Full wwPDB X-ray Structure Validation Report (i)

Apr 28, 2024 – 09:08 am BST

PDB ID	:	2IZ1
Title	:	6PDH complexed with PEX inhibitor synchrotron data
Authors	:	Sundaramoorthy, R.; Iulek, J.; Hunter, W.N.
Deposited on	:	2006-07-23
Resolution	:	2.30 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 (i) 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 (i)) were used in the production of this report:

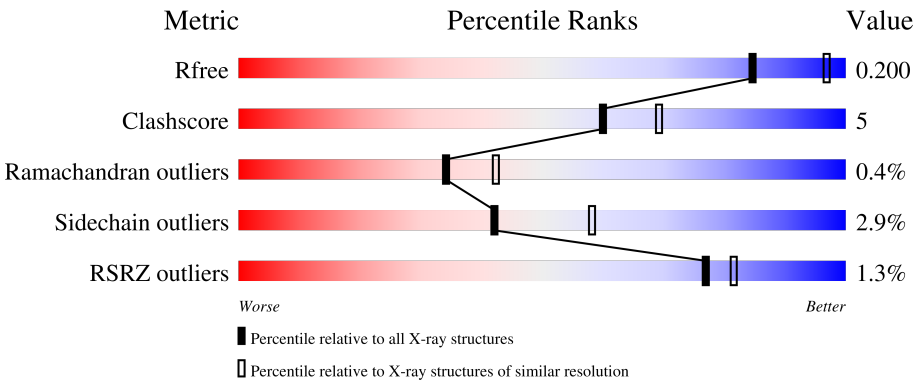
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36.2
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36.2

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 2.30 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	5042 (2.30-2.30)
Clashscore	141614	5643 (2.30-2.30)
Ramachandran outliers	138981	5575 (2.30-2.30)
Sidechain outliers	138945	5575 (2.30-2.30)
RSRZ outliers	127900	4938 (2.30-2.30)

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	474	2% 85% 13%
1	B	474	% 91% 7%
1	C	474	% 90% 9%

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ATR	A	1470[A]	X	-	-	-
2	ATR	A	1470[B]	X	-	-	-
2	ATR	B	1470[A]	X	-	-	-
2	ATR	B	1470[B]	X	-	-	-
2	ATR	C	1470[A]	X	-	-	-
2	ATR	C	1470[B]	X	-	-	-
4	P33	A	1472	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 13480 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.

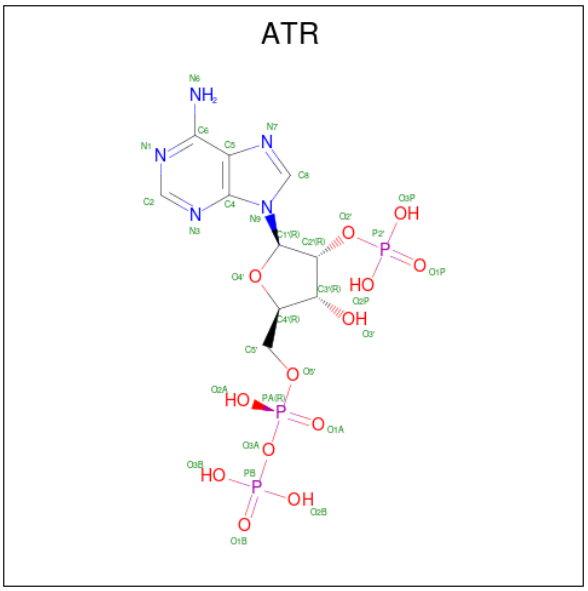
- Molecule 1 is a protein called 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	470	3814	2444	619	736	15	0	26	1
1	B	472	3795	2422	621	737	15	0	20	1
1	C	469	3780	2422	617	728	13	0	21	1

There are 9 discrepancies between the modelled and reference sequences:

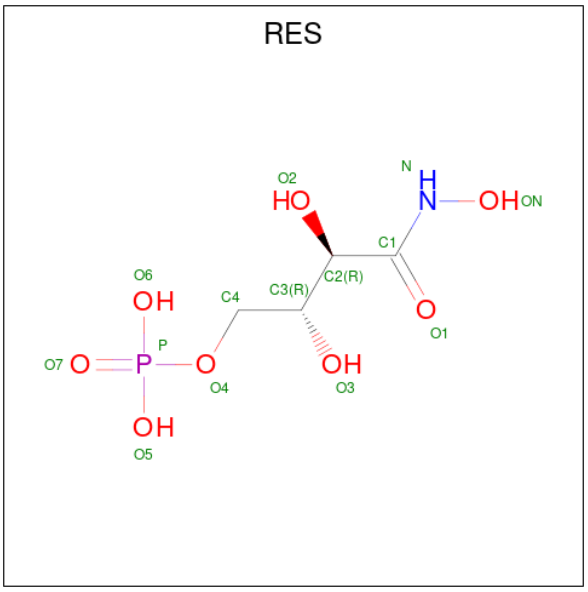
Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	HIS	-	expression tag	UNP P96789
A	0	HIS	-	expression tag	UNP P96789
A	43	PHE	TYR	conflict	UNP P96789
B	-1	HIS	-	expression tag	UNP P96789
B	0	HIS	-	expression tag	UNP P96789
B	43	PHE	TYR	conflict	UNP P96789
C	-1	HIS	-	expression tag	UNP P96789
C	0	HIS	-	expression tag	UNP P96789
C	43	PHE	TYR	conflict	UNP P96789

- Molecule 2 is 2'-MONOPHOSPHOADENOSINE-5'-DIPHOSPHATE (three-letter code: ATR) (formula: $C_{10}H_{16}N_5O_{13}P_3$).



