Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 03:55 PM UTC

PDB ID	:	2WVJ / pdb_00002wvj
Title	:	Mutation of Thr163 to Ser in Human Thymidine Kinase Shifts the Specificity from Thymidine towards the Nucleoside Analogue Azidothymidine
Authors	:	Skovgaard, T.; Uhlin, U.; Munch-Petersen, B.
Deposited on	:	2009-10-17
Resolution	:	2.20 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at *validation@mail.wwpdb.org*
A user guide is available at
https://www.wwpdb.org/validation/2017/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at
http://www.wwpdb.org/validation/2017/FAQs#types.

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

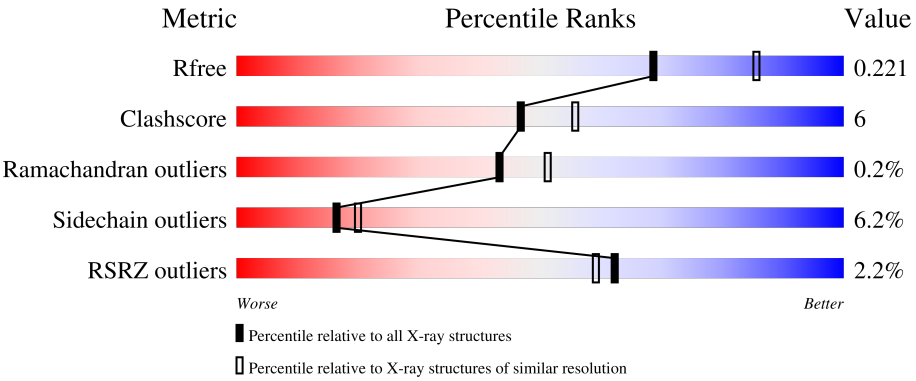
MolProbity	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

1 Overall quality at a glance (i)

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

The reported resolution of this entry is 2.20 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	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for >=3, 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions <=5% The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	193	2% 72% 10% • 17%
1	B	193	2% 74% 8% • 17%
1	C	193	2% 70% 12% • 17%
1	D	193	3% 70% 11% • 16%
1	E	193	2% 69% 12% • 17%

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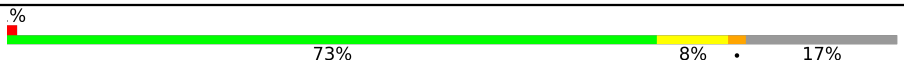
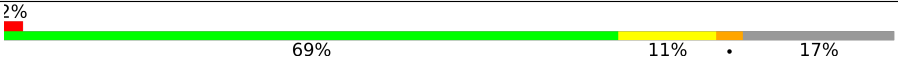
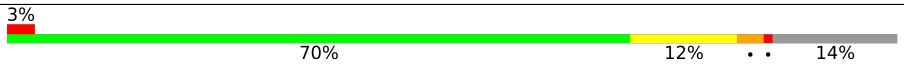
Mol	Chain	Length	Quality of chain
1	F	193	
1	G	193	
1	H	193	

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 11307 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.

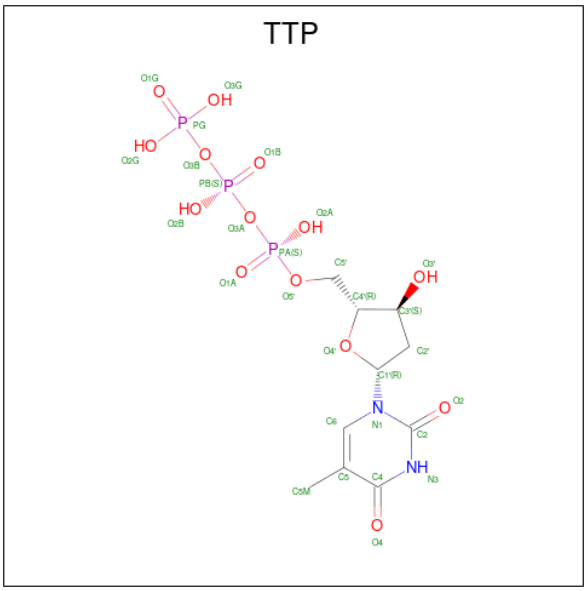
- Molecule 1 is a protein called THYMIDINE KINASE, CYTOSOLIC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	160	Total	C	N	O	S	0	0	0
			1238	793	215	219	11			
1	B	161	Total	C	N	O	S	0	0	0
			1247	799	217	220	11			
1	C	160	Total	C	N	O	S	0	0	0
			1238	793	215	219	11			
1	D	162	Total	C	N	O	S	0	0	0
			1256	805	217	223	11			
1	E	160	Total	C	N	O	S	0	0	0
			1238	793	215	219	11			
1	F	160	Total	C	N	O	S	0	0	0
			1238	793	215	219	11			
1	G	161	Total	C	N	O	S	0	0	0
			1250	802	216	221	11			
1	H	166	Total	C	N	O	S	0	0	0
			1285	821	221	231	12			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	163	SER	THR	engineered mutation	UNP P04183
B	163	SER	THR	engineered mutation	UNP P04183
C	163	SER	THR	engineered mutation	UNP P04183
D	163	SER	THR	engineered mutation	UNP P04183
E	163	SER	THR	engineered mutation	UNP P04183
F	163	SER	THR	engineered mutation	UNP P04183
G	163	SER	THR	engineered mutation	UNP P04183
H	163	SER	THR	engineered mutation	UNP P04183

- Molecule 2 is THYMIDINE-5'-TRIPHOSPHATE (CCD ID: TTP) (formula: $C_{10}H_{17}N_2O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	B	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	C	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	D	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	E	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	F	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	G	1	Total	C	N	O	P	0	0
			29	10	2	14	3		
2	H	1	Total	C	N	O	P	0	0
			29	10	2	14	3		

- Molecule 3 is ZINC ION (CCD ID: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		
3	B	1	Total	Zn	0	0
			1	1		
3	C	1	Total	Zn	0	0
			1	1		
3	D	1	Total	Zn	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	E	1	Total Zn 1 1	0	0
3	F	1	Total Zn 1 1	0	0
3	G	1	Total Zn 1 1	0	0
3	H	1	Total Zn 1 1	0	0

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	D	1	Total Mg 1 1	0	0
4	G	1	Total Mg 1 1	0	0
4	H	1	Total Mg 1 1	0	0

- Molecule 5 is water.

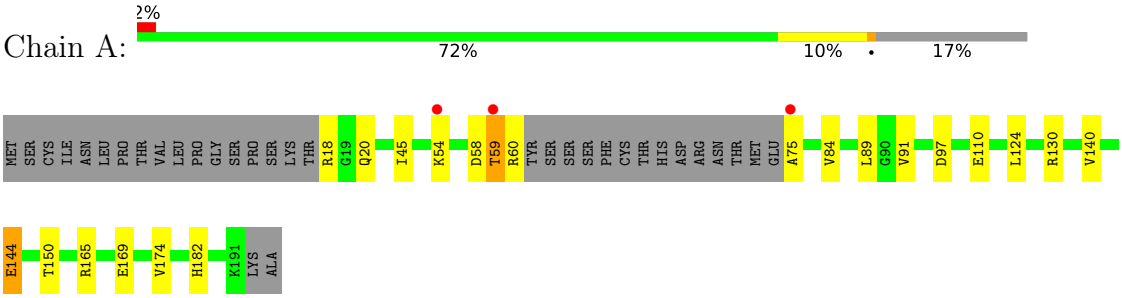
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	119	Total O 119 119	0	0
5	B	139	Total O 139 139	0	0
5	C	123	Total O 123 123	0	0
5	D	138	Total O 138 138	0	0
5	E	119	Total O 119 119	0	0
5	F	119	Total O 119 119	0	0
5	G	164	Total O 164 164	0	0
5	H	153	Total O 153 153	0	0

3 Residue-property plots (i)

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

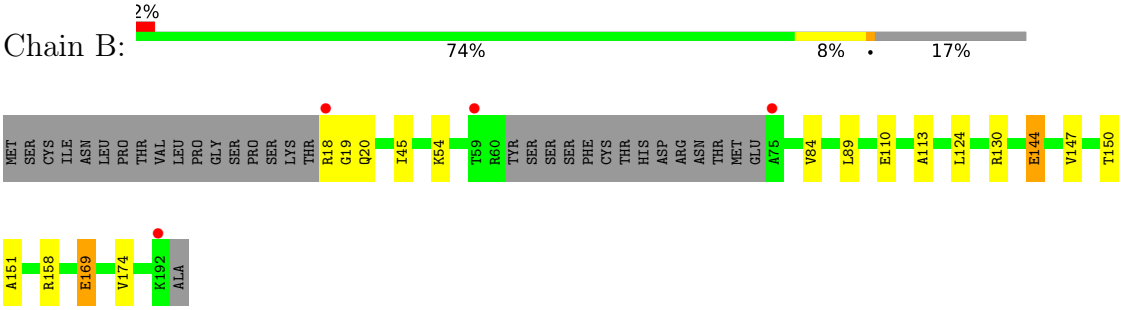
• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

Chain A:



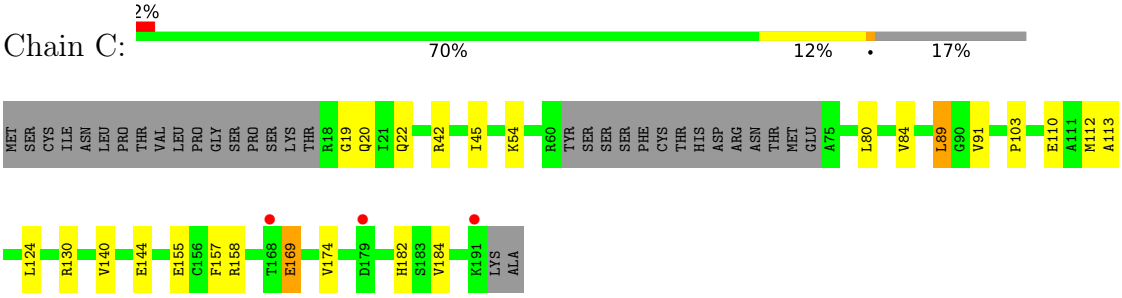
• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

Chain B:



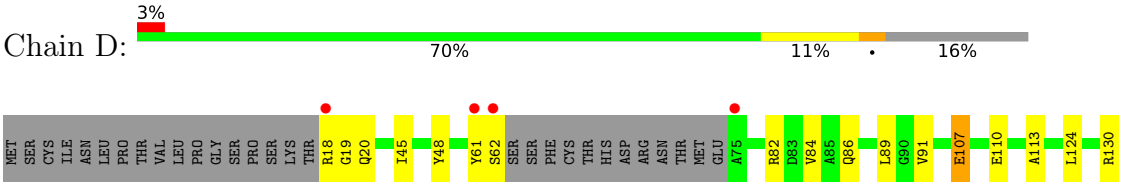
• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

