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	456	-	4,4,4	1.04	0	6,6,6	0.65	0
2	SO4	D	434	-	4,4,4	1.03	0	6,6,6	0.66	0
2	SO4	C	436	-	4,4,4	1.00	0	6,6,6	0.67	0
4	U5P	B	456	-	18,22,22	1.79	5 (27%)	21,33,33	0.92	0
2	SO4	D	444	-	4,4,4	1.00	0	6,6,6	0.67	0
2	SO4	A	440	-	4,4,4	1.05	0	6,6,6	0.68	0
2	SO4	C	446	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	434	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	A	433	-	4,4,4	1.00	0	6,6,6	0.65	0
2	SO4	B	435	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	435	-	4,4,4	1.03	0	6,6,6	0.65	0
2	SO4	A	445	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	455	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	453	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	A	439	-	4,4,4	0.99	0	6,6,6	0.68	0
2	SO4	A	450	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	451	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	B	434	-	4,4,4	1.04	0	6,6,6	0.64	0
2	SO4	D	439	-	4,4,4	1.00	0	6,6,6	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	A	448	-	4,4,4	1.03	0	6,6,6	0.66	0
2	SO4	A	444	-	4,4,4	0.97	0	6,6,6	0.67	0
2	SO4	B	441	-	4,4,4	1.01	0	6,6,6	0.67	0
2	SO4	B	448	-	4,4,4	1.03	0	6,6,6	0.64	0
2	SO4	D	445	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	A	442	-	4,4,4	1.01	0	6,6,6	0.65	0
3	FLC	A	464	-	3,12,12	0.95	0	3,17,17	0.65	0
2	SO4	C	456	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	A	446	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	452	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	D	437	-	4,4,4	1.00	0	6,6,6	0.64	0
2	SO4	B	440	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	C	434	-	4,4,4	1.00	0	6,6,6	0.67	0
3	FLC	B	455	-	3,12,12	1.27	0	3,17,17	0.48	0
2	SO4	A	463	-	4,4,4	0.99	0	6,6,6	0.66	0
2	SO4	C	448	-	4,4,4	1.01	0	6,6,6	0.64	0
2	SO4	A	432	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	B	454	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	A	452	-	4,4,4	1.03	0	6,6,6	0.65	0
2	SO4	A	436	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	A	459	-	4,4,4	0.99	0	6,6,6	0.66	0
4	U5P	A	465	-	18,22,22	1.79	5 (27%)	21,33,33	1.01	1 (4%)
2	SO4	D	436	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	D	440	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	440	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	462	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	C	454	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	D	441	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	C	450	-	4,4,4	1.03	0	6,6,6	0.65	0
2	SO4	D	435	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	451	-	4,4,4	1.01	0	6,6,6	0.65	0
4	U5P	B	457	-	18,22,22	1.87	6 (33%)	21,33,33	1.06	1 (4%)
2	SO4	B	447	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	A	441	-	4,4,4	1.01	0	6,6,6	0.67	0
2	SO4	A	460	-	4,4,4	1.04	0	6,6,6	0.65	0
2	SO4	B	437	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	C	437	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	A	454	-	4,4,4	0.98	0	6,6,6	0.65	0
2	SO4	C	449	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	C	438	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	A	457	-	4,4,4	0.99	0	6,6,6	0.66	0
2	SO4	C	447	-	4,4,4	1.01	0	6,6,6	0.66	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	SO4	B	452	-	4,4,4	0.99	0	6,6,6	0.69	0
2	SO4	C	443	-	4,4,4	1.03	0	6,6,6	0.64	0
2	SO4	C	444	-	4,4,4	1.02	0	6,6,6	0.66	0
2	SO4	A	451	-	4,4,4	0.98	0	6,6,6	0.66	0
2	SO4	D	446	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	C	442	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	C	432	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	D	443	-	4,4,4	0.99	0	6,6,6	0.65	0
2	SO4	A	447	-	4,4,4	1.02	0	6,6,6	0.65	0
4	U5P	A	466	-	18,22,22	1.98	6 (33%)	21,33,33	1.14	1 (4%)
2	SO4	D	447	-	4,4,4	1.01	0	6,6,6	0.66	0
2	SO4	B	439	-	4,4,4	1.03	0	6,6,6	0.64	0
2	SO4	C	433	-	4,4,4	1.02	0	6,6,6	0.66	0
4	U5P	C	457	-	18,22,22	1.87	6 (33%)	21,33,33	0.94	1 (4%)
2	SO4	D	432	-	4,4,4	1.00	0	6,6,6	0.66	0
2	SO4	B	436	-	4,4,4	0.95	0	6,6,6	0.69	0
2	SO4	C	435	-	4,4,4	1.00	0	6,6,6	0.64	0
2	SO4	C	439	-	4,4,4	1.01	0	6,6,6	0.65	0
2	SO4	B	450	-	4,4,4	1.02	0	6,6,6	0.65	0
2	SO4	B	444	-	4,4,4	1.01	0	6,6,6	0.64	0
2	SO4	D	433	-	4,4,4	1.00	0	6,6,6	0.65	0
2	SO4	A	443	-	4,4,4	1.02	0	6,6,6	0.66	0
4	U5P	D	448	-	18,22,22	1.91	6 (33%)	21,33,33	0.91	0
2	SO4	B	442	-	4,4,4	1.01	0	6,6,6	0.65	0
4	U5P	A	467	-	18,22,22	1.89	6 (33%)	21,33,33	0.96	1 (4%)
2	SO4	C	453	-	4,4,4	1.01	0	6,6,6	0.66	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
4	U5P	A	465	-	-	6/8/26/26	0/2/2/2
3	FLC	B	455	-	-	0/6/16/16	-
4	U5P	B	457	-	-	4/8/26/26	0/2/2/2
4	U5P	B	456	-	-	3/8/26/26	0/2/2/2
4	U5P	A	467	-	-	3/8/26/26	0/2/2/2
4	U5P	C	457	-	-	2/8/26/26	0/2/2/2
3	FLC	A	464	-	-	0/6/16/16	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	U5P	A	466	-	-	4/8/26/26	0/2/2/2
4	U5P	D	448	-	-	2/8/26/26	0/2/2/2

All (40) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	466	U5P	C6-N1	4.26	1.41	1.35
4	A	466	U5P	C4-N3	4.08	1.40	1.33
4	D	448	U5P	C6-N1	4.01	1.40	1.35
4	A	467	U5P	C6-N1	3.99	1.40	1.35
4	B	456	U5P	C4-N3	3.87	1.39	1.33
4	C	457	U5P	C6-N1	3.83	1.40	1.35
4	A	465	U5P	C4-N3	3.75	1.39	1.33
4	A	467	U5P	C4-N3	3.74	1.39	1.33
4	D	448	U5P	C4-N3	3.72	1.39	1.33
4	C	457	U5P	C4-N3	3.64	1.39	1.33
4	B	456	U5P	C6-N1	3.61	1.40	1.35
4	B	457	U5P	C6-N1	3.56	1.40	1.35
4	B	457	U5P	O4'-C1'	3.49	1.45	1.41
4	B	457	U5P	C4-N3	3.27	1.38	1.33
4	A	465	U5P	C6-N1	3.12	1.39	1.35
4	C	457	U5P	P-O5'	-3.08	1.50	1.60
4	A	466	U5P	O4'-C1'	3.05	1.45	1.41
4	D	448	U5P	O4'-C1'	3.01	1.45	1.41
4	A	465	U5P	O4'-C1'	2.99	1.45	1.41
4	A	465	U5P	P-O5'	-2.97	1.50	1.60
4	D	448	U5P	P-O5'	-2.95	1.50	1.60
4	B	456	U5P	P-O5'	-2.88	1.50	1.60
4	A	466	U5P	C6-C5	2.88	1.44	1.38
4	A	467	U5P	O4'-C1'	2.84	1.45	1.41
4	A	467	U5P	P-O5'	-2.80	1.51	1.60
4	B	457	U5P	C6-C5	2.80	1.44	1.38
4	A	467	U5P	C6-C5	2.77	1.44	1.38
4	C	457	U5P	C6-C5	2.76	1.44	1.38
4	D	448	U5P	C6-C5	2.69	1.44	1.38
4	B	457	U5P	P-O5'	-2.64	1.51	1.60
4	B	456	U5P	C6-C5	2.54	1.43	1.38
4	A	466	U5P	P-O5'	-2.52	1.52	1.60
4	C	457	U5P	O4'-C1'	2.47	1.44	1.41
4	A	465	U5P	C6-C5	2.46	1.43	1.38
4	B	456	U5P	O4'-C1'	2.37	1.44	1.41
4	A	466	U5P	P-O2P	2.34	1.63	1.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	457	U5P	P-O2P	2.27	1.63	1.54
4	B	457	U5P	P-O2P	2.24	1.63	1.54
4	D	448	U5P	P-O2P	2.15	1.63	1.54
4	A	467	U5P	P-O2P	2.11	1.63	1.54