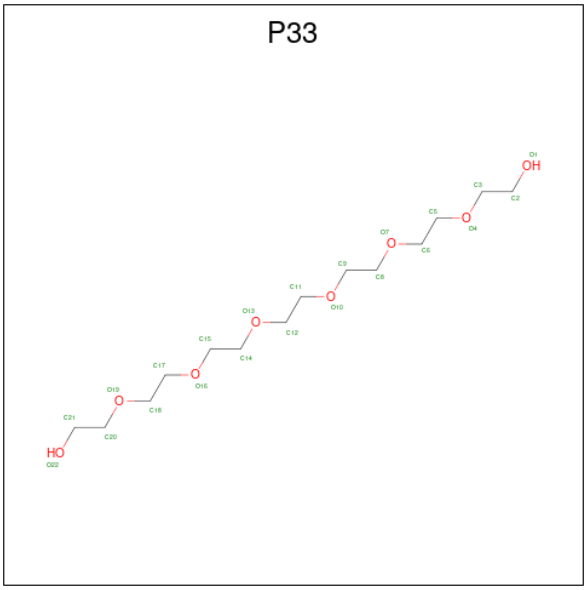
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
2	A	1	42	12	5	20	5	0	1
			Total	C	N	O	P		
2	B	1	42	12	5	20	5	0	1
			Total	C	N	O	P		
2	C	1	42	12	5	20	5	0	1

- Molecule 3 is 4-PHOSPHO-D-ERYTHRONOHYDROXAMIC ACID (three-letter code: RES) (formula: $C_4H_{10}NO_8P$).



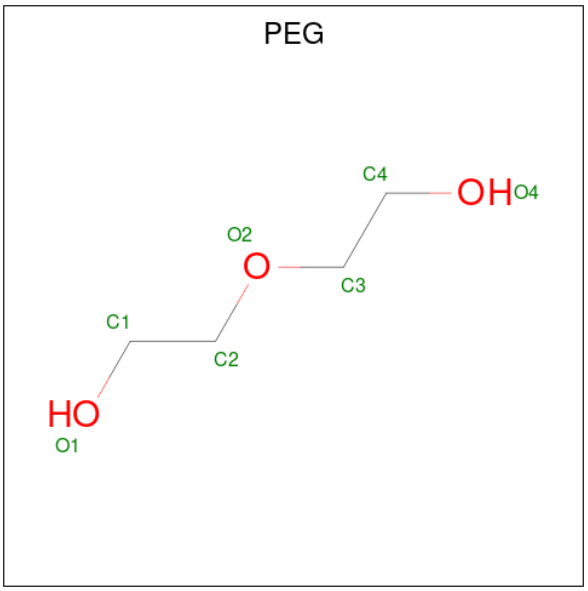
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
			Total	C	N	O	P		
3	A	1	14	4	1	8	1	0	0

- Molecule 4 is 3,6,9,12,15,18-HEXAOXAICOSANE-1,20-DIOL (three-letter code: P33) (formula: $C_{14}H_{30}O_8$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	O			
4	A	1	22	14	8		0	0
4	C	1	19	12	7		0	0

- Molecule 5 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: $C_4H_{10}O_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total C O 7 4 3	0	0

- Molecule 6 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	B	2	Total Cl 2 2	0	0
6	C	2	Total Cl 2 2	0	0

- Molecule 7 is water.

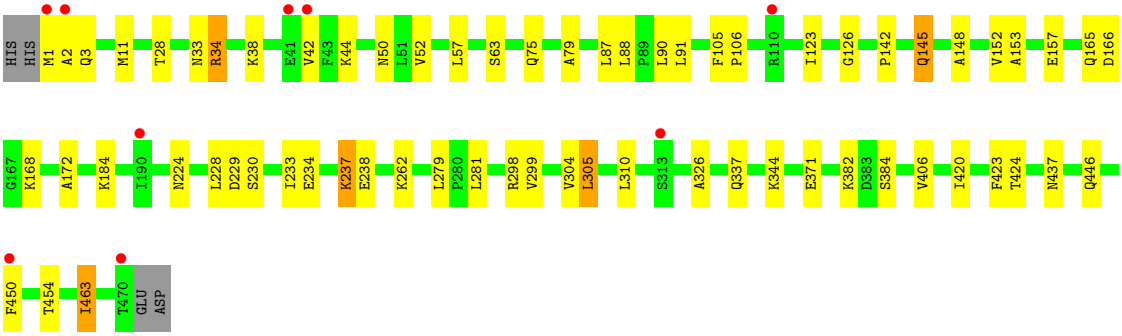
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	A	573	Total O 573 573	0	1
7	B	655	Total O 655 655	0	0
7	C	671	Total O 671 671	0	0

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.