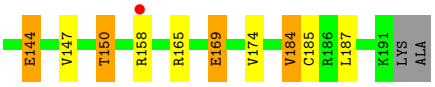
Chain C:



• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

Chain D:

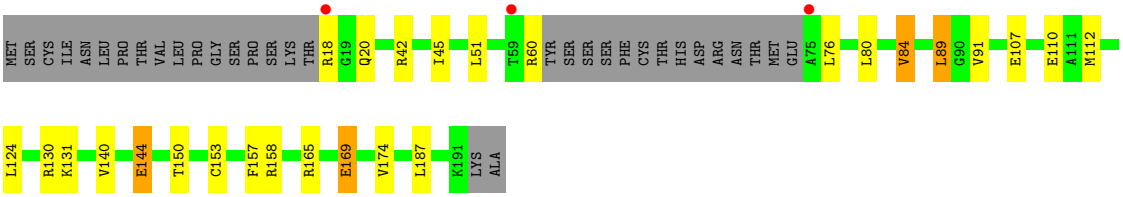




• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

Chain E:

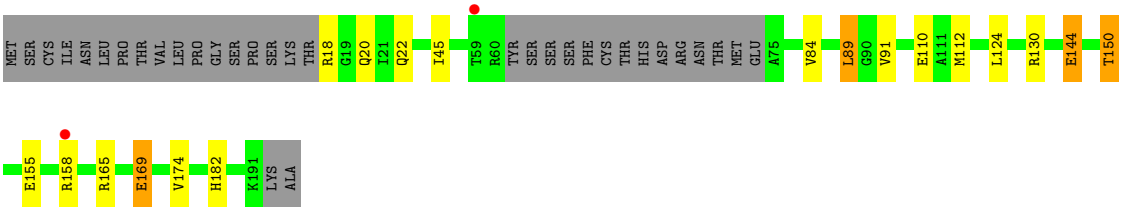




• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

Chain F:

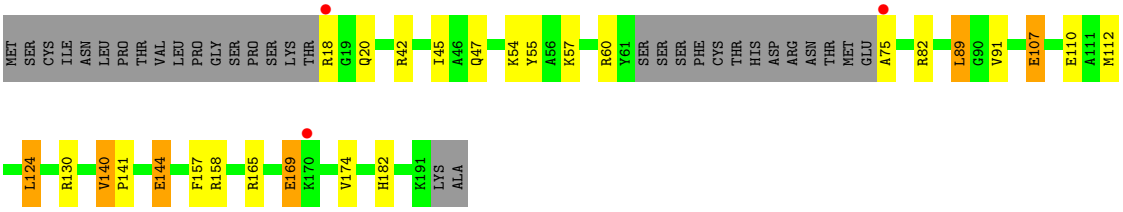




• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

Chain G:

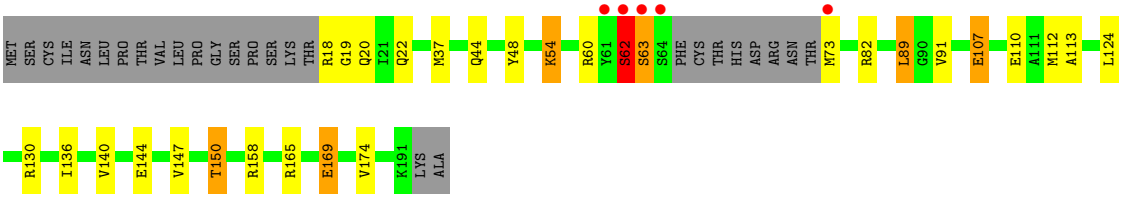




• Molecule 1: THYMIDINE KINASE, CYTOSOLIC

Chain H:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	156.90Å 123.25Å 121.02Å 90.00° 132.98° 90.00°	Depositor
Resolution (Å)	49.81 – 2.20 49.81 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.9 (49.81-2.20) 99.8 (49.81-2.20)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.76 (at 2.20Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.173 , 0.221 0.173 , 0.221	Depositor DCC
R_{free} test set	4263 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	21.3	Xtriage
Anisotropy	0.264	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.38 , 48.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Estimated twinning fraction	0.015 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.95	EDS
Total number of atoms	11307	wwPDB-VP
Average B, all atoms (Å^2)	21.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.90% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: ZN, TTP, 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	0.58	1/1256 (0.1%)	0.79	0/1688
1	B	0.57	0/1265	0.78	0/1699
1	C	0.60	1/1256 (0.1%)	0.80	0/1688
1	D	0.56	0/1275	0.80	0/1714
1	E	0.58	1/1256 (0.1%)	0.80	0/1688
1	F	0.54	0/1256	0.79	0/1688
1	G	0.60	1/1269 (0.1%)	0.80	0/1706
1	H	0.60	1/1304 (0.1%)	0.84	3/1752 (0.2%)
All	All	0.58	5/10137 (0.0%)	0.80	3/13623 (0.0%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	G	140	VAL	CA-CB	7.18	1.57	1.54
1	C	140	VAL	CA-CB	7.01	1.57	1.54
1	E	140	VAL	CA-CB	6.53	1.57	1.54
1	H	140	VAL	CA-CB	5.46	1.56	1.54
1	A	140	VAL	CA-CB	5.26	1.56	1.54

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	H	62	SER	CA-C-N	6.63	133.64	121.70
1	H	62	SER	C-N-CA	6.63	133.64	121.70
1	H	136	ILE	N-CA-C	5.23	115.95	110.62

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	1238	0	1278	14	0
1	B	1247	0	1291	14	0
1	C	1238	0	1278	13	0
1	D	1256	0	1292	21	0
1	E	1238	0	1278	18	0
1	F	1238	0	1278	16	0
1	G	1250	0	1287	20	0
1	H	1285	0	1317	26	0
2	A	29	0	13	0	0
2	B	29	0	13	0	0
2	C	29	0	13	0	0
2	D	29	0	13	0	0
2	E	29	0	13	1	0
2	F	29	0	13	0	0
2	G	29	0	13	1	0
2	H	29	0	13	0	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
3	E	1	0	0	0	0
3	F	1	0	0	0	0
3	G	1	0	0	0	0
3	H	1	0	0	0	0
4	D	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	119	0	0	4	0
5	B	139	0	0	3	0
5	C	123	0	0	2	0
5	D	138	0	0	4	0
5	E	119	0	0	1	0
5	F	119	0	0	3	0
5	G	164	0	0	4	0
5	H	153	0	0	4	0
All	All	11307	0	10403	118	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 6.