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	466	U5P	C3'-C2'-C1'	2.71	105.06	100.98
4	A	465	U5P	C3'-C2'-C1'	2.55	104.82	100.98
4	C	457	U5P	C3'-C2'-C1'	2.26	104.37	100.98
4	A	467	U5P	C3'-C2'-C1'	2.06	104.08	100.98
4	B	457	U5P	C3'-C2'-C1'	2.05	104.07	100.98

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	456	U5P	O4'-C1'-N1-C6
4	A	465	U5P	O4'-C1'-N1-C6
4	A	465	U5P	C5'-O5'-P-O2P
4	A	465	U5P	C5'-O5'-P-O3P
4	B	457	U5P	C3'-C4'-C5'-O5'
4	B	457	U5P	C5'-O5'-P-O2P
4	B	457	U5P	C5'-O5'-P-O3P
4	A	466	U5P	C5'-O5'-P-O2P
4	A	466	U5P	C5'-O5'-P-O3P
4	C	457	U5P	C2'-C1'-N1-C6
4	C	457	U5P	O4'-C1'-N1-C6
4	D	448	U5P	C2'-C1'-N1-C6
4	D	448	U5P	O4'-C1'-N1-C6
4	B	457	U5P	O4'-C4'-C5'-O5'
4	A	465	U5P	O4'-C4'-C5'-O5'
4	A	465	U5P	C5'-O5'-P-O1P
4	A	465	U5P	C3'-C4'-C5'-O5'
4	A	467	U5P	C5'-O5'-P-O2P
4	A	466	U5P	C3'-C4'-C5'-O5'
4	A	466	U5P	O4'-C4'-C5'-O5'
4	B	456	U5P	C5'-O5'-P-O1P
4	A	467	U5P	C5'-O5'-P-O1P
4	B	456	U5P	C5'-O5'-P-O2P
4	A	467	U5P	C4'-C5'-O5'-P

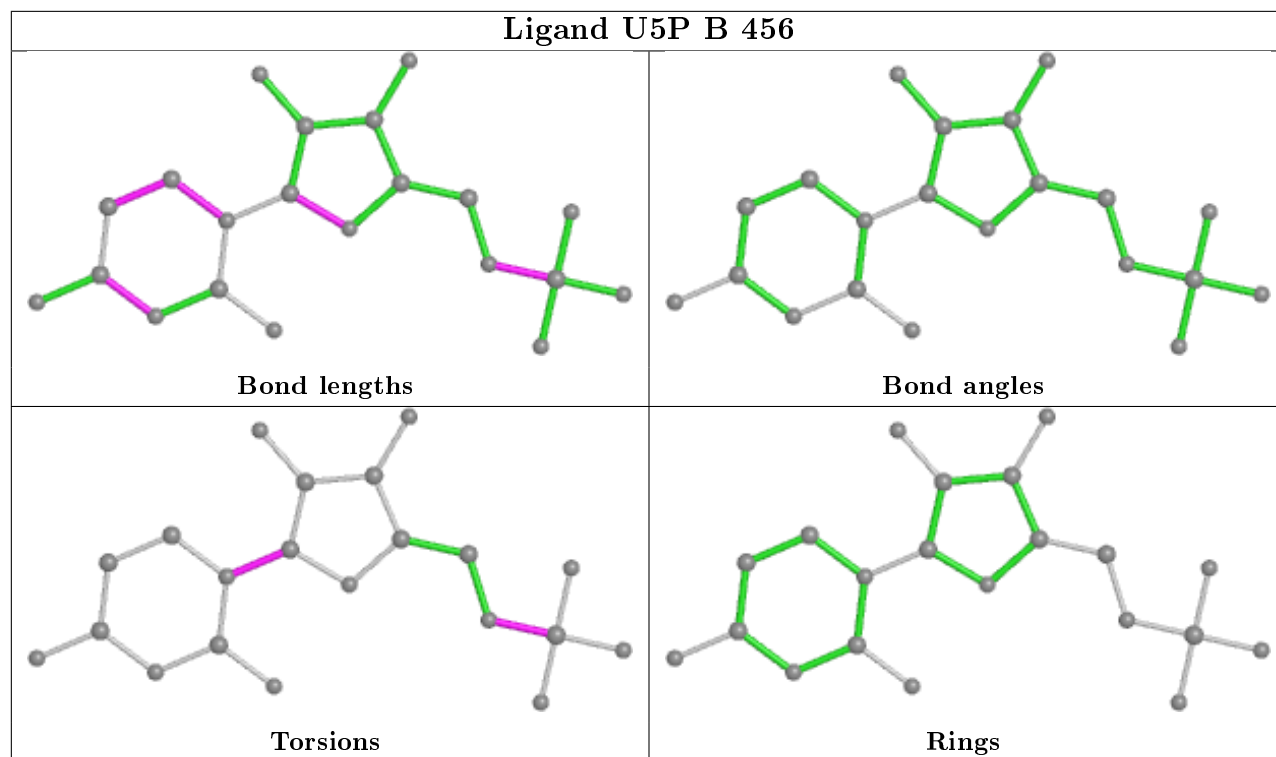
There are no ring outliers.

16 monomers are involved in 22 short contacts:

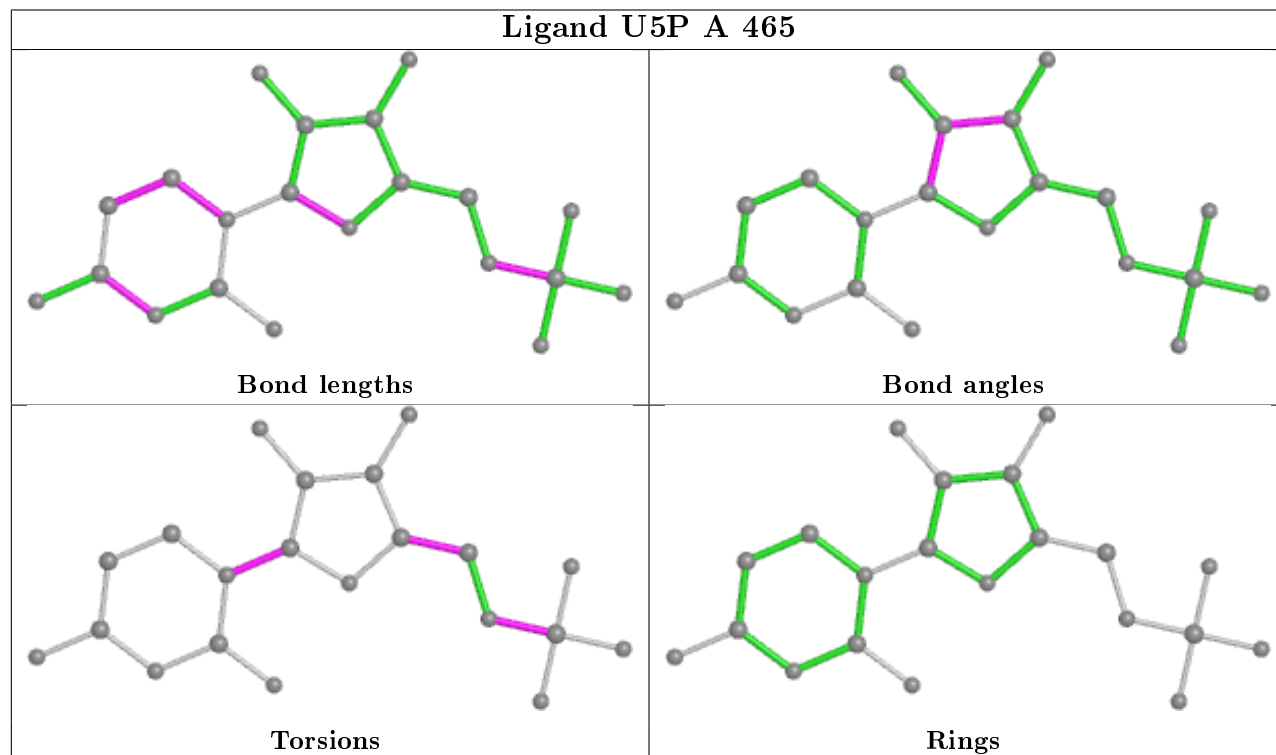
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	456	U5P	1	0
2	A	433	SO4	3	0
2	A	444	SO4	1	0
3	A	464	FLC	1	0
3	B	455	FLC	2	0
2	A	463	SO4	1	0
2	A	459	SO4	1	0
4	A	465	U5P	2	0
2	C	454	SO4	1	0
2	C	451	SO4	1	0
4	B	457	U5P	1	0
2	A	451	SO4	1	0
2	D	443	SO4	1	0
2	C	433	SO4	1	0
2	A	443	SO4	2	0
2	C	453	SO4	2	0

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.