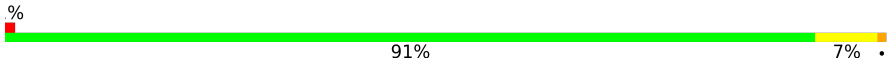
• Molecule 1: 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING

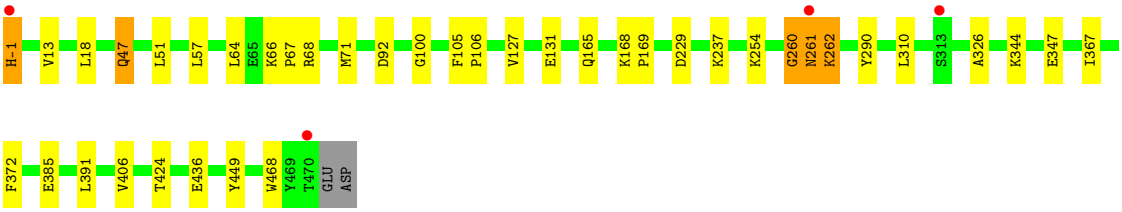
Chain A:



• Molecule 1: 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING

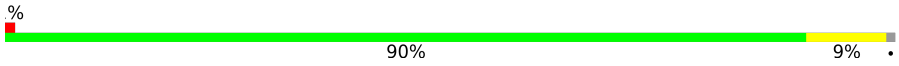
Chain B:

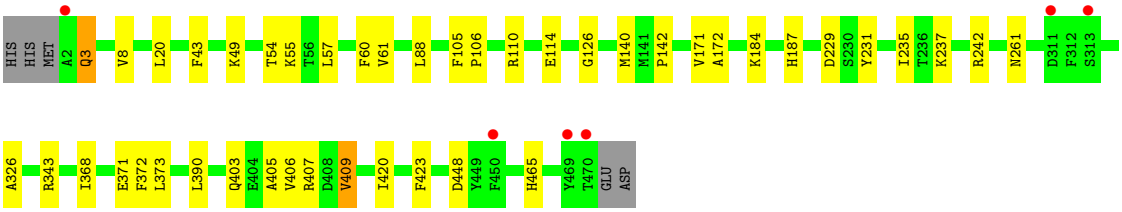




• Molecule 1: 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING

Chain C:





4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α, β, γ	71.07Å 104.88Å 240.54Å 90.00° 98.31° 90.00°	Depositor
Resolution (Å)	34.08 – 2.30 34.08 – 2.30	Depositor EDS
% Data completeness (in resolution range)	94.5 (34.08-2.30) 94.5 (34.08-2.30)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	8.85 (at 2.29Å)	Xtriage
Refinement program	REFMAC 5.2.0005	Depositor
R, R_{free}	0.137 , 0.198 0.139 , 0.200	Depositor DCC
R_{free} test set	3670 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å^2)	20.3	Xtriage
Anisotropy	0.580	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 60.8	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	0.011 for h,-k,-h-l	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	13480	wwPDB-VP
Average B, all atoms (Å^2)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.78% 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 (i)

5.1 Standard geometry (i)

Bond lengths and bond angles in the following residue types are not validated in this section: ATR, RES, P33, CL, PEG

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	0.47	0/3962	0.57	1/5348 (0.0%)
1	B	0.49	0/3930	0.55	0/5312
1	C	0.51	0/3916	0.57	0/5289
All	All	0.49	0/11808	0.56	1/15949 (0.0%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	298	ARG	NE-CZ-NH2	-5.25	117.68	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	260	GLY	Peptide

5.2 Too-close contacts (i)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen

atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	3814	0	3835	48	0
1	B	3795	0	3776	30	0
1	C	3780	0	3794	20	0
2	A	42	0	10	0	0
2	B	42	0	10	1	0
2	C	42	0	10	1	0
3	A	14	0	10	0	0
4	A	22	0	30	12	0
4	C	19	0	25	4	0
5	A	7	0	10	1	0
6	B	2	0	0	0	0
6	C	2	0	0	0	0
7	A	573	0	0	12	0
7	B	655	0	0	4	0
7	C	671	0	0	10	0
All	All	13480	0	11510	106	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 5.

All (106) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:28:THR:HB	7:A:2030:HOH:O	1.48	1.12
4:A:1472:P33:H32	7:C:2668:HOH:O	1.50	1.10
1:A:371:GLU:HG2	4:A:1472:P33:H212	1.44	0.97
4:A:1472:P33:H31	4:A:1472:P33:H92	1.51	0.93
4:C:1473:P33:H151	7:C:2667:HOH:O	1.73	0.87
1:A:371:GLU:HG2	4:A:1472:P33:C21	2.04	0.86
7:A:2340:HOH:O	1:B:262:LYS:HG3	1.81	0.80
4:A:1472:P33:H52	4:A:1472:P33:C9	2.13	0.78
1:A:28:THR:HG23	7:C:2294:HOH:O	1.83	0.78
1:C:49:LYS:O	4:C:1473:P33:H142	1.87	0.74
1:B:-1[A]:HIS:CE1	7:B:2003:HOH:O	2.43	0.72
2:B:1470[B]:ATR:H4'	2:B:1470[B]:ATR:O1A	1.91	0.69
1:A:145:GLN:HG2	7:A:2180:HOH:O	1.91	0.68
1:B:262:LYS:NZ	7:B:2425:HOH:O	2.25	0.68
4:A:1472:P33:H92	4:A:1472:P33:H52	1.77	0.67
1:C:326:ALA:HA	1:C:406:VAL:HG22	1.77	0.66