All (118) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:H:62:SER:CB	1:H:63:SER:HB2	2.00	0.91
1:H:62:SER:HB2	1:H:63:SER:HB2	1.56	0.86
1:F:20:GLN:NE2	1:F:22:GLN:HE21	1.75	0.83
1:H:54:LYS:HE3	1:H:63:SER:O	1.84	0.77
1:B:130:ARG:NH2	1:D:110:GLU:OE1	2.18	0.76
1:B:110:GLU:OE1	1:D:130:ARG:NH2	2.21	0.74
1:E:42:ARG:HH21	1:F:150:THR:HG22	1.53	0.73
1:H:62:SER:HB3	5:H:2153:HOH:O	1.89	0.71
1:H:169:GLU:HG3	1:H:174:VAL:HG21	1.73	0.70
1:F:110:GLU:OE1	1:H:130:ARG:NH2	2.22	0.70
1:A:110:GLU:OE1	1:C:130:ARG:NH2	2.23	0.70
1:G:169:GLU:HG3	1:G:174:VAL:HG21	1.74	0.69
1:F:130:ARG:NH2	1:H:110:GLU:OE1	2.19	0.69
1:B:169:GLU:HG3	1:B:174:VAL:HG21	1.75	0.69
1:B:20:GLN:HG2	1:B:144:GLU:CG	2.24	0.68
1:H:37:MET:HE1	1:H:73:MET:HE1	1.75	0.68
1:F:20:GLN:HB2	1:F:144:GLU:CG	2.24	0.68
1:F:169:GLU:HG3	1:F:174:VAL:HG21	1.76	0.68
1:E:51:LEU:HD11	1:E:76:LEU:HD12	1.78	0.65
1:E:130:ARG:NH2	1:G:110:GLU:OE1	2.28	0.65
1:D:165:ARG:HD3	1:D:169:GLU:HG2	1.79	0.64
1:C:42:ARG:HH21	1:D:150:THR:HG22	1.63	0.64
1:D:169:GLU:HG3	1:D:174:VAL:HG21	1.79	0.64
1:E:169:GLU:HG3	1:E:174:VAL:HG21	1.81	0.62
1:H:20:GLN:NE2	1:H:22:GLN:HE21	2.00	0.59
1:B:20:GLN:HG2	1:B:144:GLU:HG2	1.85	0.59
1:A:169:GLU:HG3	1:A:174:VAL:HG21	1.84	0.59
1:D:61:TYR:O	1:D:62:SER:HB3	2.03	0.57
1:F:20:GLN:HE21	1:F:22:GLN:HE21	1.51	0.57
1:C:169:GLU:HG3	1:C:174:VAL:HG21	1.87	0.57
1:D:61:TYR:O	1:D:62:SER:CB	2.53	0.56
1:B:158:ARG:HD3	1:D:18:ARG:NH2	2.19	0.56
1:A:20:GLN:HB2	1:A:144:GLU:CG	2.36	0.55
1:C:54:LYS:HG2	5:C:2038:HOH:O	2.07	0.55
1:D:84:VAL:HG12	1:D:84:VAL:O	2.06	0.55
1:B:158:ARG:HD3	1:D:18:ARG:CZ	2.37	0.54
1:F:20:GLN:HB2	1:F:144:GLU:HG3	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:82:ARG:HD3	5:G:2079:HOH:O	2.08	0.54
1:B:18:ARG:NH1	1:D:187:LEU:HD12	2.22	0.53
1:E:18:ARG:CZ	1:G:158:ARG:HD3	2.38	0.53
1:F:165:ARG:HD3	1:F:169:GLU:HG2	1.91	0.53
1:G:182:HIS:HE1	5:G:2154:HOH:O	1.91	0.53
1:B:20:GLN:NE2	5:B:2007:HOH:O	2.41	0.53
1:E:110:GLU:OE1	1:G:130:ARG:NH2	2.36	0.52
1:E:107:GLU:HG3	5:E:2062:HOH:O	2.09	0.52
5:B:2096:HOH:O	1:D:147:VAL:HG23	2.10	0.51
1:C:84:VAL:HG12	1:C:84:VAL:O	2.10	0.51
1:D:20:GLN:HG2	1:D:144:GLU:CG	2.40	0.51
1:B:54:LYS:HG3	5:B:2043:HOH:O	2.11	0.51
1:H:44:GLN:NE2	1:H:73:MET:HB2	2.26	0.51
1:D:82:ARG:NH2	5:D:2045:HOH:O	2.32	0.50
1:D:158:ARG:HD2	5:D:2106:HOH:O	2.11	0.50
1:G:165:ARG:HD3	1:G:169:GLU:HG2	1.93	0.50
1:A:130:ARG:NH2	1:C:110:GLU:OE1	2.31	0.49
1:A:54:LYS:HG2	1:A:97:ASP:HB3	1.94	0.48
1:E:165:ARG:HD3	1:E:169:GLU:HG2	1.95	0.48
1:D:184:VAL:HG13	1:D:185:CYS:O	2.13	0.48
1:E:89:LEU:HD13	1:E:112:MET:HE1	1.95	0.48
1:E:187:LEU:HD12	1:G:18:ARG:NH1	2.29	0.47
1:H:165:ARG:HD3	1:H:169:GLU:HG2	1.96	0.47
1:G:75:ALA:N	5:G:2069:HOH:O	2.47	0.47
5:F:2086:HOH:O	1:H:147:VAL:HG23	2.15	0.47
1:E:42:ARG:HH21	1:F:150:THR:CG2	2.26	0.47
1:F:89:LEU:HD13	1:F:112:MET:HE1	1.96	0.47
1:A:54:LYS:HG3	5:A:2038:HOH:O	2.15	0.46
1:G:60:ARG:HD2	5:G:2062:HOH:O	2.16	0.46
1:A:18:ARG:CZ	1:C:158:ARG:HD3	2.46	0.45
1:G:42:ARG:HH21	1:H:150:THR:HG23	1.80	0.45
1:H:19:GLY:HA3	1:H:113:ALA:O	2.16	0.45
1:D:84:VAL:O	1:D:84:VAL:CG1	2.64	0.45
1:C:20:GLN:NE2	1:C:22:GLN:HE21	2.15	0.45
1:E:20:GLN:HB2	1:E:144:GLU:CG	2.47	0.44
1:C:157:PHE:HB3	1:D:48:TYR:OH	2.18	0.44
5:F:2086:HOH:O	1:H:147:VAL:CG2	2.65	0.44
1:H:54:LYS:HG2	5:H:2040:HOH:O	2.17	0.44
1:A:20:GLN:HB2	1:A:144:GLU:HG3	2.01	0.43
1:H:62:SER:HB3	1:H:63:SER:HB2	1.92	0.43
1:H:60:ARG:O	1:H:63:SER:HB3	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:G:20:GLN:HB2	1:G:144:GLU:CG	2.49	0.43
1:C:89:LEU:HD13	1:C:112:MET:HE1	2.00	0.43
1:A:59:THR:O	1:A:60:ARG:C	2.62	0.43
1:D:19:GLY:HA3	1:D:113:ALA:O	2.18	0.42
1:F:182:HIS:HE1	5:F:2109:HOH:O	2.01	0.42
1:C:155:GLU:OE1	1:C:182:HIS:HD2	2.01	0.42
1:G:47:GLN:HG3	5:H:2069:HOH:O	2.20	0.42
1:A:165:ARG:HD3	1:A:169:GLU:HG2	2.01	0.42
1:B:147:VAL:HG23	5:D:2096:HOH:O	2.19	0.42
1:A:59:THR:HB	5:A:2034:HOH:O	2.20	0.42
1:C:80:LEU:HD23	1:C:103:PRO:HD2	2.02	0.42
1:G:89:LEU:HD13	1:G:112:MET:HE1	2.01	0.42
1:G:107:GLU:H	1:G:107:GLU:CD	2.27	0.42
1:D:107:GLU:H	1:D:107:GLU:CD	2.28	0.42
1:H:37:MET:CE	1:H:73:MET:HE1	2.47	0.41
1:H:82:ARG:NH2	5:H:2060:HOH:O	2.40	0.41
1:A:58:ASP:OD1	1:A:60:ARG:HD3	2.20	0.41
1:E:42:ARG:NH2	1:F:150:THR:HG22	2.26	0.41
1:F:18:ARG:CZ	1:H:158:ARG:HD3	2.51	0.41
1:A:182:HIS:HE1	5:A:2107:HOH:O	2.04	0.41
1:C:19:GLY:HA3	1:C:113:ALA:O	2.21	0.41
1:E:84:VAL:O	1:E:84:VAL:HG13	2.20	0.41
1:H:62:SER:CB	1:H:63:SER:CB	2.87	0.41
1:B:20:GLN:CG	1:B:144:GLU:HG3	2.51	0.41
1:B:150:THR:HG22	1:B:151:ALA:O	2.21	0.41
1:D:165:ARG:HG3	5:D:2111:HOH:O	2.20	0.41
1:F:155:GLU:OE1	1:F:182:HIS:HD2	2.04	0.41
1:B:19:GLY:HA3	1:B:113:ALA:O	2.21	0.40
5:C:2058:HOH:O	1:E:131:LYS:HD3	2.21	0.40
1:G:140:VAL:HB	1:G:141:PRO:HD3	2.02	0.40
1:G:157:PHE:HB3	1:H:48:TYR:OH	2.22	0.40
1:G:124:LEU:HD22	2:G:1192:TTP:H5'2	2.03	0.40
1:E:60:ARG:NH2	2:E:1192:TTP:H5'1	2.36	0.40
1:G:55:TYR:CE2	1:G:57:LYS:HB2	2.57	0.40
1:H:107:GLU:H	1:H:107:GLU:CD	2.28	0.40
1:E:153:CYS:O	1:E:157:PHE:HA	2.21	0.40
1:F:158:ARG:HD3	1:H:18:ARG:CZ	2.51	0.40
1:A:75:ALA:HB1	5:A:2038:HOH:O	2.21	0.40
1:E:158:ARG:HD3	1:G:18:ARG:CZ	2.51	0.40
1:H:89:LEU:HD13	1:H:112:MET:HE1	2.04	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	156/193 (81%)	153 (98%)	3 (2%)	0	100 100
1	B	157/193 (81%)	155 (99%)	2 (1%)	0	100 100
1	C	156/193 (81%)	154 (99%)	2 (1%)	0	100 100
1	D	158/193 (82%)	157 (99%)	1 (1%)	0	100 100
1	E	156/193 (81%)	153 (98%)	3 (2%)	0	100 100
1	F	156/193 (81%)	155 (99%)	1 (1%)	0	100 100
1	G	157/193 (81%)	156 (99%)	1 (1%)	0	100 100
1	H	162/193 (84%)	159 (98%)	1 (1%)	2 (1%)	10 8
All	All	1258/1544 (82%)	1242 (99%)	14 (1%)	2 (0%)	43 51

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	H	63	SER
1	H	62	SER

5.3.2 Protein sidechains (i)

In the following table, the Percentiles column shows the percent sidechain outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the sidechain conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	A	130/161 (81%)	122 (94%)	8 (6%)	16 20
1	B	131/161 (81%)	125 (95%)	6 (5%)	24 32
1	C	130/161 (81%)	123 (95%)	7 (5%)	20 25

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
1	D	132/161 (82%)	122 (92%)	10 (8%)	12 14
1	E	130/161 (81%)	121 (93%)	9 (7%)	14 16
1	F	130/161 (81%)	122 (94%)	8 (6%)	16 20
1	G	131/161 (81%)	123 (94%)	8 (6%)	17 20
1	H	136/161 (84%)	127 (93%)	9 (7%)	15 18
All	All	1050/1288 (82%)	985 (94%)	65 (6%)	16 20

All (65) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	45	ILE
1	A	59	THR
1	A	84	VAL
1	A	89	LEU
1	A	91	VAL
1	A	124	LEU
1	A	144	GLU
1	A	150	THR
1	B	45	ILE
1	B	84	VAL
1	B	89	LEU
1	B	124	LEU
1	B	144	GLU
1	B	169	GLU
1	C	45	ILE
1	C	89	LEU
1	C	91	VAL
1	C	124	LEU
1	C	144	GLU
1	C	169	GLU
1	C	184	VAL
1	D	45	ILE
1	D	86	GLN
1	D	89	LEU
1	D	91	VAL
1	D	107	GLU
1	D	124	LEU
1	D	144	GLU
1	D	150	THR
1	D	169	GLU

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Mol	Chain	Res	Type
1	D	184	VAL
1	E	45	ILE
1	E	80	LEU
1	E	84	VAL
1	E	89	LEU
1	E	91	VAL
1	E	124	LEU
1	E	144	GLU
1	E	150	THR
1	E	169	GLU
1	F	45	ILE
1	F	84	VAL
1	F	89	LEU
1	F	91	VAL
1	F	124	LEU
1	F	144	GLU
1	F	150	THR
1	F	169	GLU
1	G	45	ILE
1	G	54	LYS
1	G	89	LEU
1	G	91	VAL
1	G	107	GLU
1	G	124	LEU
1	G	144	GLU
1	G	169	GLU
1	H	54	LYS
1	H	62	SER
1	H	89	LEU
1	H	91	VAL
1	H	107	GLU
1	H	124	LEU
1	H	144	GLU
1	H	150	THR
1	H	169	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (17) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	20	GLN
1	A	182	HIS
1	B	86	GLN

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Mol	Chain	Res	Type
1	B	182	HIS
1	C	20	GLN
1	C	182	HIS
1	D	47	GLN
1	D	138	ASN
1	D	182	HIS
1	F	20	GLN
1	F	138	ASN
1	F	182	HIS
1	G	182	HIS
1	H	20	GLN
1	H	129	GLN
1	H	138	ASN
1	H	182	HIS

5.3.3 RNA (i)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates (i)

There are no oligosaccharides in this entry.