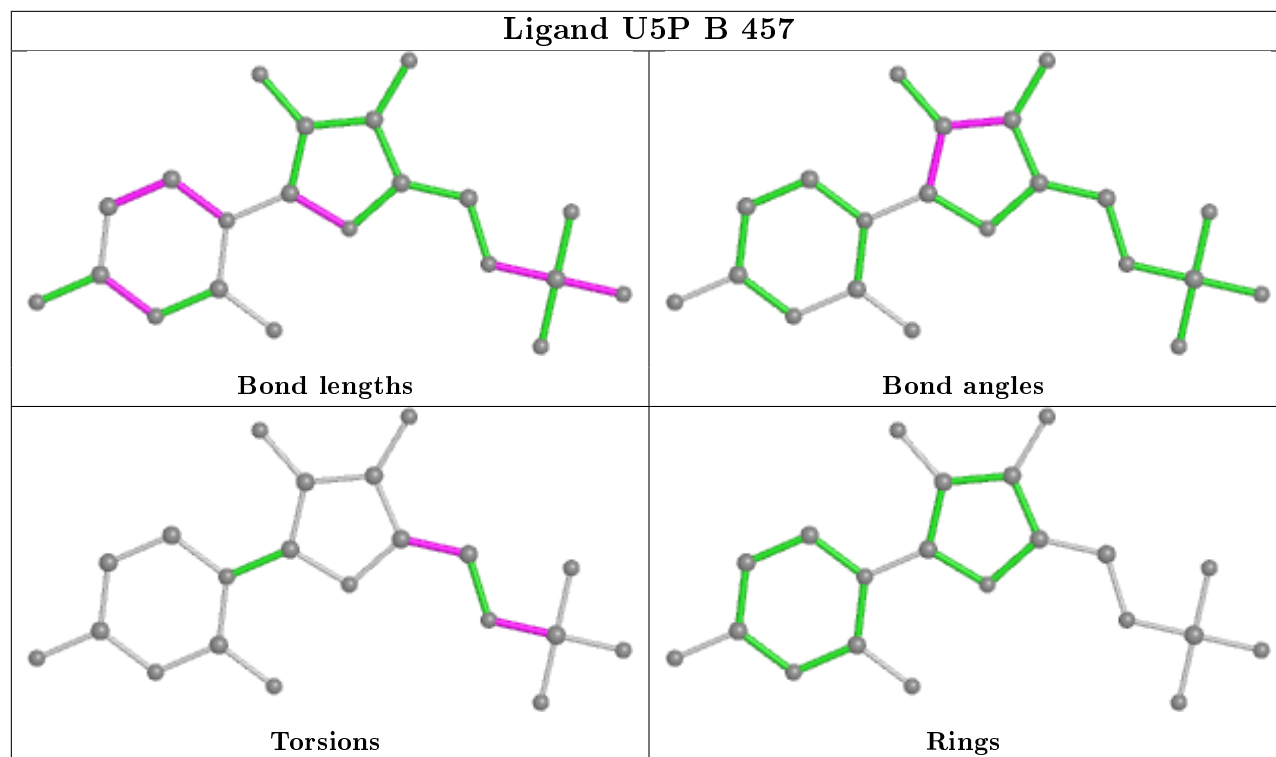
Ligand U5P B 456



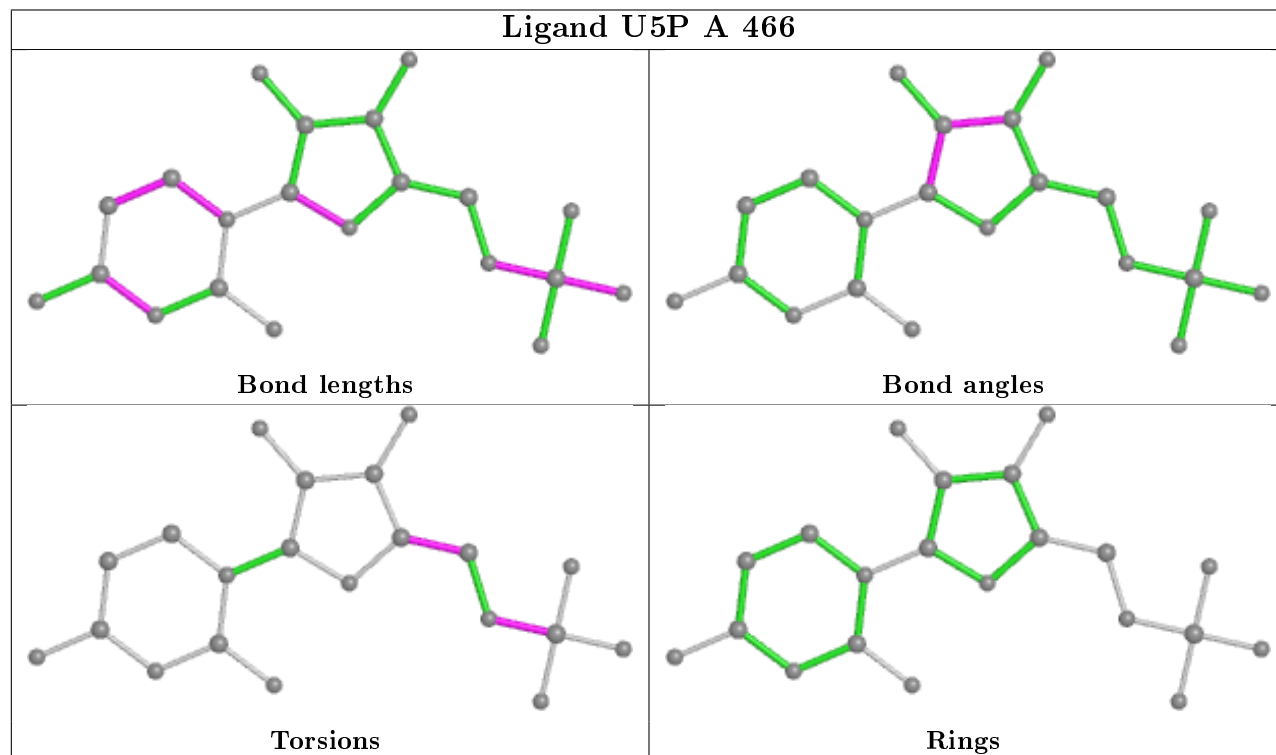
Ligand U5P A 465



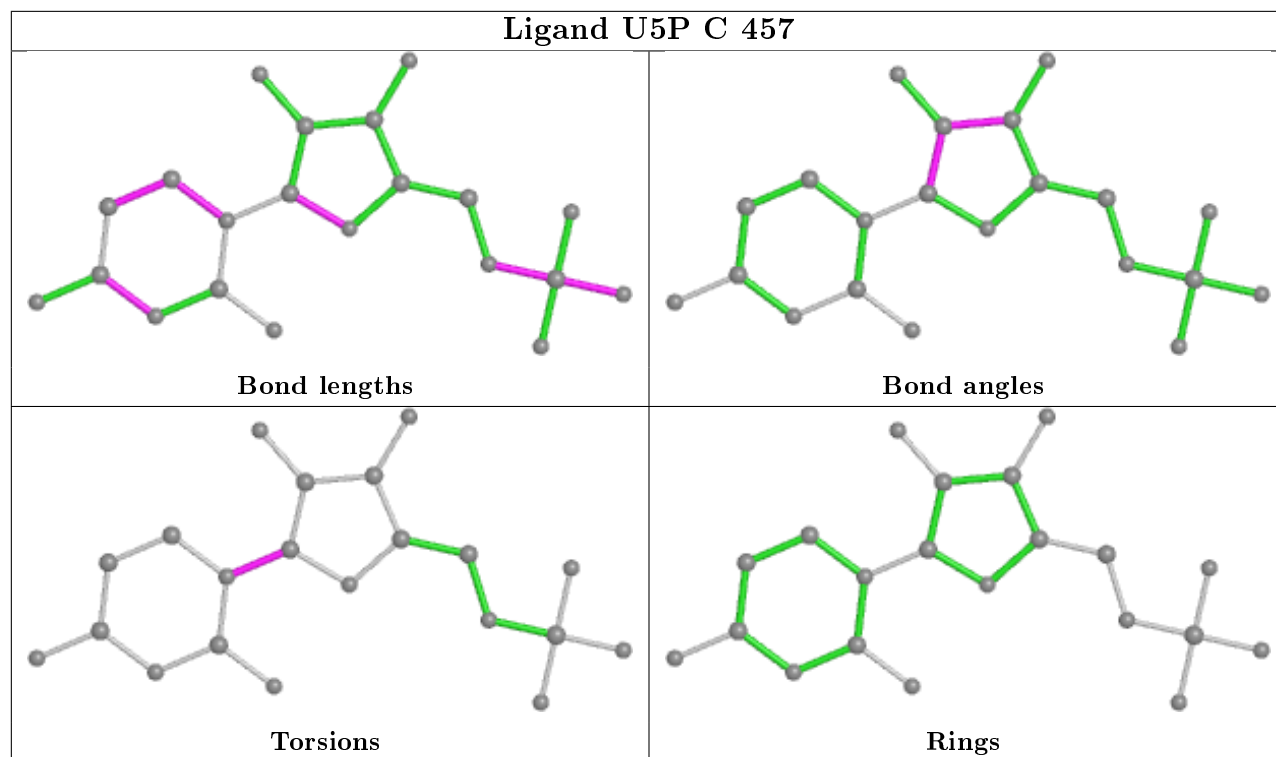
Ligand U5P B 457



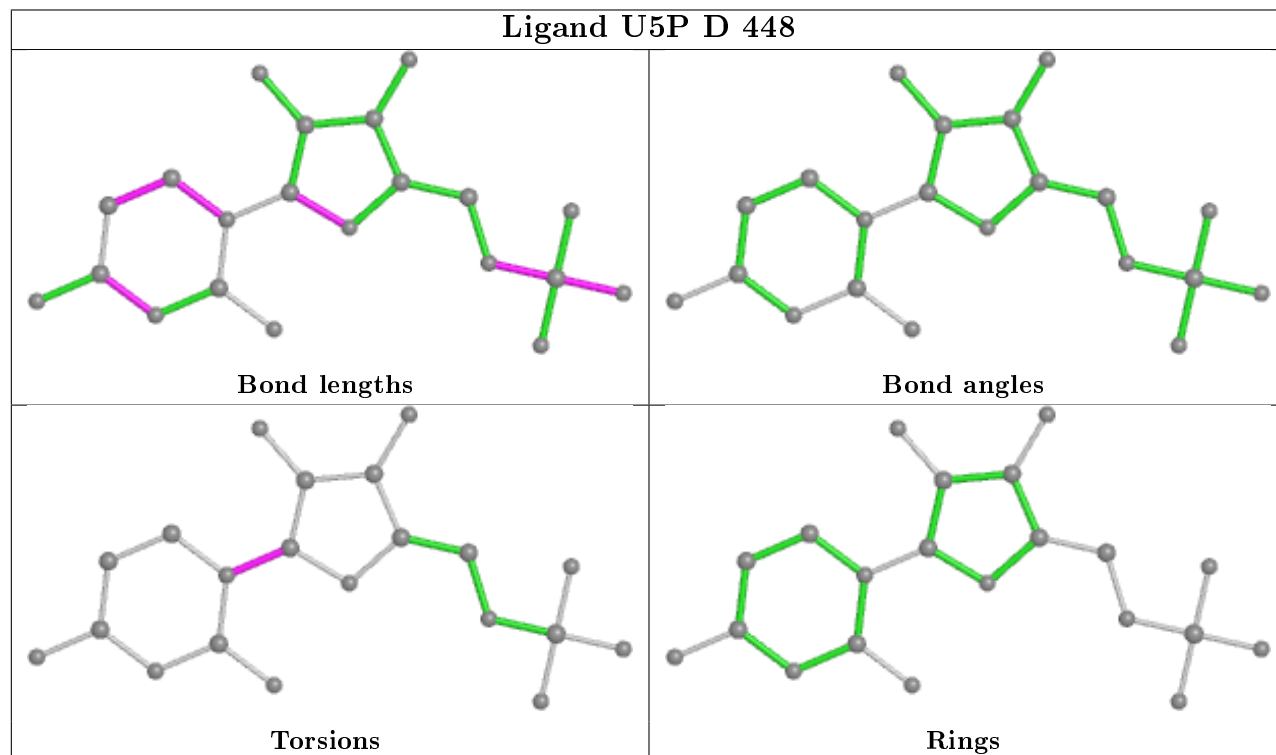
Ligand U5P A 466

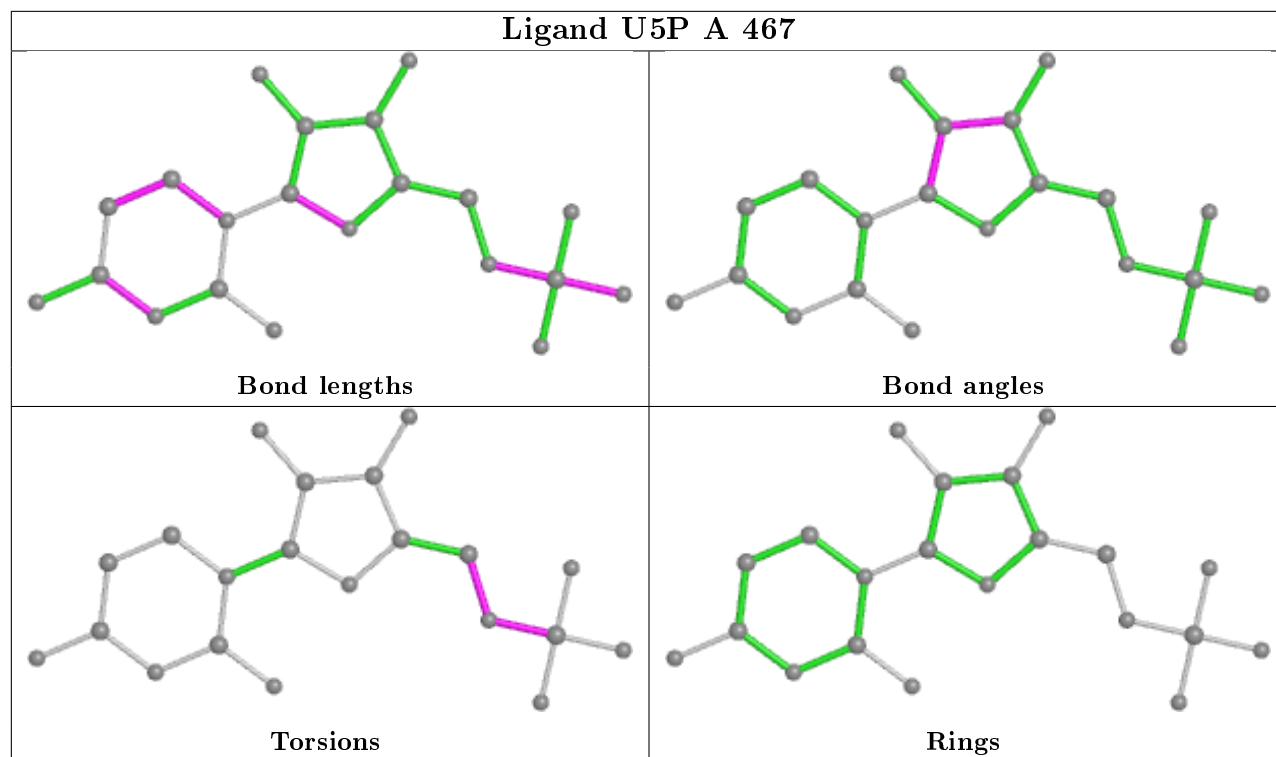


Ligand U5P C 457



Ligand U5P D 448





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	431/431 (100%)	0.30	11 (2%) 56 65	26, 39, 62, 83	0
1	B	431/431 (100%)	0.23	7 (1%) 72 80	23, 40, 64, 83	0
1	C	431/431 (100%)	1.30	110 (25%) 0 1	26, 61, 109, 121	0
1	D	431/431 (100%)	1.55	128 (29%) 0 0	36, 69, 124, 144	0
All	All	1724/1724 (100%)	0.85	256 (14%) 2 3	23, 48, 111, 144	0