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:448:ASP:OD1	1:C:465:HIS:HD2	1.82	0.62
1:A:344[A]:LYS:HE3	7:A:2346:HOH:O	2.00	0.62
2:C:1470[A]:ATR:H4'	2:C:1470[A]:ATR:O1A	2.00	0.62
4:A:1472:P33:H92	4:A:1472:P33:C5	2.29	0.61
1:B:-1[A]:HIS:HE1	7:B:2003:HOH:O	1.81	0.61
1:B:261:ASN:O	1:B:262:LYS:HB2	2.00	0.60
1:A:424:THR:HB	1:B:424:THR:HB	1.85	0.57
1:A:142:PRO:HD2	1:A:172:ALA:O	2.05	0.57
1:B:326:ALA:HA	1:B:406:VAL:HG22	1.86	0.57
1:C:43:PHE:HE1	4:C:1473:P33:H172	1.70	0.57
1:C:3:GLN:NE2	7:C:2002:HOH:O	2.37	0.57
1:A:165:GLN:HG3	4:A:1472:P33:H152	1.87	0.56
1:C:261:ASN:ND2	7:C:2410:HOH:O	2.37	0.56
1:A:105:PHE:CD1	1:A:106:PRO:HD3	2.40	0.56
1:A:1[A]:MET:HB3	1:A:63:SER:HA	1.87	0.56
1:A:57:LEU:HD22	1:A:87:LEU:HD13	1.88	0.54
1:B:-1[A]:HIS:CD2	1:B:-1[A]:HIS:H1	2.26	0.53
1:B:68[B]:ARG:NH2	1:B:92:ASP:OD2	2.41	0.53
1:C:343[A]:ARG:NH1	7:C:2503:HOH:O	2.42	0.53
1:A:224:ASN:HD21	1:A:230:SER:H	1.55	0.53
1:B:-1[A]:HIS:CD2	1:B:-1[A]:HIS:H3	2.26	0.52
1:C:54:THR:HG21	1:C:60:PHE:HA	1.92	0.52
1:B:64:LEU:CB	1:B:68[B]:ARG:HG2	2.40	0.51
1:C:405:ALA:O	1:C:409:VAL:HG13	2.11	0.51
1:B:18[A]:LEU:HD21	1:B:71:MET:SD	2.51	0.51
1:A:28:THR:HG22	1:A:50:ASN:HB3	1.93	0.51
1:A:454:THR:HB	1:A:463:ILE:HD12	1.92	0.50
5:A:1473:PEG:H32	7:C:2669:HOH:O	2.12	0.50
1:B:13[B]:VAL:HG11	1:B:131:GLU:OE2	2.12	0.49
1:A:153:ALA:O	1:A:157:GLU:HG3	2.11	0.49
1:C:420:ILE:HB	1:C:423:PHE:HB2	1.94	0.49
1:C:57:LEU:O	1:C:61[A]:VAL:HG13	2.13	0.48
1:C:110:ARG:O	1:C:114:GLU:HG3	2.13	0.48
1:A:126:GLY:HA3	1:A:184:LYS:HB2	1.95	0.48
4:C:1473:P33:H182	4:C:1473:P33:H212	1.72	0.47
4:A:1472:P33:C3	7:C:2668:HOH:O	2.31	0.47
1:B:262:LYS:HE2	7:B:2427:HOH:O	2.14	0.47
1:A:299:VAL:HG22	1:B:436:GLU:HG3	1.97	0.47
1:C:105:PHE:CD1	1:C:106:PRO:HD3	2.50	0.47
1:B:64:LEU:HB2	1:B:68[B]:ARG:HG2	1.98	0.46
1:A:310[A]:LEU:HD12	7:A:2377:HOH:O	2.15	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:403:GLN:O	1:C:407:ARG:HG3	2.15	0.46
1:A:224:ASN:ND2	1:A:230:SER:H	2.14	0.46
1:A:234:GLU:O	1:A:237[A]:LYS:HG3	2.15	0.46
1:A:326:ALA:HA	1:A:406:VAL:HG22	1.98	0.46
7:A:2362:HOH:O	1:B:391:LEU:HD11	2.15	0.46
1:A:123[A]:ILE:HD11	1:A:148:ALA:HB1	1.97	0.46
1:A:371:GLU:HA	4:A:1472:P33:H211	1.97	0.46
1:B:105:PHE:CD1	1:B:106:PRO:HD3	2.50	0.46
1:A:437:ASN:ND2	7:A:2508:HOH:O	2.48	0.46
1:A:446:GLN:O	1:A:450[B]:PHE:CD2	2.69	0.46
1:C:126:GLY:HA3	1:C:184:LYS:HB2	1.97	0.46
1:A:463:ILE:O	1:A:463:ILE:HG13	2.14	0.45
1:A:304:VAL:HG12	1:A:305:LEU:HD13	1.97	0.45
1:A:11:MET:HB2	1:A:33:ASN:HB2	1.99	0.45
1:A:28:THR:CG2	7:C:2294:HOH:O	2.55	0.45
1:B:-1[A]:HIS:H3	1:B:-1[A]:HIS:HD2	1.64	0.45
1:B:449:TYR:HA	1:B:468:TRP:CD1	2.52	0.44
1:A:166:ASP:CG	1:A:168:LYS:HD3	2.38	0.44
1:A:371:GLU:HG2	4:A:1472:P33:H211	1.94	0.44
1:A:123[B]:ILE:HD13	1:A:152:VAL:HG21	1.99	0.44
1:A:420:ILE:HB	1:A:423:PHE:HB2	1.99	0.44
1:C:231:TYR:CE2	1:C:235:ILE:HD11	2.52	0.44
1:B:64:LEU:HB3	1:B:68[B]:ARG:HG2	2.00	0.44
1:A:262:LYS:NZ	7:A:2334:HOH:O	2.52	0.43
1:B:47[A]:GLN:NE2	1:B:47[A]:GLN:H	2.16	0.43
1:A:237[B]:LYS:NZ	1:A:238:GLU:OE2	2.50	0.42
4:A:1472:P33:C12	4:A:1472:P33:H81	2.49	0.42
1:A:228:LEU:HB3	1:A:233:ILE:HD13	2.02	0.42
1:A:279:LEU:HD12	1:A:337:GLN:HB3	2.01	0.42
1:A:52:VAL:HG23	7:A:2030:HOH:O	2.19	0.41
1:A:450[B]:PHE:CD2	1:B:367:ILE:CD1	3.03	0.41
1:A:454:THR:CB	1:A:463:ILE:HD12	2.51	0.41
1:A:281:LEU:HB2	7:A:2493:HOH:O	2.21	0.41
1:A:384:SER:HB3	7:A:2448:HOH:O	2.21	0.41
1:A:450[B]:PHE:CD2	1:B:367:ILE:HD11	2.56	0.41
1:B:262:LYS:HD2	1:B:290:TYR:CE1	2.56	0.41
1:C:187:HIS:CD2	1:C:368:ILE:HG12	2.56	0.41
1:C:142:PRO:HD2	1:C:172:ALA:O	2.21	0.40
1:A:75:GLN:O	1:A:79:ALA:HB3	2.21	0.40
1:A:382[B]:LYS:NZ	7:A:2441:HOH:O	2.45	0.40
1:B:100:GLY:O	1:B:127[B]:VAL:HG22	2.20	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:MET:HB2	1:C:171:VAL:HG23	2.03	0.40
1:C:242:ARG:HD3	7:C:2379:HOH:O	2.22	0.40
1:B:168:LYS:HA	1:B:169:PRO:HD3	1.91	0.40
1:B:260:GLY:O	1:B:261:ASN:OD1	2.39	0.40
1:B:66:LYS:HA	1:B:67:PRO:C	2.42	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	492/474 (104%)	478 (97%)	12 (2%)	2 (0%)	34	42
1	B	489/474 (103%)	475 (97%)	12 (2%)	2 (0%)	34	42
1	C	488/474 (103%)	474 (97%)	12 (2%)	2 (0%)	34	42
All	All	1469/1422 (103%)	1427 (97%)	36 (2%)	6 (0%)	34	42