5.6 Ligand geometry (i)

Of 19 ligands modelled in this entry, 11 are monoatomic - leaving 8 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	TTP	H	1192	4	29,30,30	1.53	7 (24%)	43,47,47	1.65	6 (13%)
2	TTP	B	1193	-	29,30,30	1.52	7 (24%)	43,47,47	1.72	7 (16%)
2	TTP	G	1192	4	29,30,30	1.46	7 (24%)	43,47,47	1.76	8 (18%)
2	TTP	F	1192	-	29,30,30	1.40	5 (17%)	43,47,47	1.75	9 (20%)
2	TTP	C	1192	-	29,30,30	1.47	7 (24%)	43,47,47	1.76	10 (23%)
2	TTP	A	1192	-	29,30,30	1.43	5 (17%)	43,47,47	1.70	7 (16%)
2	TTP	E	1192	-	29,30,30	1.48	7 (24%)	43,47,47	1.72	7 (16%)
2	TTP	D	1192	4	29,30,30	1.51	8 (27%)	43,47,47	1.68	8 (18%)

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	TTP	H	1192	4	-	2/22/34/34	0/2/2/2
2	TTP	B	1193	-	-	1/22/34/34	0/2/2/2
2	TTP	G	1192	4	-	2/22/34/34	0/2/2/2
2	TTP	F	1192	-	-	1/22/34/34	0/2/2/2
2	TTP	C	1192	-	-	1/22/34/34	0/2/2/2
2	TTP	A	1192	-	-	2/22/34/34	0/2/2/2
2	TTP	E	1192	-	-	1/22/34/34	0/2/2/2
2	TTP	D	1192	4	-	2/22/34/34	0/2/2/2

All (53) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	H	1192	TTP	PA-O3A	3.52	1.63	1.59
2	H	1192	TTP	C6-C5	3.30	1.40	1.34
2	F	1192	TTP	C6-C5	3.25	1.39	1.34
2	C	1192	TTP	C6-C5	3.23	1.39	1.34
2	E	1192	TTP	C6-C5	3.20	1.39	1.34
2	B	1193	TTP	C6-C5	3.16	1.39	1.34
2	A	1192	TTP	C6-C5	3.14	1.39	1.34
2	B	1193	TTP	C2-N1	3.12	1.43	1.38
2	G	1192	TTP	C4-C5	3.05	1.49	1.44
2	C	1192	TTP	C4-C5	3.05	1.49	1.44
2	D	1192	TTP	PA-O3A	3.05	1.62	1.59
2	D	1192	TTP	C6-C5	3.01	1.39	1.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	1193	TTP	C4-C5	3.00	1.49	1.44
2	A	1192	TTP	PB-O3B	2.99	1.62	1.59
2	G	1192	TTP	C6-C5	2.95	1.39	1.34
2	A	1192	TTP	C4-C5	2.93	1.49	1.44
2	E	1192	TTP	PB-O3B	2.91	1.62	1.59
2	C	1192	TTP	C2-N1	2.91	1.43	1.38
2	B	1193	TTP	PB-O3B	2.89	1.62	1.59
2	D	1192	TTP	C4-C5	2.87	1.49	1.44
2	G	1192	TTP	PA-O3A	2.81	1.62	1.59
2	F	1192	TTP	C4-C5	2.78	1.49	1.44
2	D	1192	TTP	C4-N3	-2.74	1.33	1.38
2	A	1192	TTP	C2-N1	2.74	1.42	1.38
2	H	1192	TTP	C4-N3	-2.71	1.33	1.38
2	E	1192	TTP	C4-C5	2.68	1.49	1.44
2	H	1192	TTP	C4-C5	2.60	1.49	1.44
2	E	1192	TTP	C4-N3	-2.58	1.34	1.38
2	F	1192	TTP	C4-N3	-2.47	1.34	1.38
2	E	1192	TTP	C2-N1	2.44	1.42	1.38
2	H	1192	TTP	C2-N1	2.39	1.42	1.38
2	C	1192	TTP	C4-N3	-2.38	1.34	1.38
2	E	1192	TTP	PB-O3A	2.36	1.62	1.59
2	F	1192	TTP	C2-N1	2.35	1.42	1.38
2	G	1192	TTP	C2-N1	2.34	1.42	1.38
2	G	1192	TTP	C4-N3	-2.33	1.34	1.38
2	F	1192	TTP	PB-O3B	2.31	1.62	1.59
2	D	1192	TTP	PB-O3A	2.31	1.62	1.59
2	B	1193	TTP	C4-N3	-2.30	1.34	1.38
2	D	1192	TTP	C2-N3	-2.30	1.34	1.38
2	A	1192	TTP	C4-N3	-2.30	1.34	1.38
2	H	1192	TTP	C2-N3	-2.22	1.34	1.38
2	B	1193	TTP	PA-O3A	2.19	1.61	1.59
2	G	1192	TTP	C2-N3	-2.17	1.34	1.38
2	D	1192	TTP	C2-N1	2.15	1.41	1.38
2	D	1192	TTP	PB-O3B	2.13	1.61	1.59
2	E	1192	TTP	PA-O3A	2.13	1.61	1.59
2	G	1192	TTP	PB-O3B	2.13	1.61	1.59
2	H	1192	TTP	PB-O3A	2.12	1.61	1.59
2	C	1192	TTP	C2-N3	-2.11	1.34	1.38
2	B	1193	TTP	PB-O3A	2.11	1.61	1.59
2	C	1192	TTP	PB-O3B	2.10	1.61	1.59
2	C	1192	TTP	PB-O3A	2.04	1.61	1.59

All (62) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	C	1192	TTP	N3-C2-N1	5.27	121.75	114.89
2	G	1192	TTP	C4-N3-C2	-5.03	120.75	127.34
2	F	1192	TTP	N3-C2-N1	5.03	121.44	114.89
2	B	1193	TTP	N3-C2-N1	4.94	121.32	114.89
2	B	1193	TTP	C4-N3-C2	-4.87	120.96	127.34
2	C	1192	TTP	C4-N3-C2	-4.86	120.97	127.34
2	E	1192	TTP	N3-C2-N1	4.85	121.20	114.89
2	D	1192	TTP	N3-C2-N1	4.83	121.18	114.89
2	F	1192	TTP	C4-N3-C2	-4.75	121.11	127.34
2	G	1192	TTP	N3-C2-N1	4.73	121.05	114.89
2	A	1192	TTP	C4-N3-C2	-4.72	121.15	127.34
2	D	1192	TTP	C4-N3-C2	-4.70	121.17	127.34
2	A	1192	TTP	N3-C2-N1	4.70	121.00	114.89
2	H	1192	TTP	C5-C4-N3	4.65	119.37	115.32
2	E	1192	TTP	C4-N3-C2	-4.55	121.37	127.34
2	H	1192	TTP	C4-N3-C2	-4.53	121.40	127.34
2	G	1192	TTP	C5-C4-N3	4.52	119.25	115.32
2	H	1192	TTP	N3-C2-N1	4.35	120.55	114.89
2	D	1192	TTP	C5-C4-N3	4.34	119.09	115.32
2	B	1193	TTP	C5-C4-N3	4.33	119.09	115.32
2	A	1192	TTP	C5-C4-N3	4.11	118.89	115.32
2	F	1192	TTP	C5-C4-N3	4.10	118.88	115.32
2	H	1192	TTP	C5-C6-N1	-3.96	119.01	123.31
2	G	1192	TTP	C5-C6-N1	-3.95	119.03	123.31
2	E	1192	TTP	C5-C4-N3	3.94	118.75	115.32
2	D	1192	TTP	C5-C6-N1	-3.91	119.07	123.31
2	C	1192	TTP	C5-C4-N3	3.84	118.66	115.32
2	F	1192	TTP	O4'-C1'-N1	3.64	114.32	107.86
2	E	1192	TTP	O4'-C1'-N1	3.57	114.19	107.86
2	A	1192	TTP	C5-C6-N1	-3.49	119.53	123.31
2	C	1192	TTP	C5-C6-N1	-3.42	119.59	123.31
2	A	1192	TTP	O4-C4-C5	-3.39	121.03	124.92
2	E	1192	TTP	C5-C6-N1	-3.35	119.67	123.31
2	B	1193	TTP	O4-C4-C5	-3.32	121.12	124.92
2	H	1192	TTP	O4-C4-C5	-3.22	121.24	124.92
2	F	1192	TTP	C5-C6-N1	-3.18	119.86	123.31
2	B	1193	TTP	C5-C6-N1	-3.09	119.95	123.31
2	G	1192	TTP	O4-C4-C5	-3.05	121.42	124.92
2	F	1192	TTP	O4-C4-C5	-2.95	121.54	124.92
2	E	1192	TTP	O4-C4-C5	-2.92	121.57	124.92
2	A	1192	TTP	O4'-C1'-N1	2.92	113.04	107.86
2	C	1192	TTP	O4'-C1'-N1	2.81	112.85	107.86
2	C	1192	TTP	O4-C4-C5	-2.78	121.73	124.92

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	B	1193	TTP	O4'-C1'-N1	2.71	112.67	107.86
2	G	1192	TTP	O2-C2-N1	-2.65	119.35	122.80
2	D	1192	TTP	O2G-PG-O3B	2.51	113.05	104.64
2	G	1192	TTP	C5M-C5-C4	2.50	121.45	118.78
2	D	1192	TTP	O4-C4-C5	-2.48	122.08	124.92
2	C	1192	TTP	C5M-C5-C4	2.45	121.40	118.78
2	A	1192	TTP	O2-C2-N1	-2.44	119.62	122.80
2	F	1192	TTP	C5M-C5-C4	2.42	121.37	118.78
2	D	1192	TTP	O2-C2-N1	-2.41	119.66	122.80
2	F	1192	TTP	O2-C2-N1	-2.40	119.67	122.80
2	H	1192	TTP	O2-C2-N1	-2.38	119.70	122.80
2	E	1192	TTP	O2-C2-N1	-2.24	119.88	122.80
2	B	1193	TTP	C5M-C5-C4	2.21	121.14	118.78
2	C	1192	TTP	C5M-C5-C6	-2.21	119.87	122.85
2	F	1192	TTP	O2B-PB-O3B	2.19	113.19	107.27
2	G	1192	TTP	O2G-PG-O3B	2.10	111.67	104.64
2	D	1192	TTP	O2B-PB-O3B	2.09	112.94	107.27
2	C	1192	TTP	O2-C2-N1	-2.08	120.08	122.80
2	C	1192	TTP	O2A-PA-O3A	2.05	112.81	107.27

There are no chirality outliers.

All (12) torsion outliers are listed below:

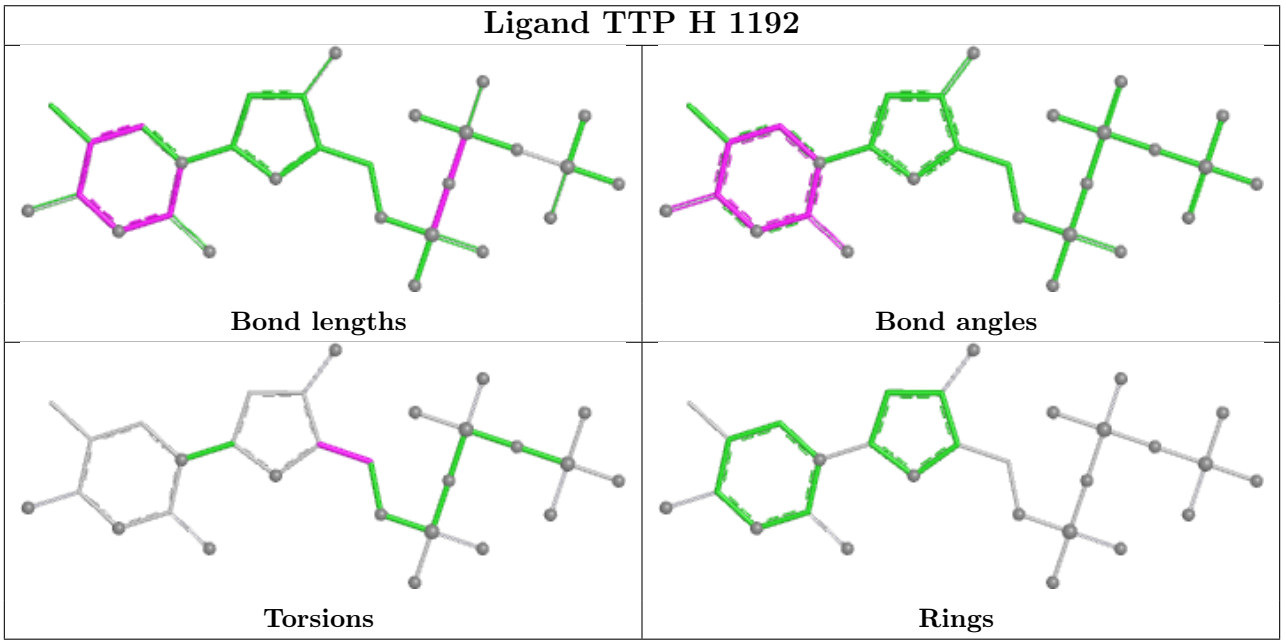
Mol	Chain	Res	Type	Atoms
2	D	1192	TTP	O4'-C4'-C5'-O5'
2	D	1192	TTP	C3'-C4'-C5'-O5'
2	G	1192	TTP	C3'-C4'-C5'-O5'
2	G	1192	TTP	O4'-C4'-C5'-O5'
2	H	1192	TTP	O4'-C4'-C5'-O5'
2	H	1192	TTP	C3'-C4'-C5'-O5'
2	A	1192	TTP	PG-O3B-PB-O2B
2	E	1192	TTP	PG-O3B-PB-O2B
2	F	1192	TTP	PG-O3B-PB-O2B
2	A	1192	TTP	PG-O3B-PB-O1B
2	B	1193	TTP	PA-O3A-PB-O2B
2	C	1192	TTP	PG-O3B-PB-O2B

There are no ring outliers.

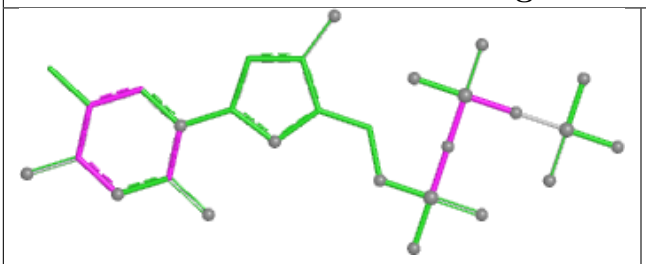
2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	G	1192	TTP	1	0
2	E	1192	TTP	1	0

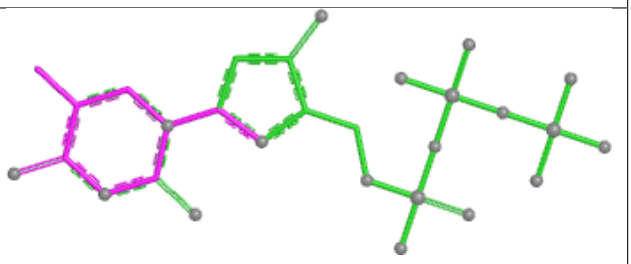
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