All (256) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	212	LEU	9.0
1	D	363	GLU	8.4
1	D	306	PRO	7.8
1	D	325	LEU	7.7
1	D	208	LEU	7.1
1	D	334	ASN	6.9
1	D	244	ARG	6.9
1	C	333	ARG	6.8
1	D	332	PRO	6.7
1	C	301	ASN	6.7
1	C	329	LEU	6.6
1	D	286	ALA	6.4
1	D	205	LEU	6.2
1	D	240	HIS	6.1
1	D	242	LEU	6.1
1	D	241	ARG	6.1
1	C	242	LEU	6.0
1	D	213	SER	6.0
1	D	214	GLN	5.8
1	D	335	ALA	5.7
1	D	365	VAL	5.6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	329	LEU	5.6
1	C	241	ARG	5.6
1	D	285	PRO	5.6
1	D	299	ALA	5.6
1	C	210	LYS	5.4
1	D	250	ASP	5.4
1	D	333	ARG	5.3
1	C	307	MET	5.3
1	C	216	GLY	5.3
1	D	367	LEU	5.3
1	D	300	LEU	5.2
1	C	367	LEU	5.2
1	D	249	LEU	5.2
1	C	297	SER	5.2
1	C	326	LYS	5.1
1	C	415	LEU	5.1
1	D	358	VAL	5.1
1	D	239	GLY	5.0
1	C	240	HIS	5.0
1	D	201	VAL	5.0
1	C	286	ALA	4.9
1	C	244	ARG	4.8
1	C	214	GLN	4.8
1	C	300	LEU	4.8
1	D	351	ILE	4.8
1	D	327	HIS	4.6
1	D	360	ILE	4.6
1	C	354	ARG	4.6
1	D	308	VAL	4.6
1	C	213	SER	4.6
1	D	102	ASP	4.6
1	D	210	LYS	4.6
1	D	100	VAL	4.5
1	C	292	GLU	4.5
1	C	212	LEU	4.5
1	C	334	ASN	4.4
1	D	324	HIS	4.4
1	C	215	GLY	4.3
1	D	209	GLU	4.3
1	D	368	ARG	4.3
1	C	199	GLU	4.3
1	D	218	VAL	4.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	D	415	LEU	4.2
1	D	297	SER	4.2
1	C	335	ALA	4.2
1	D	377	PHE	4.2
1	D	302	ARG	4.2
1	C	280	LYS	4.2
1	D	293	HIS	4.1
1	C	248	TYR	4.1
1	D	291	VAL	4.1
1	C	296	ALA	4.1
1	D	339	VAL	4.1
1	C	332	PRO	4.1
1	D	246	PRO	4.1
1	D	207	ILE	4.0
1	D	301	ASN	4.0
1	D	245	ALA	4.0
1	D	243	PRO	4.0
1	D	338	PHE	4.0
1	C	323	HIS	3.9
1	C	295	GLU	3.9
1	D	307	MET	3.9
1	C	196	PRO	3.9
1	D	354	ARG	3.9
1	A	362	GLY	3.9
1	C	356	PRO	3.9
1	D	369	ALA	3.8
1	C	245	ALA	3.8
1	D	292	GLU	3.8
1	D	108	PRO	3.7
1	D	280	LYS	3.6
1	C	358	VAL	3.6
1	D	216	GLY	3.6
1	D	359	ARG	3.5
1	D	219	LEU	3.5
1	D	314	GLY	3.5
1	C	219	LEU	3.5
1	D	361	LEU	3.5
1	C	293	HIS	3.5
1	D	330	SER	3.5
1	D	248	TYR	3.4
1	C	288	LEU	3.4
1	C	359	ARG	3.4

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	303	ALA	3.4
1	D	234	VAL	3.4
1	D	252	PRO	3.4
1	A	149	VAL	3.4
1	D	253	MET	3.4
1	D	290	VAL	3.3
1	C	357	ALA	3.3
1	D	199	GLU	3.3
1	C	148	VAL	3.3
1	D	238	HIS	3.3
1	C	238	HIS	3.3
1	C	209	GLU	3.3
1	C	208	LEU	3.2
1	C	202	ARG	3.2
1	C	246	PRO	3.2
1	C	361	LEU	3.2
1	D	310	LEU	3.2
1	A	365	VAL	3.2
1	D	296	ALA	3.2
1	C	362	GLY	3.2
1	C	412	LEU	3.2
1	D	336	LEU	3.2
1	C	320	ARG	3.2
1	D	101	MET	3.2
1	D	149	VAL	3.2
1	C	289	GLU	3.2
1	C	243	PRO	3.2
1	C	306	PRO	3.2
1	C	294	THR	3.1
1	C	365	VAL	3.1
1	C	363	GLU	3.1
1	D	104	PRO	3.1
1	D	316	LEU	3.1
1	C	211	THR	3.1
1	C	353	ALA	3.1
1	C	58	THR	3.0
1	C	366	PRO	3.0
1	C	360	ILE	3.0
1	D	217	LYS	3.0
1	C	207	ILE	3.0
1	C	287	GLY	3.0
1	C	276	PHE	3.0