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	2	ALA
1	C	3	GLN
1	B	261	ASN
1	A	229	ASP
1	B	229	ASP
1	C	229	ASP

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	410/390 (105%)	398 (97%)	12 (3%)	42	58
1	B	407/390 (104%)	390 (96%)	17 (4%)	30	42
1	C	405/390 (104%)	393 (97%)	12 (3%)	41	57
All	All	1222/1170 (104%)	1181 (97%)	41 (3%)	42	51

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	34	ARG
1	A	38	LYS
1	A	42	VAL
1	A	44	LYS
1	A	88	LEU
1	A	90	LEU
1	A	91	LEU
1	A	145	GLN
1	A	237[A]	LYS
1	A	237[B]	LYS
1	A	305	LEU
1	A	463	ILE
1	B	-1[A]	HIS
1	B	-1[B]	HIS
1	B	47[A]	GLN
1	B	47[B]	GLN
1	B	51	LEU
1	B	57	LEU
1	B	165	GLN
1	B	237	LYS
1	B	254	LYS
1	B	262	LYS
1	B	310	LEU
1	B	344	LYS
1	B	347[A]	GLU
1	B	347[B]	GLU
1	B	372	PHE
1	B	385[A]	GLU
1	B	385[B]	GLU
1	C	8	VAL