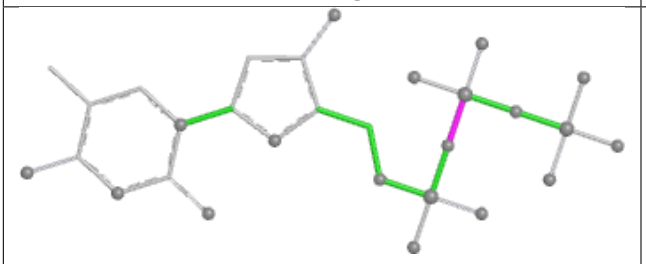
Ligand TTP B 1193



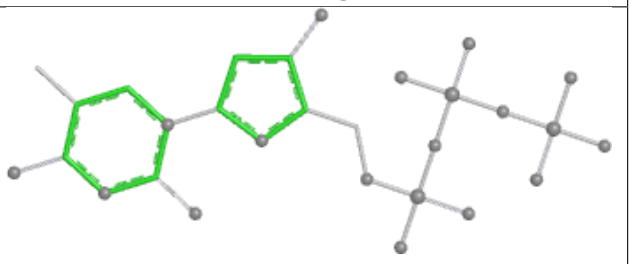
Bond lengths



Bond angles

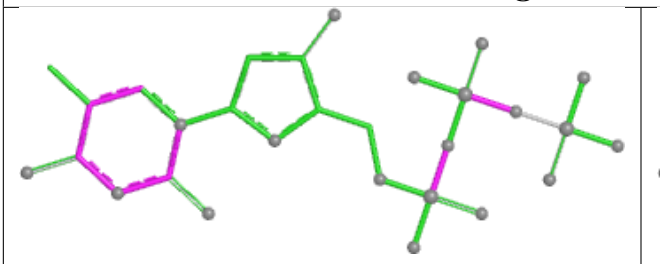


Torsions

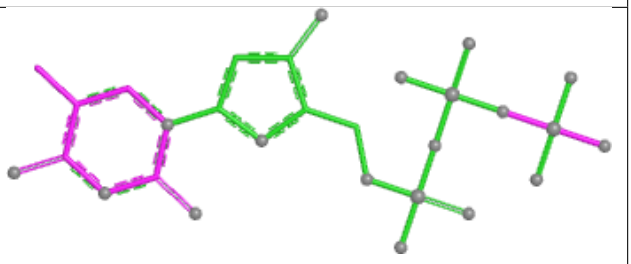


Rings

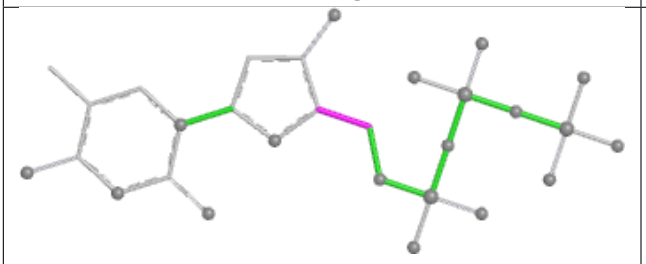
Ligand TTP G 1192



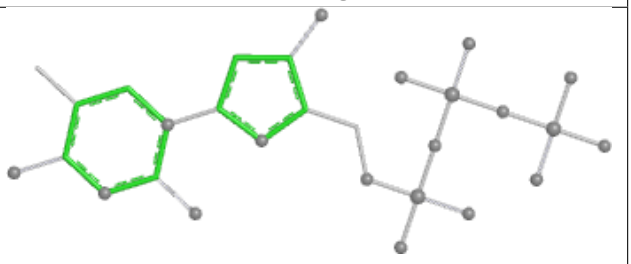
Bond lengths



Bond angles

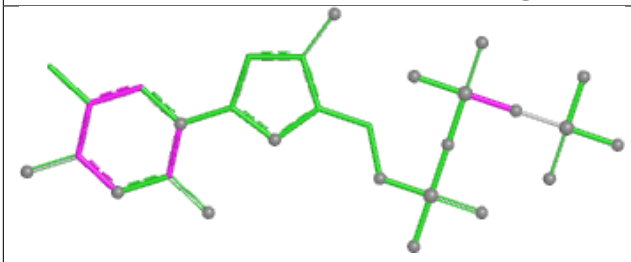


Torsions

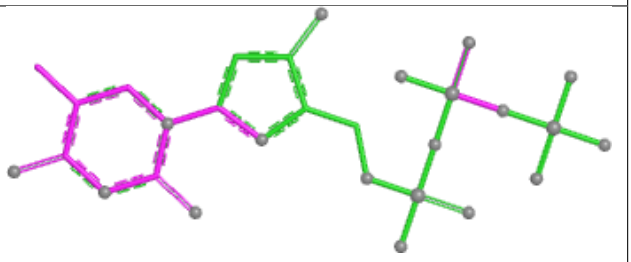


Rings

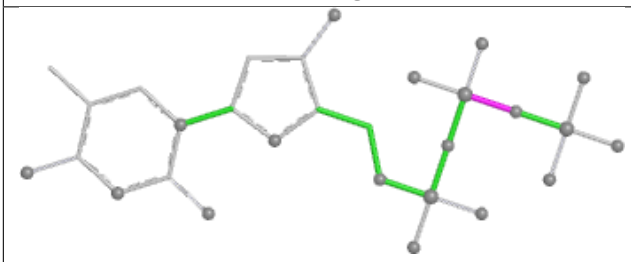
Ligand TTP F 1192



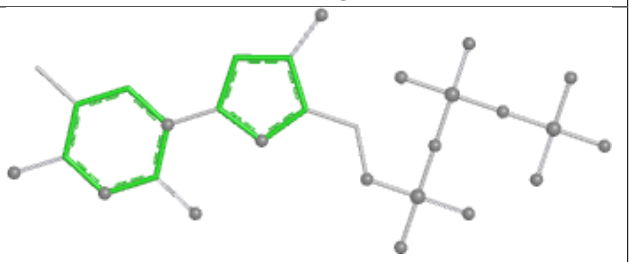
Bond lengths



Bond angles

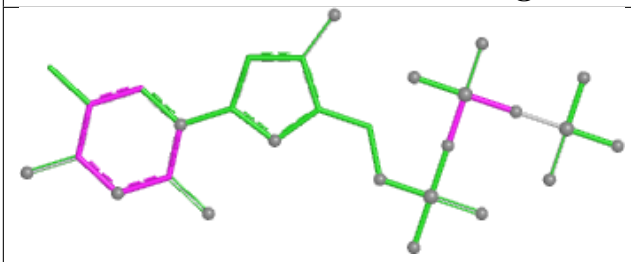


Torsions

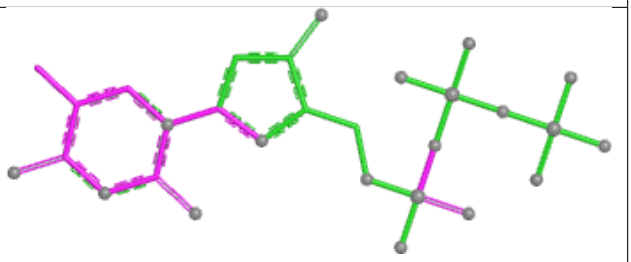


Rings

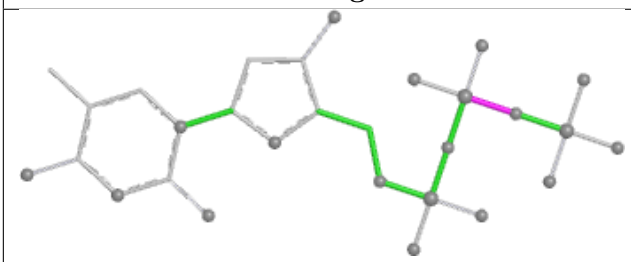
Ligand TTP C 1192



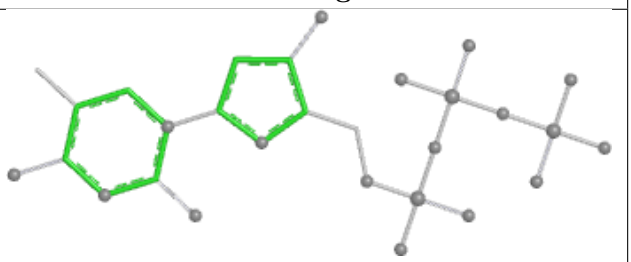
Bond lengths



Bond angles

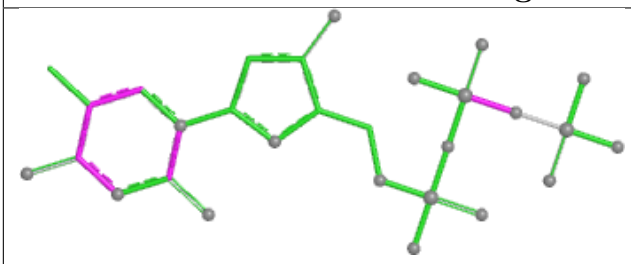


Torsions

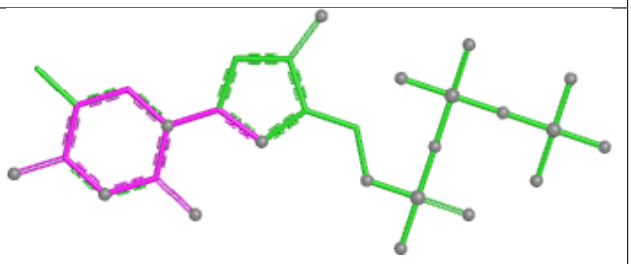


Rings

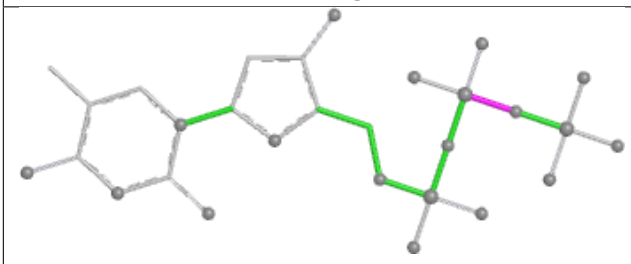
Ligand TTP A 1192



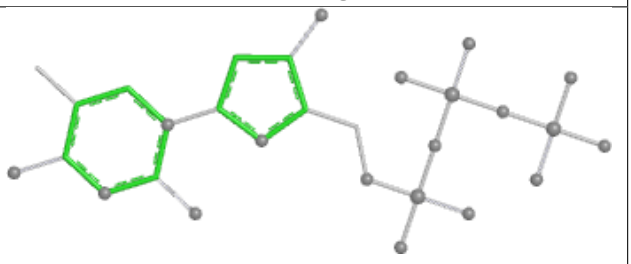
Bond lengths



Bond angles

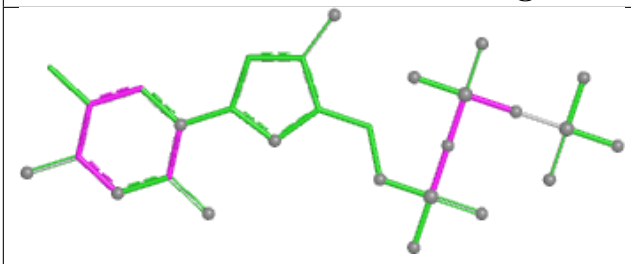


Torsions



Rings

Ligand TTP E 1192



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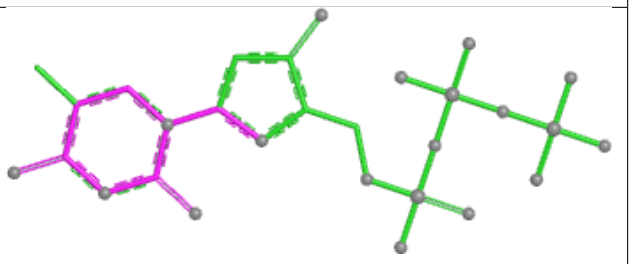
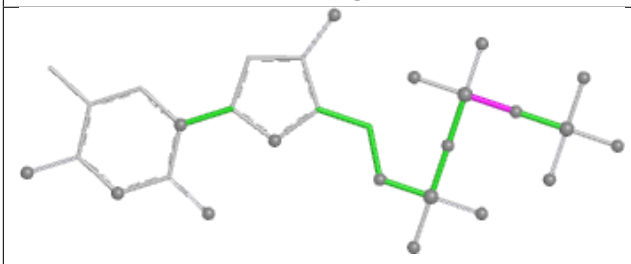
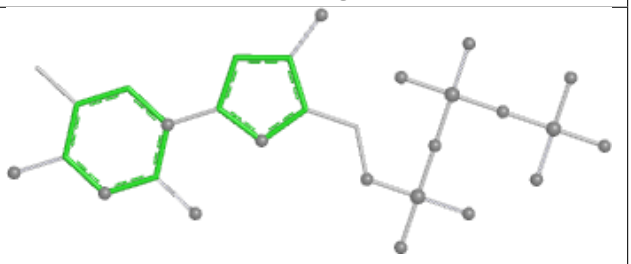


Bond angles

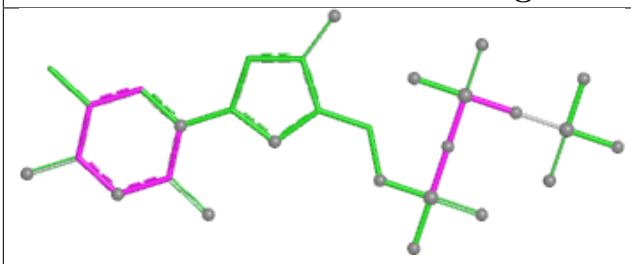


Torsions

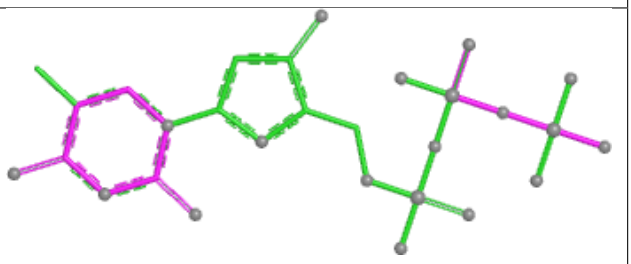


Rings

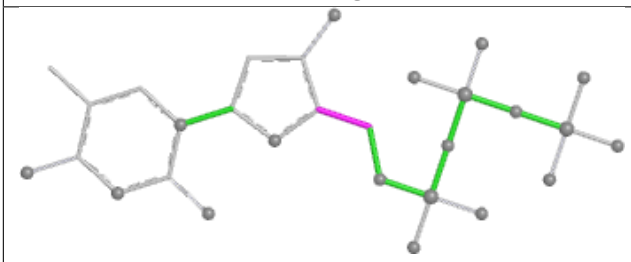
Ligand TTP D 1192



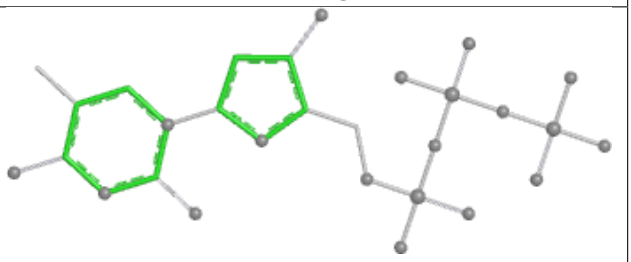
Bond lengths



Bond angles



Torsions



Rings

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled '#RSRZ> 2' contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled 'Q< 0.9' lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2			OWAB(Å^2)	Q<0.9
1	A	160/193 (82%)	-0.17	3 (1%)	66	63	10, 19, 30, 39	0
1	B	161/193 (83%)	-0.03	4 (2%)	58	55	9, 18, 31, 41	0
1	C	160/193 (82%)	-0.05	3 (1%)	66	63	11, 20, 33, 36	0
1	D	162/193 (83%)	-0.17	5 (3%)	51	48	10, 17, 28, 36	0
1	E	160/193 (82%)	-0.01	3 (1%)	66	63	12, 19, 32, 37	0
1	F	160/193 (82%)	-0.15	2 (1%)	75	73	11, 18, 30, 39	0
1	G	161/193 (83%)	-0.20	3 (1%)	66	63	10, 18, 27, 32	0
1	H	166/193 (86%)	-0.17	5 (3%)	52	49	9, 17, 30, 40	0
All	All	1290/1544 (83%)	-0.12	28 (2%)	62	59	9, 18, 31, 41	0

All (28) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	59	THR	5.0
1	D	75	ALA	3.7
1	D	61	TYR	3.4
1	H	63	SER	3.4
1	H	64	SER	3.4
1	G	75	ALA	3.3
1	B	75	ALA	2.9
1	F	158	ARG	2.7
1	H	73	MET	2.7
1	A	75	ALA	2.6
1	C	168	THR	2.6
1	F	59	THR	2.6
1	H	61	TYR	2.6
1	E	75	ALA	2.5
1	A	59	THR	2.5
1	D	158	ARG	2.4

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Mol	Chain	Res	Type	RSRZ
1	H	62	SER	2.3
1	B	18	ARG	2.3
1	E	59	THR	2.3
1	C	191	LYS	2.2
1	D	18	ARG	2.1
1	B	192	LYS	2.1
1	C	179	ASP	2.1
1	D	62	SER	2.1
1	A	54	LYS	2.1
1	E	18	ARG	2.0
1	G	18	ARG	2.0
1	G	170	LYS	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(Å^2)	Q<0.9
4	MG	D	1193	1/1	0.93	0.28	45,45,45,45	0
2	TTP	D	1192	29/29	0.95	0.07	11,13,23,23	0
2	TTP	E	1192	29/29	0.95	0.08	16,20,29,29	0
2	TTP	H	1192	29/29	0.95	0.07	10,12,21,22	0
2	TTP	C	1192	29/29	0.95	0.08	19,21,25,26	0
4	MG	G	1193	1/1	0.95	0.06	23,23,23,23	0
2	TTP	A	1192	29/29	0.96	0.07	16,17,23,25	0
2	TTP	F	1192	29/29	0.96	0.07	16,17,25,25	0
2	TTP	G	1192	29/29	0.96	0.07	10,12,19,19	0
2	TTP	B	1193	29/29	0.97	0.07	12,15,21,22	0
4	MG	H	1193	1/1	0.97	0.07	27,27,27,27	0