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	325	LEU	3.0
1	B	241	ARG	3.0
1	B	36	LYS	3.0
1	C	239	GLY	3.0
1	D	340	GLY	3.0
1	D	362	GLY	2.9
1	D	366	PRO	2.9
1	C	305	GLY	2.9
1	C	355	PRO	2.9
1	C	198	ARG	2.9
1	C	247	ILE	2.8
1	C	373	THR	2.8
1	C	364	GLU	2.8
1	C	302	ARG	2.8
1	D	211	THR	2.8
1	D	288	LEU	2.8
1	B	240	HIS	2.8
1	D	370	SER	2.8
1	C	350	GLU	2.8
1	B	22	GLY	2.7
1	C	235	LEU	2.7
1	D	295	GLU	2.7
1	D	112	GLU	2.7
1	C	319	GLY	2.7
1	C	299	ALA	2.7
1	D	223	PHE	2.7
1	C	147	PHE	2.7
1	A	354	ARG	2.7
1	C	368	ARG	2.7
1	D	158	VAL	2.7
1	C	236	TYR	2.6
1	A	302	ARG	2.6
1	D	94	LEU	2.6
1	C	370	SER	2.6
1	D	185	ALA	2.6
1	C	304	PRO	2.6
1	C	327	HIS	2.6
1	D	372	HIS	2.6
1	D	236	TYR	2.6
1	A	158	VAL	2.5
1	D	204	PHE	2.5
1	C	250	ASP	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	283	PHE	2.5
1	C	324	HIS	2.5
1	D	352	ILE	2.5
1	A	23	GLY	2.5
1	C	160	SER	2.5
1	D	320	ARG	2.5
1	A	135	ALA	2.5
1	B	43	ALA	2.5
1	D	303	ALA	2.5
1	D	389	TRP	2.4
1	D	319	GLY	2.4
1	D	202	ARG	2.4
1	A	358	VAL	2.4
1	C	274	ALA	2.4
1	C	290	VAL	2.4
1	C	414	ALA	2.4
1	C	205	LEU	2.4
1	D	233	TYR	2.4
1	D	195	ARG	2.4
1	D	305	GLY	2.4
1	C	322	LEU	2.4
1	D	76	TYR	2.3
1	C	371	VAL	2.3
1	D	99	LYS	2.3
1	D	237	THR	2.3
1	C	298	LYS	2.3
1	D	284	ARG	2.3
1	B	280	LYS	2.3
1	C	217	LYS	2.3
1	C	135	ALA	2.3
1	D	51	GLU	2.2
1	C	369	ALA	2.2
1	D	135	ALA	2.2
1	D	356	PRO	2.2
1	C	279	GLY	2.2
1	D	109	GLU	2.2
1	D	222	THR	2.2
1	C	266	ARG	2.2
1	D	347	LEU	2.2
1	A	129	LEU	2.2
1	D	163	LEU	2.2
1	D	251	SER	2.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	159	TYR	2.1
1	C	225	VAL	2.1
1	D	247	ILE	2.1
1	C	57	LEU	2.1
1	B	197	TYR	2.1
1	C	158	VAL	2.1
1	A	357	ALA	2.1
1	D	110	ASP	2.1
1	D	49	PRO	2.1
1	C	146	ALA	2.1
1	D	147	PHE	2.1
1	D	198	ARG	2.1
1	D	225	VAL	2.1
1	D	309	VAL	2.1
1	D	197	TYR	2.1
1	C	163	LEU	2.1
1	C	233	TYR	2.1
1	D	105	PHE	2.1
1	D	283	PHE	2.1
1	C	112	GLU	2.0
1	C	56	LEU	2.0
1	D	312	GLY	2.0
1	D	276	PHE	2.0
1	C	175	SER	2.0
1	D	36	LYS	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	C	447	5/5	0.41	0.42	186,186,186,186	0
3	FLC	A	464	13/13	0.42	0.53	125,127,128,128	0
2	SO4	D	443	5/5	0.43	0.43	185,185,185,185	0
2	SO4	A	436	5/5	0.51	0.27	159,159,159,159	0
3	FLC	B	455	13/13	0.52	0.47	84,97,99,100	0
2	SO4	D	446	5/5	0.59	0.29	165,165,166,166	0
2	SO4	A	446	5/5	0.60	0.42	167,167,167,167	0
2	SO4	C	452	5/5	0.62	0.34	149,149,149,149	0
2	SO4	B	440	5/5	0.62	0.42	140,140,140,141	0
4	U5P	B	457	21/21	0.62	0.38	106,108,110,111	0
2	SO4	D	442	5/5	0.65	0.67	167,167,167,167	0
2	SO4	C	453	5/5	0.67	0.36	152,152,152,152	0
2	SO4	D	441	5/5	0.68	0.30	173,173,173,174	0
4	U5P	A	467	21/21	0.69	0.40	140,144,145,146	0
2	SO4	B	438	5/5	0.70	0.25	133,133,133,133	0
2	SO4	C	433	5/5	0.71	0.39	138,138,138,138	0
2	SO4	A	443	5/5	0.71	0.29	141,141,142,142	0
2	SO4	D	440	5/5	0.71	0.20	139,139,139,139	0
2	SO4	C	450	5/5	0.71	0.35	142,142,143,143	0
2	SO4	A	442	5/5	0.72	0.68	159,159,159,159	0
2	SO4	A	434	5/5	0.72	0.22	140,140,140,140	0
2	SO4	A	444	5/5	0.73	0.49	138,138,138,138	0
2	SO4	C	454	5/5	0.73	0.22	143,144,144,144	0
2	SO4	C	456	5/5	0.74	0.15	136,137,137,137	0
2	SO4	C	440	5/5	0.75	0.35	174,174,174,174	0
2	SO4	A	447	5/5	0.75	0.24	145,145,145,146	0
2	SO4	A	450	5/5	0.76	0.35	166,166,166,166	0
2	SO4	A	451	5/5	0.76	0.43	130,130,130,130	0
2	SO4	D	433	5/5	0.76	0.40	141,141,142,142	0
2	SO4	C	442	5/5	0.77	0.27	150,151,151,151	0
2	SO4	B	451	5/5	0.77	0.20	143,143,143,143	0
2	SO4	A	435	5/5	0.78	0.21	126,126,127,127	0
2	SO4	B	454	5/5	0.78	0.24	147,147,148,148	0
2	SO4	A	461	5/5	0.79	0.26	125,125,126,126	0
2	SO4	A	438	5/5	0.79	0.38	143,144,144,144	0
2	SO4	A	433	5/5	0.79	0.66	157,158,158,158	0
2	SO4	D	437	5/5	0.79	0.41	141,141,142,142	0
2	SO4	D	447	5/5	0.79	0.25	161,161,161,161	0
2	SO4	B	435	5/5	0.80	0.23	132,132,133,133	0
2	SO4	C	448	5/5	0.81	0.29	141,141,141,141	0
2	SO4	D	445	5/5	0.81	0.19	131,131,132,132	0
2	SO4	A	463	5/5	0.81	0.30	142,142,143,143	0
2	SO4	C	438	5/5	0.81	0.26	123,123,124,124	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	A	458	5/5	0.83	0.30	124,124,125,125	0
2	SO4	A	459	5/5	0.83	0.39	118,119,119,119	0
2	SO4	C	441	5/5	0.83	0.18	130,130,130,130	0
2	SO4	A	439	5/5	0.83	0.26	131,131,131,131	0
5	ZN	C	458	1/1	0.83	0.09	96,96,96,96	0
4	U5P	A	466	21/21	0.83	0.23	60,71,74,76	0
2	SO4	A	448	5/5	0.84	0.24	125,125,125,125	0
2	SO4	A	452	5/5	0.84	0.28	120,120,120,120	0
2	SO4	D	434	5/5	0.85	0.23	123,123,123,123	0
2	SO4	C	443	5/5	0.85	0.17	117,117,118,118	0
2	SO4	C	444	5/5	0.85	0.15	124,124,124,124	0
2	SO4	B	449	5/5	0.85	0.26	141,141,141,141	0
2	SO4	C	455	5/5	0.85	0.28	138,138,139,139	0
2	SO4	C	437	5/5	0.86	0.38	142,142,142,142	0
2	SO4	C	449	5/5	0.86	0.30	148,148,148,148	0
2	SO4	D	439	5/5	0.86	0.43	131,131,132,132	0
2	SO4	B	441	5/5	0.87	0.15	107,107,108,109	0
2	SO4	D	432	5/5	0.87	0.14	132,132,132,132	0
2	SO4	B	436	5/5	0.87	0.38	94,95,95,97	0
2	SO4	A	460	5/5	0.87	0.19	101,101,101,102	0
2	SO4	B	437	5/5	0.87	0.20	119,119,119,119	0
2	SO4	B	446	5/5	0.87	0.26	135,135,135,136	0
2	SO4	B	439	5/5	0.87	0.22	135,135,135,135	0
2	SO4	B	452	5/5	0.88	0.22	103,103,103,104	0
2	SO4	C	446	5/5	0.88	0.32	155,155,155,156	0
5	ZN	D	449	1/1	0.88	0.07	106,106,106,106	0
2	SO4	A	456	5/5	0.88	0.12	90,90,91,91	0
2	SO4	B	442	5/5	0.88	0.12	106,106,107,107	0
2	SO4	D	438	5/5	0.88	0.12	159,159,159,159	0
2	SO4	A	432	5/5	0.88	0.11	123,123,124,124	0
2	SO4	A	455	5/5	0.89	0.24	114,114,114,114	0
2	SO4	A	449	5/5	0.89	0.25	156,156,156,156	0
2	SO4	A	445	5/5	0.89	0.17	125,125,125,126	0
2	SO4	B	448	5/5	0.89	0.11	105,105,106,106	0
2	SO4	A	457	5/5	0.89	0.17	129,129,129,130	0
2	SO4	B	447	5/5	0.90	0.17	142,142,142,142	0
2	SO4	C	445	5/5	0.90	0.20	99,99,100,100	0
4	U5P	D	448	21/21	0.90	0.21	88,94,95,96	0
2	SO4	C	436	5/5	0.90	0.21	129,130,130,130	0
5	ZN	D	450	1/1	0.90	0.05	102,102,102,102	0
2	SO4	B	444	5/5	0.90	0.17	109,110,110,110	0
2	SO4	B	450	5/5	0.91	0.16	122,122,123,123	0

Continued on next page...