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	C	20	LEU
1	C	55	LYS
1	C	88	LEU
1	C	237	LYS
1	C	371[A]	GLU
1	C	371[B]	GLU
1	C	372	PHE
1	C	373	LEU
1	C	390[A]	LEU
1	C	390[B]	LEU
1	C	409	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	HIS
1	A	47	GLN
1	A	224	ASN
1	A	437	ASN
1	B	102	ASN
1	B	261	ASN
1	C	3	GLN
1	C	47	GLN
1	C	217	GLN
1	C	261	ASN
1	C	437	ASN
1	C	465	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 14 ligands modelled in this entry, 4 are monoatomic - leaving 10 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	ATR	C	1470[B]	-	27,33,33	1.06	1 (3%)	35,52,52	1.28	3 (8%)
2	ATR	B	1470[B]	-	27,33,33	0.94	1 (3%)	35,52,52	1.36	3 (8%)
3	RES	A	1471	-	12,13,13	0.57	0	14,18,18	0.87	0
4	P33	C	1473	-	18,18,21	0.60	0	17,17,20	0.54	0
2	ATR	A	1470[A]	-	27,33,33	0.96	1 (3%)	35,52,52	1.31	2 (5%)
2	ATR	C	1470[A]	-	27,33,33	1.06	1 (3%)	35,52,52	1.37	5 (14%)
4	P33	A	1472	-	21,21,21	0.61	0	20,20,20	0.68	0
2	ATR	B	1470[A]	-	27,33,33	0.92	1 (3%)	35,52,52	1.24	1 (2%)
2	ATR	A	1470[B]	-	27,33,33	0.96	1 (3%)	35,52,52	1.30	2 (5%)
5	PEG	A	1473	-	6,6,6	0.41	0	5,5,5	0.37	0

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the Chemical Component Dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ATR	C	1470[B]	-	1/1/7/7	6/17/37/37	0/3/3/3
2	ATR	B	1470[B]	-	1/1/7/7	6/17/37/37	0/3/3/3
3	RES	A	1471	-	-	2/16/16/16	-
4	P33	C	1473	-	-	7/16/16/19	-
2	ATR	A	1470[A]	-	1/1/7/7	3/17/37/37	0/3/3/3
2	ATR	C	1470[A]	-	1/1/7/7	4/17/37/37	0/3/3/3
4	P33	A	1472	-	-	13/19/19/19	-
2	ATR	B	1470[A]	-	1/1/7/7	5/17/37/37	0/3/3/3
2	ATR	A	1470[B]	-	1/1/7/7	6/17/37/37	0/3/3/3
5	PEG	A	1473	-	-	3/4/4/4	-

All (6) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	1470[A]	ATR	O4'-C1'	3.28	1.45	1.41
2	C	1470[B]	ATR	O4'-C1'	3.28	1.45	1.41
2	A	1470[A]	ATR	O4'-C1'	3.09	1.45	1.41
2	A	1470[B]	ATR	O4'-C1'	3.09	1.45	1.41
2	B	1470[A]	ATR	O4'-C1'	2.53	1.44	1.41
2	B	1470[B]	ATR	O4'-C1'	2.53	1.44	1.41

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	1470[A]	ATR	N3-C2-N1	-5.00	120.87	128.68
2	A	1470[B]	ATR	N3-C2-N1	-5.00	120.87	128.68
2	B	1470[A]	ATR	N3-C2-N1	-4.80	121.17	128.68
2	B	1470[B]	ATR	N3-C2-N1	-4.80	121.17	128.68
2	C	1470[A]	ATR	N3-C2-N1	-4.22	122.08	128.68
2	C	1470[B]	ATR	N3-C2-N1	-4.22	122.08	128.68
2	C	1470[A]	ATR	O2'-C2'-C1'	2.79	120.15	110.10
2	C	1470[B]	ATR	O2'-C2'-C1'	2.79	120.15	110.10
2	C	1470[A]	ATR	C2'-C3'-C4'	-2.53	96.49	101.99
2	B	1470[B]	ATR	O4'-C4'-C5'	2.41	117.30	109.37
2	C	1470[A]	ATR	C4-C5-N7	-2.32	106.98	109.40
2	C	1470[B]	ATR	C4-C5-N7	-2.32	106.98	109.40
2	B	1470[B]	ATR	C2'-C3'-C4'	-2.31	96.97	101.99
2	C	1470[A]	ATR	O4'-C4'-C5'	2.22	116.69	109.37
2	A	1470[A]	ATR	O2'-P2'-O1P	-2.03	101.57	109.39
2	A	1470[B]	ATR	O2'-P2'-O1P	-2.03	101.57	109.39

All (6) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
2	A	1470[A]	ATR	C4'
2	A	1470[B]	ATR	C4'
2	B	1470[A]	ATR	C4'
2	B	1470[B]	ATR	C4'
2	C	1470[A]	ATR	C4'
2	C	1470[B]	ATR	C4'

All (55) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1470[A]	ATR	C2'-O2'-P2'-O1P