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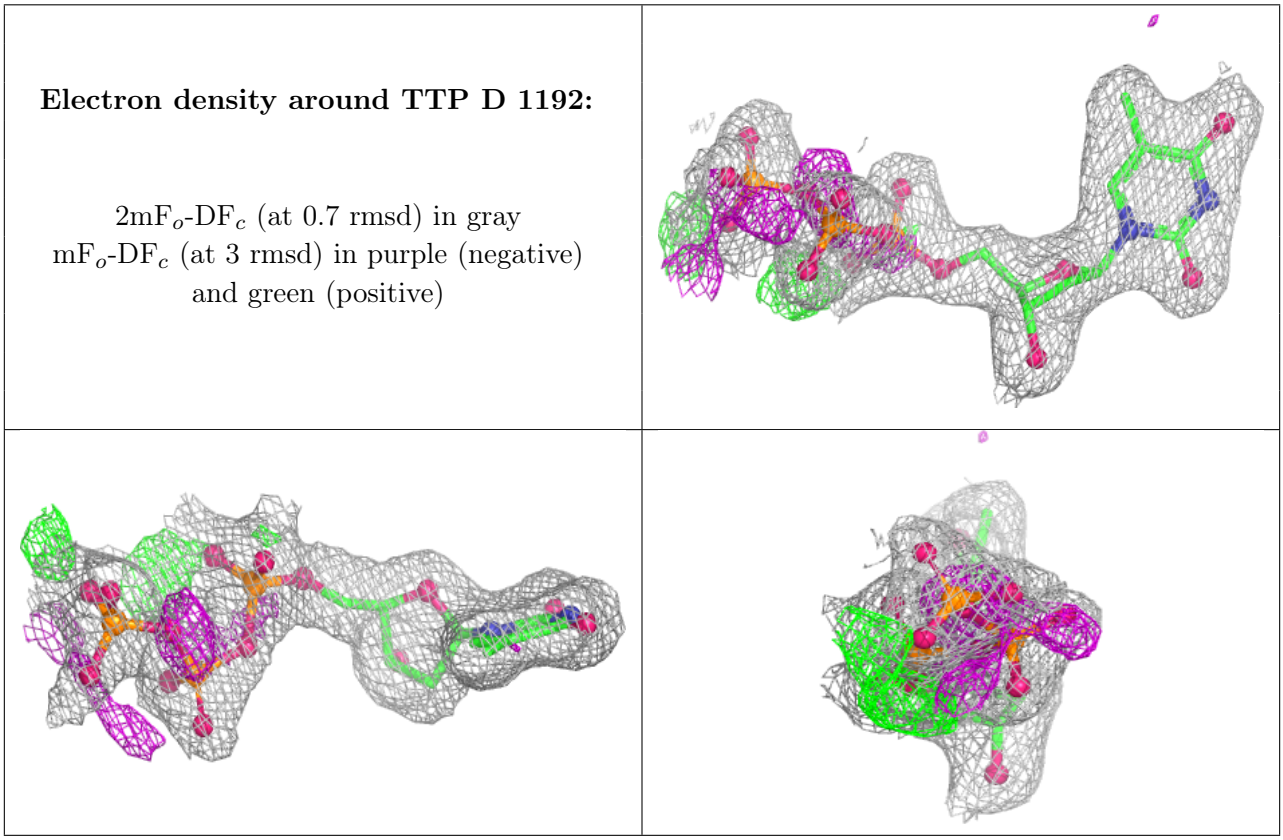
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
3	ZN	F	1193	1/1	0.99	0.02	21,21,21,21	0
3	ZN	G	1194	1/1	0.99	0.01	18,18,18,18	0
3	ZN	A	1193	1/1	0.99	0.01	19,19,19,19	0
3	ZN	C	1193	1/1	0.99	0.02	25,25,25,25	0
3	ZN	D	1194	1/1	0.99	0.01	21,21,21,21	0
3	ZN	B	1194	1/1	1.00	0.02	17,17,17,17	0
3	ZN	E	1193	1/1	1.00	0.01	21,21,21,21	0
3	ZN	H	1194	1/1	1.00	0.01	20,20,20,20	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.

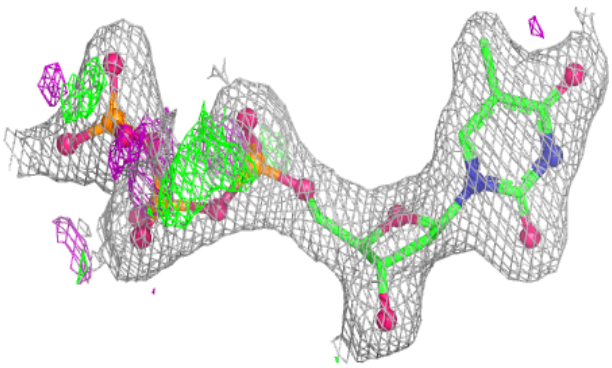
Electron density around TTP D 1192:

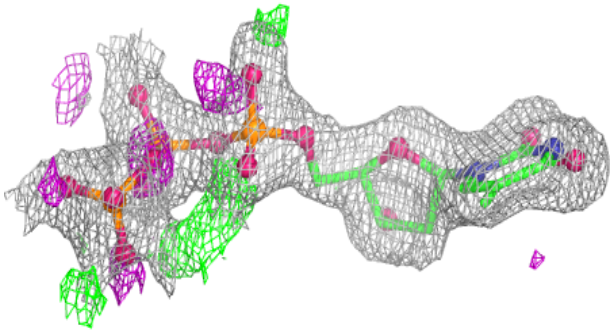
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

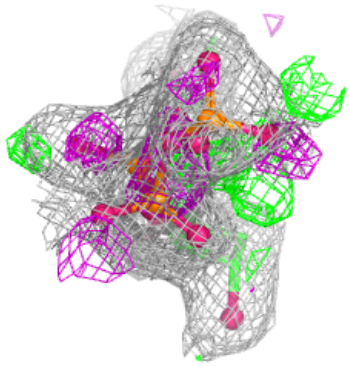


Electron density around TTP E 1192:

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

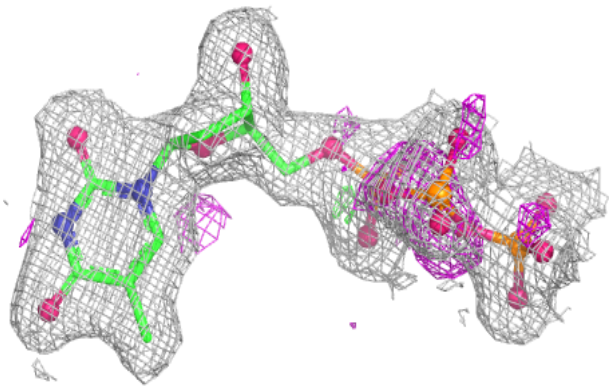


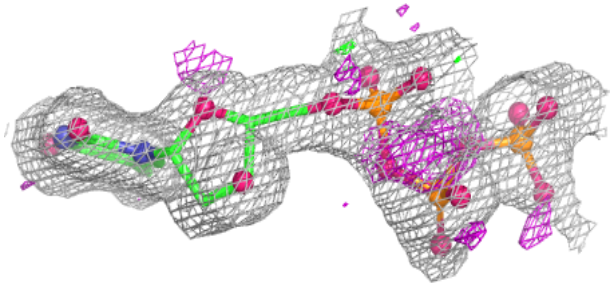


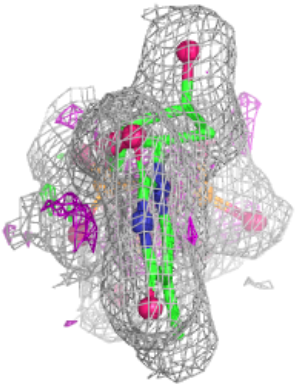


Electron density around TTP H 1192:

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

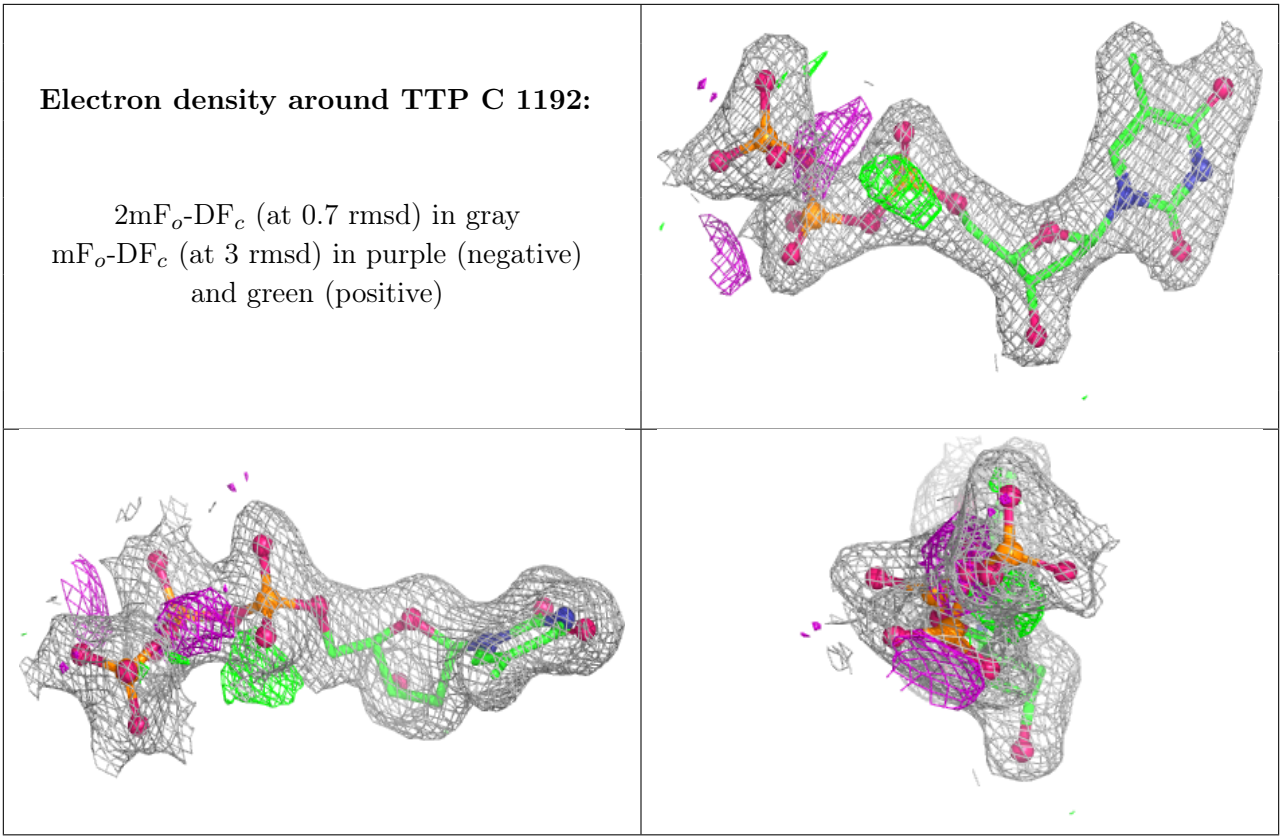






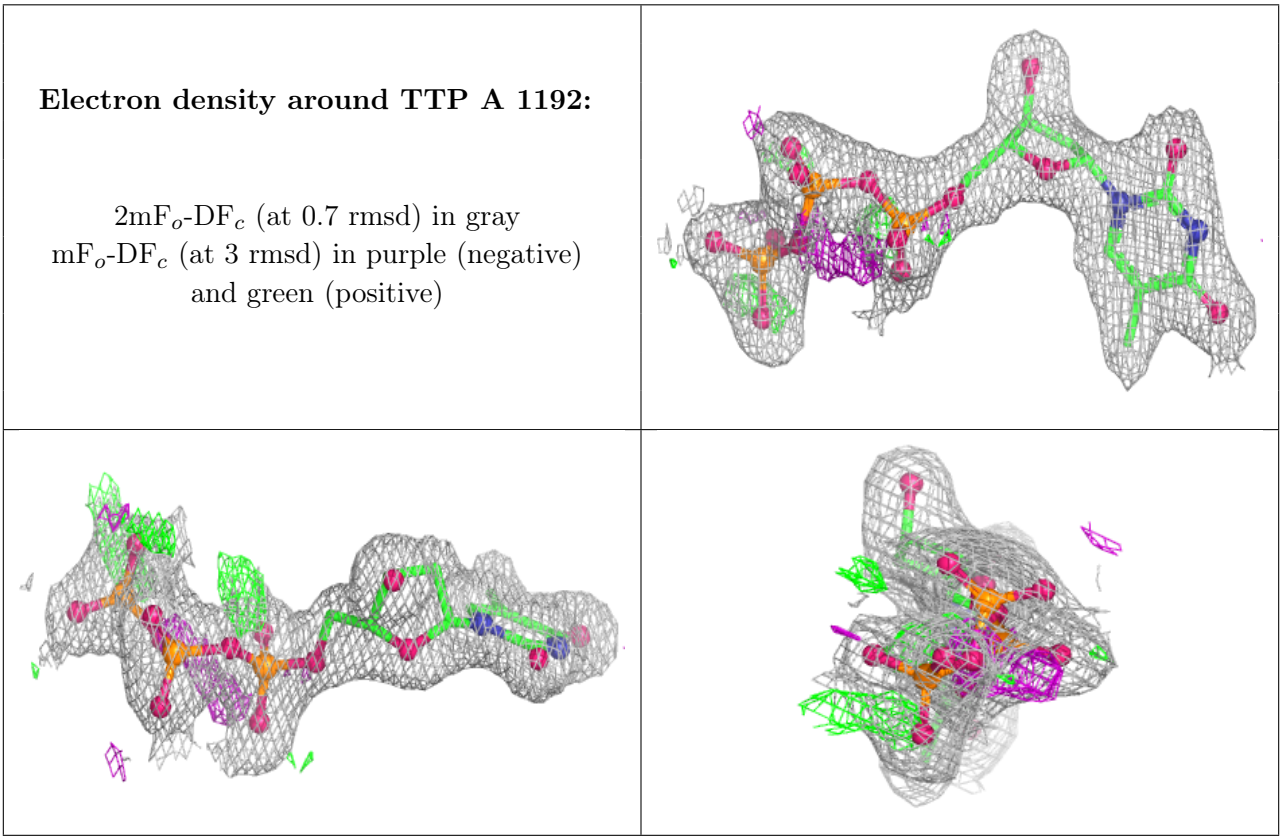
Electron density around TTP C 1192:

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



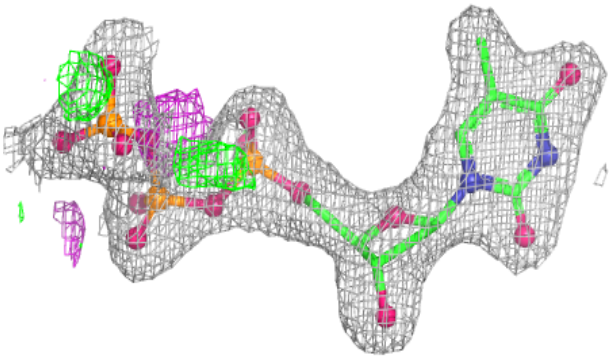
Electron density around TTP A 1192:

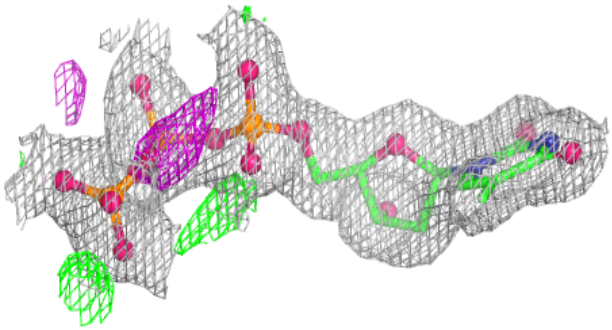
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)

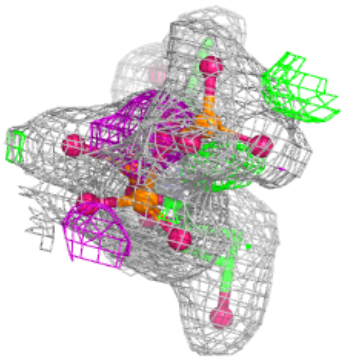


Electron density around TTP F 1192:

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

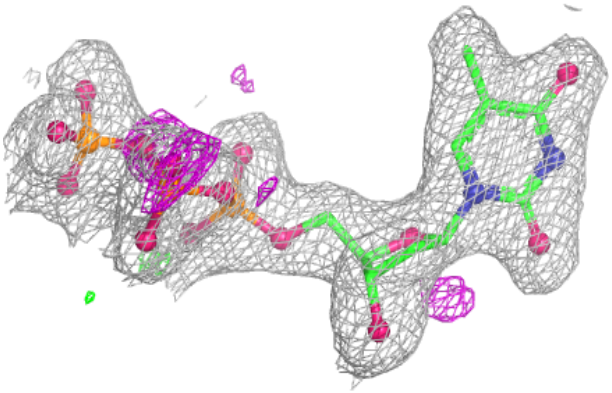


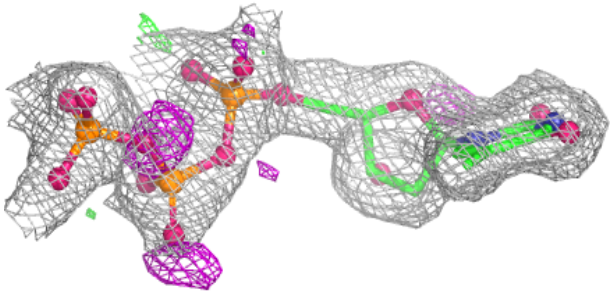


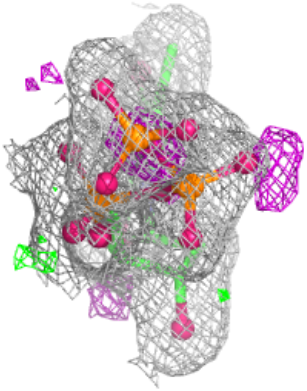


Electron density around TTP G 1192:

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

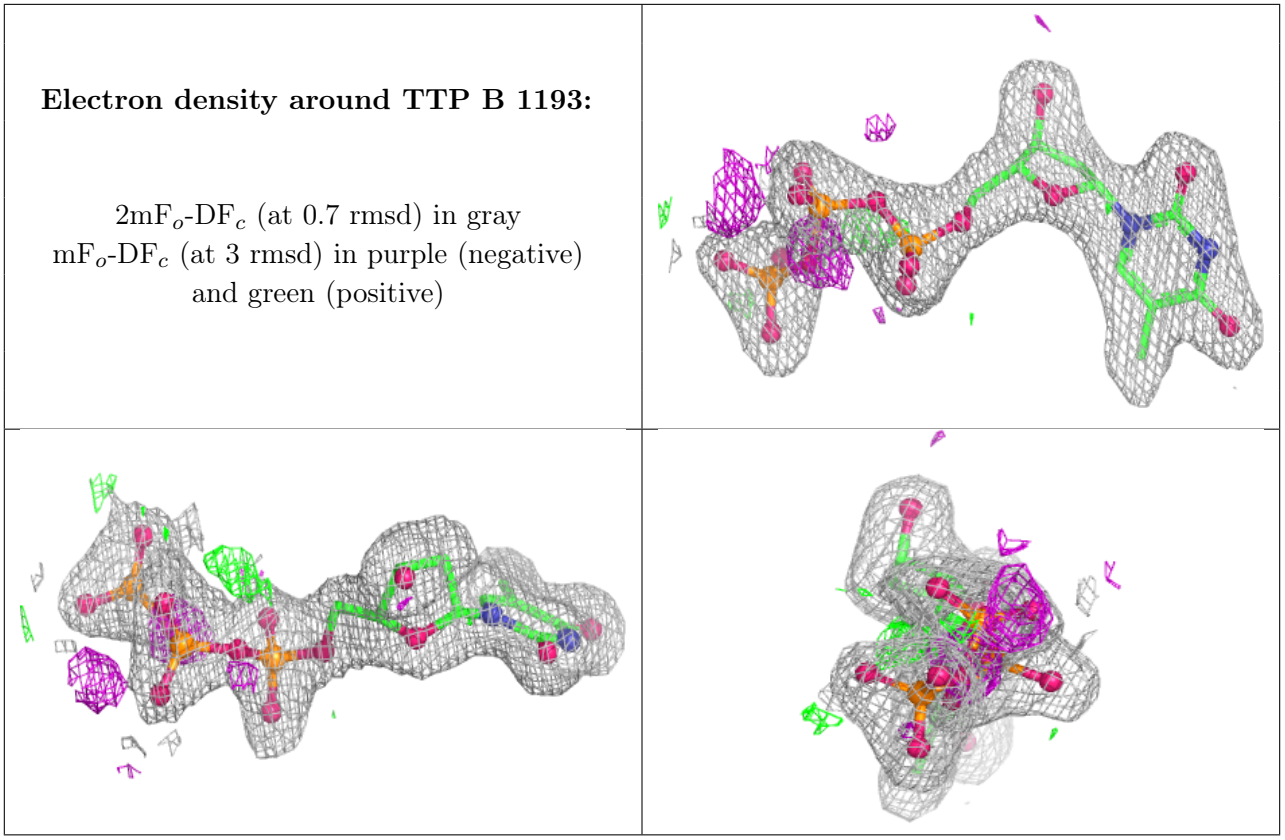






Electron density around TTP B 1193:

$2mF_o$-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.