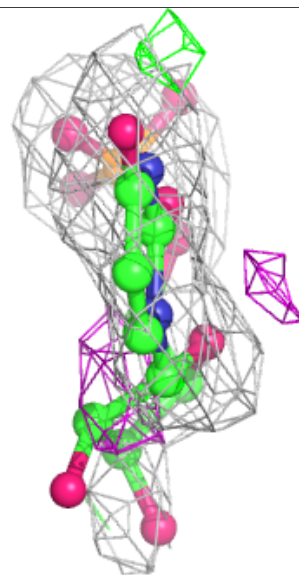
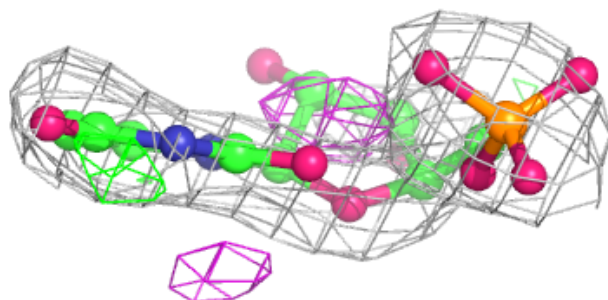
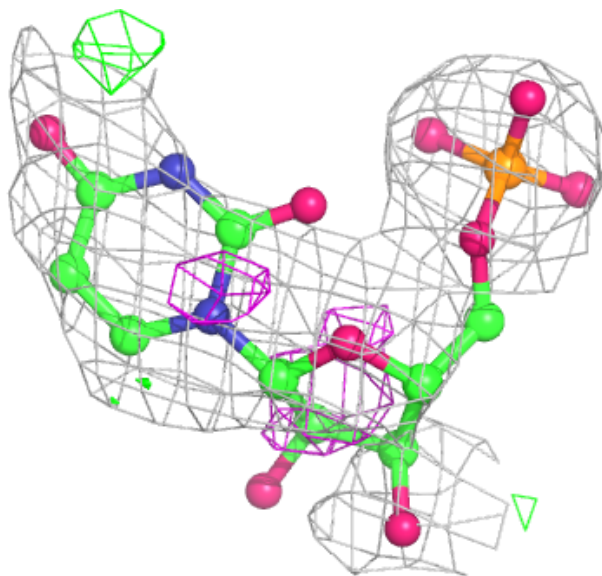
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	SO4	B	434	5/5	0.92	0.20	84,84,85,85	0
2	SO4	C	439	5/5	0.92	0.10	111,111,112,112	0
2	SO4	C	451	5/5	0.92	0.14	111,111,111,111	0
2	SO4	A	462	5/5	0.92	0.15	127,128,128,128	0
2	SO4	C	432	5/5	0.92	0.11	108,108,108,108	0
2	SO4	C	435	5/5	0.93	0.20	113,114,114,114	0
5	ZN	A	469	1/1	0.93	0.11	95,95,95,95	0
2	SO4	B	453	5/5	0.93	0.19	124,124,124,125	0
2	SO4	D	436	5/5	0.93	0.17	108,108,108,108	0
2	SO4	A	437	5/5	0.93	0.16	87,87,88,89	0
2	SO4	B	432	5/5	0.94	0.15	83,84,85,86	0
2	SO4	A	441	5/5	0.94	0.15	101,101,101,101	0
5	ZN	C	459	1/1	0.94	0.08	97,97,97,97	0
4	U5P	C	457	21/21	0.94	0.19	61,73,75,76	0
4	U5P	B	456	21/21	0.95	0.20	34,53,56,59	0
2	SO4	B	445	5/5	0.95	0.18	58,60,62,63	0
2	SO4	B	443	5/5	0.95	0.11	80,81,82,82	0
5	ZN	B	458	1/1	0.95	0.07	70,70,70,70	0
2	SO4	C	434	5/5	0.95	0.12	70,71,71,72	0
2	SO4	D	435	5/5	0.95	0.15	87,87,88,88	0
5	ZN	A	468	1/1	0.95	0.09	74,74,74,74	0
2	SO4	A	454	5/5	0.96	0.16	54,54,55,57	0
5	ZN	B	459	1/1	0.96	0.08	84,84,84,84	0
4	U5P	A	465	21/21	0.97	0.16	33,51,52,57	0
2	SO4	A	453	5/5	0.97	0.09	84,85,85,86	0
2	SO4	A	440	5/5	0.98	0.10	58,58,60,60	0
2	SO4	B	433	5/5	0.98	0.14	65,65,66,66	0
2	SO4	D	444	5/5	0.98	0.12	72,72,73,73	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.

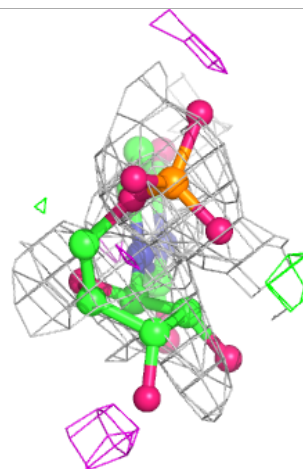
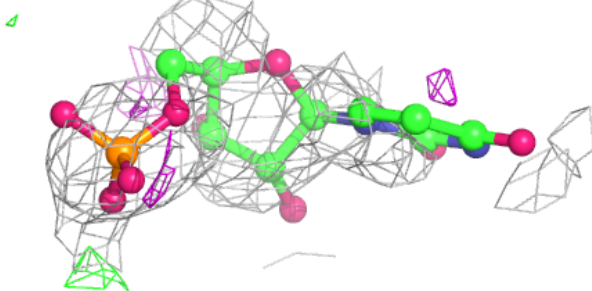
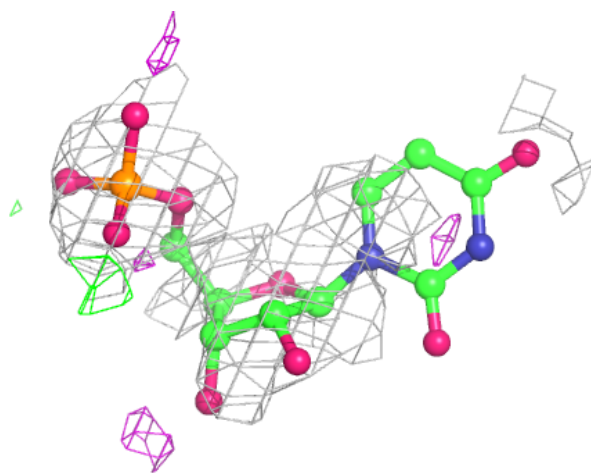
Electron density around U5P B 457:

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



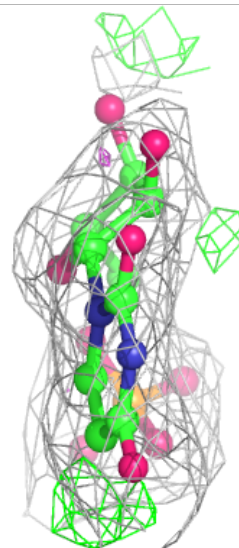
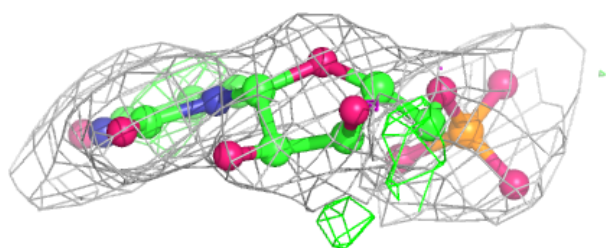
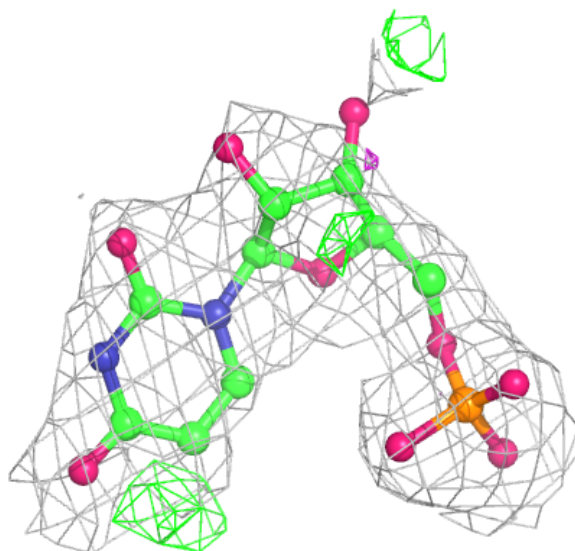
Electron density around U5P A 467:

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



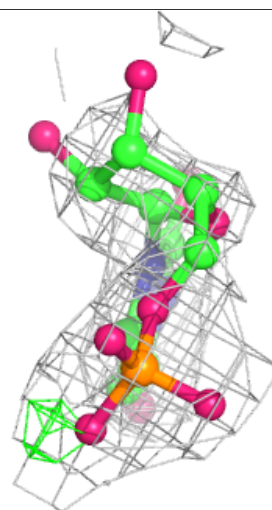
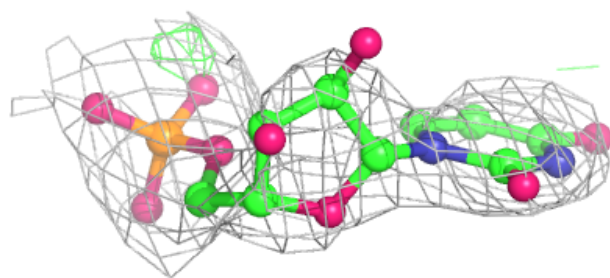
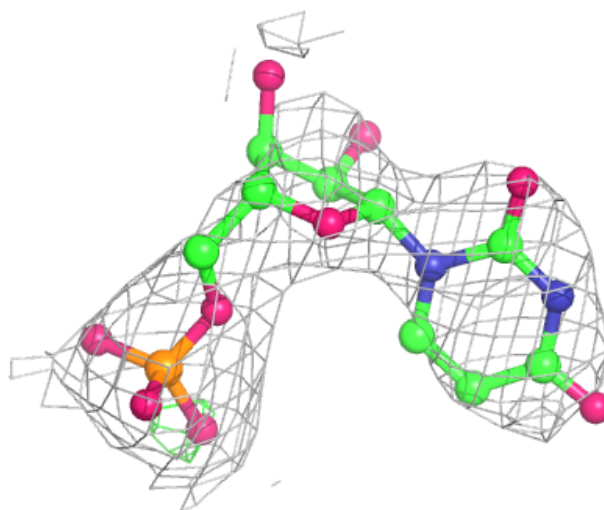
Electron density around U5P A 466:

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



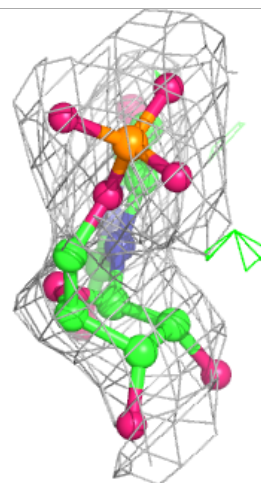
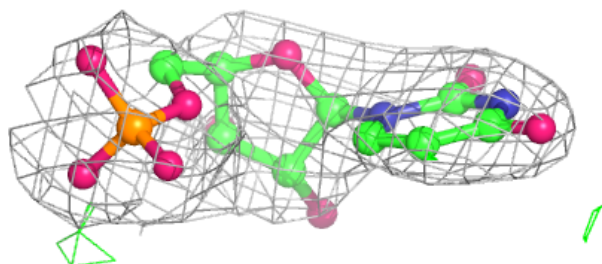
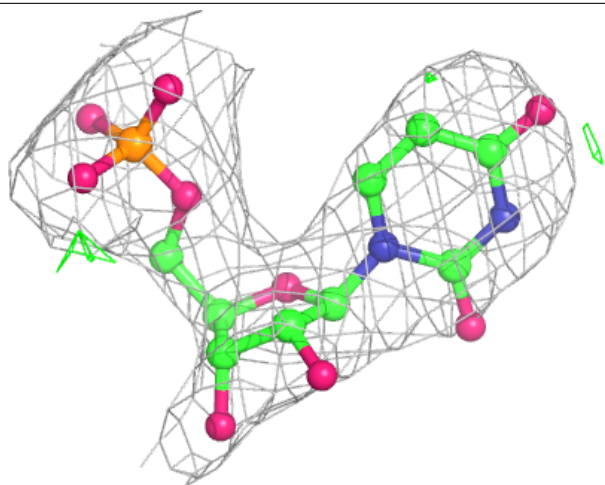
Electron density around U5P D 448:

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



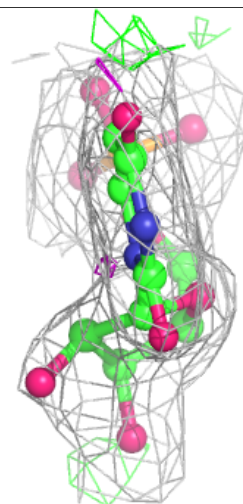
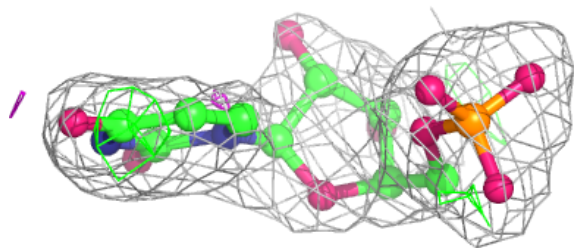
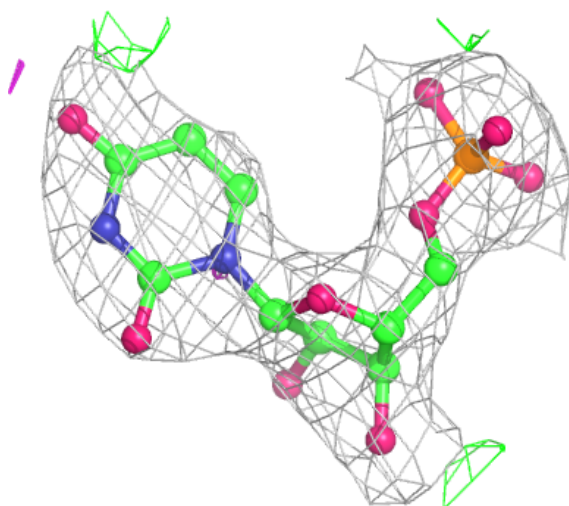
Electron density around U5P C 457:

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



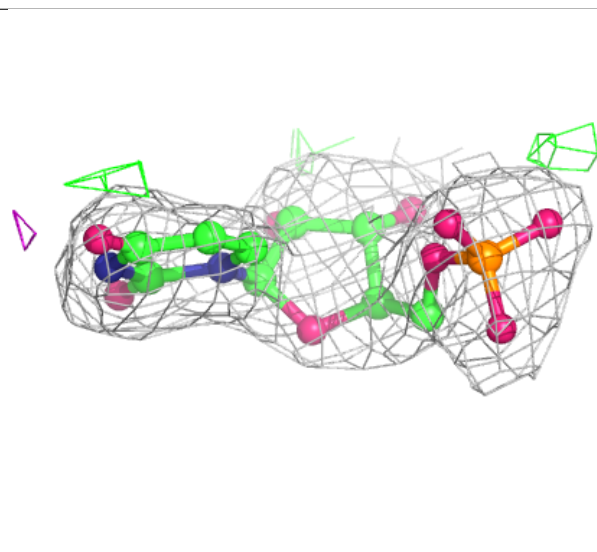
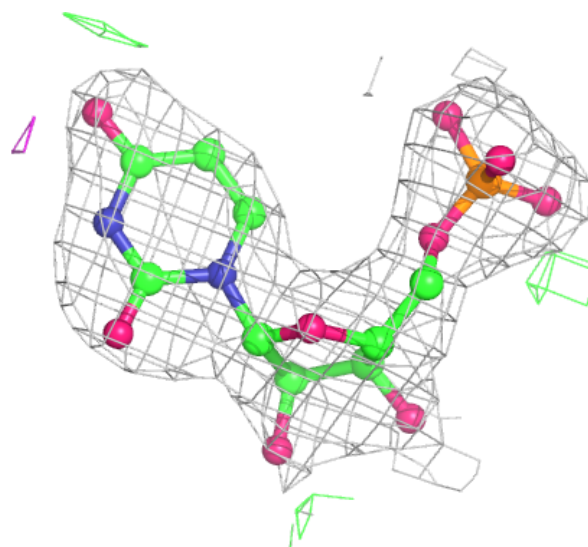
Electron density around U5P B 456:

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



Electron density around U5P A 465:

$2mF_o-DF_c$ (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.