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	A	1470[B]	ATR	C5'-O5'-PA-O2A
2	A	1470[B]	ATR	C2'-O2'-P2'-O1P
2	B	1470[A]	ATR	C5'-O5'-PA-O3A
2	B	1470[B]	ATR	C4'-C5'-O5'-PA
2	C	1470[A]	ATR	C4'-C5'-O5'-PA
2	C	1470[A]	ATR	C3'-C4'-C5'-O5'
2	C	1470[B]	ATR	C5'-O5'-PA-O1A
2	C	1470[B]	ATR	C5'-O5'-PA-O3A
4	A	1472	P33	C9-C8-O7-C6
5	A	1473	PEG	O2-C3-C4-O4
4	A	1472	P33	C5-C6-O7-C8
2	B	1470[B]	ATR	O4'-C4'-C5'-O5'
4	A	1472	P33	O16-C17-C18-O19
4	C	1473	P33	O16-C17-C18-O19
4	A	1472	P33	O10-C11-C12-O13
4	C	1473	P33	C21-C20-O19-C18
4	A	1472	P33	O7-C8-C9-O10
2	A	1470[A]	ATR	C4'-C5'-O5'-PA
4	A	1472	P33	O4-C5-C6-O7
4	C	1473	P33	O19-C20-C21-O22
4	C	1473	P33	O7-C8-C9-O10
2	C	1470[A]	ATR	O4'-C4'-C5'-O5'
2	B	1470[B]	ATR	PB-O3A-PA-O1A
4	A	1472	P33	C11-C12-O13-C14
4	A	1472	P33	C8-C9-O10-C11
2	B	1470[A]	ATR	C4'-C5'-O5'-PA
2	B	1470[B]	ATR	PB-O3A-PA-O5'
4	A	1472	P33	C2-C3-O4-C5
5	A	1473	PEG	C1-C2-O2-C3
2	A	1470[B]	ATR	C5'-O5'-PA-O3A
2	C	1470[A]	ATR	C2'-O2'-P2'-O3P
2	C	1470[B]	ATR	C2'-O2'-P2'-O3P
5	A	1473	PEG	O1-C1-C2-O2
4	C	1473	P33	C8-C9-O10-C11
4	C	1473	P33	C11-C12-O13-C14
3	A	1471	RES	C3-C4-O4-P
2	B	1470[A]	ATR	C5'-O5'-PA-O1A
2	B	1470[A]	ATR	C5'-O5'-PA-O2A
2	C	1470[B]	ATR	C5'-O5'-PA-O2A
4	A	1472	P33	C17-C18-O19-C20
2	C	1470[B]	ATR	C4'-C5'-O5'-PA
4	C	1473	P33	C12-C11-O10-C9

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
4	A	1472	P33	C6-C5-O4-C3
4	A	1472	P33	C18-C17-O16-C15
3	A	1471	RES	C4-O4-P-O5
2	B	1470[A]	ATR	C2'-O2'-P2'-O3P
2	B	1470[B]	ATR	C2'-O2'-P2'-O3P
2	A	1470[B]	ATR	C4'-C5'-O5'-PA
2	A	1470[B]	ATR	C3'-C4'-C5'-O5'
2	B	1470[B]	ATR	C3'-C4'-C5'-O5'
4	A	1472	P33	C15-C14-O13-C12
2	A	1470[B]	ATR	C5'-O5'-PA-O1A
2	A	1470[A]	ATR	O4'-C4'-C5'-O5'
2	C	1470[B]	ATR	PA-O3A-PB-O1B

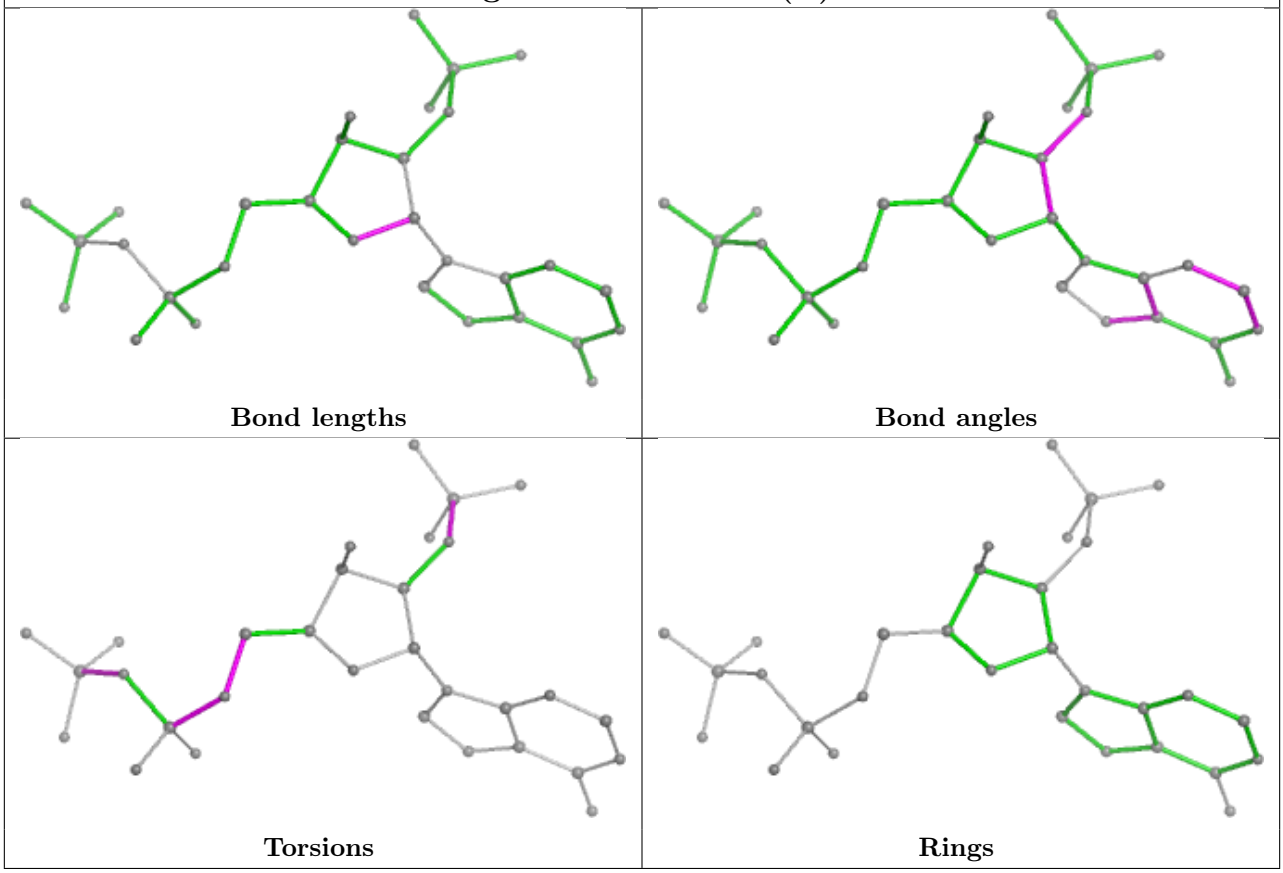
There are no ring outliers.

5 monomers are involved in 19 short contacts:

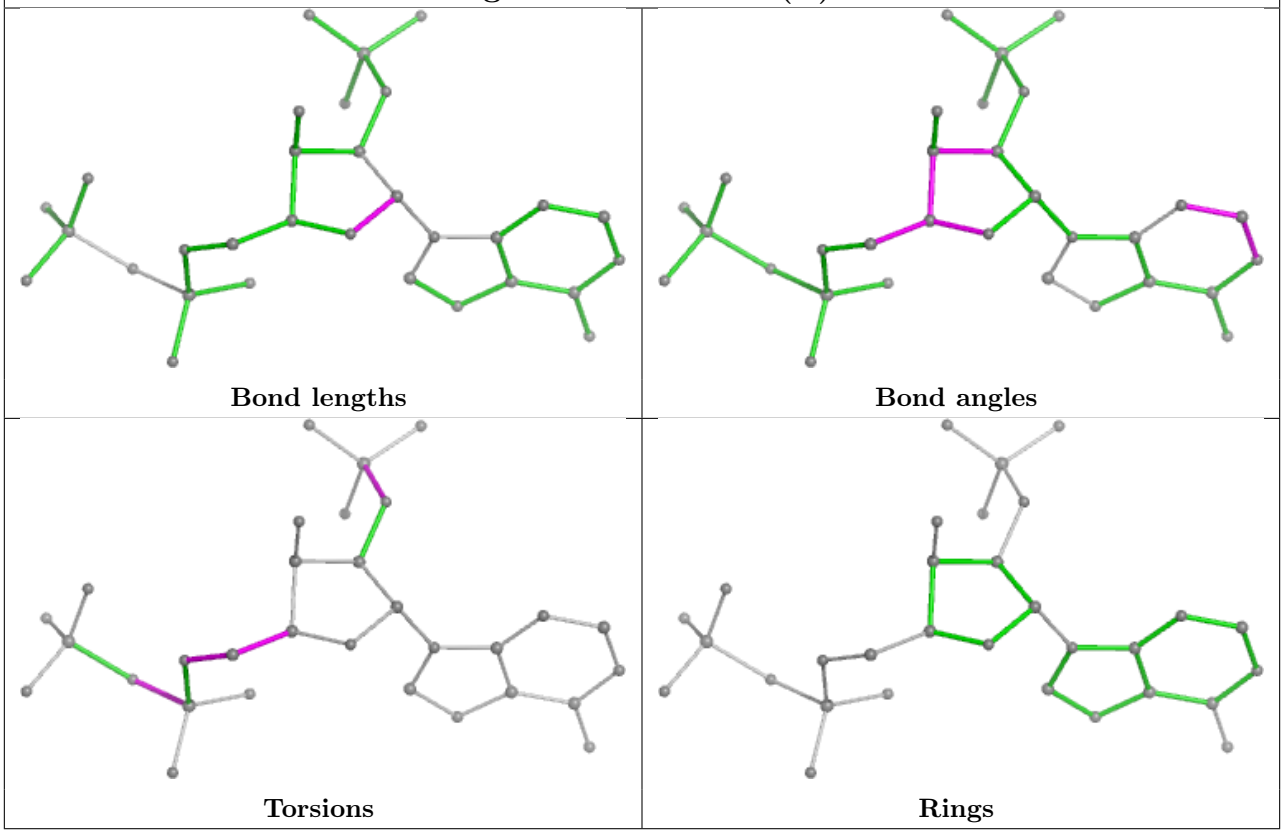
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1470[B]	ATR	1	0
4	C	1473	P33	4	0
2	C	1470[A]	ATR	1	0
4	A	1472	P33	12	0
5	A	1473	PEG	1	0

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.

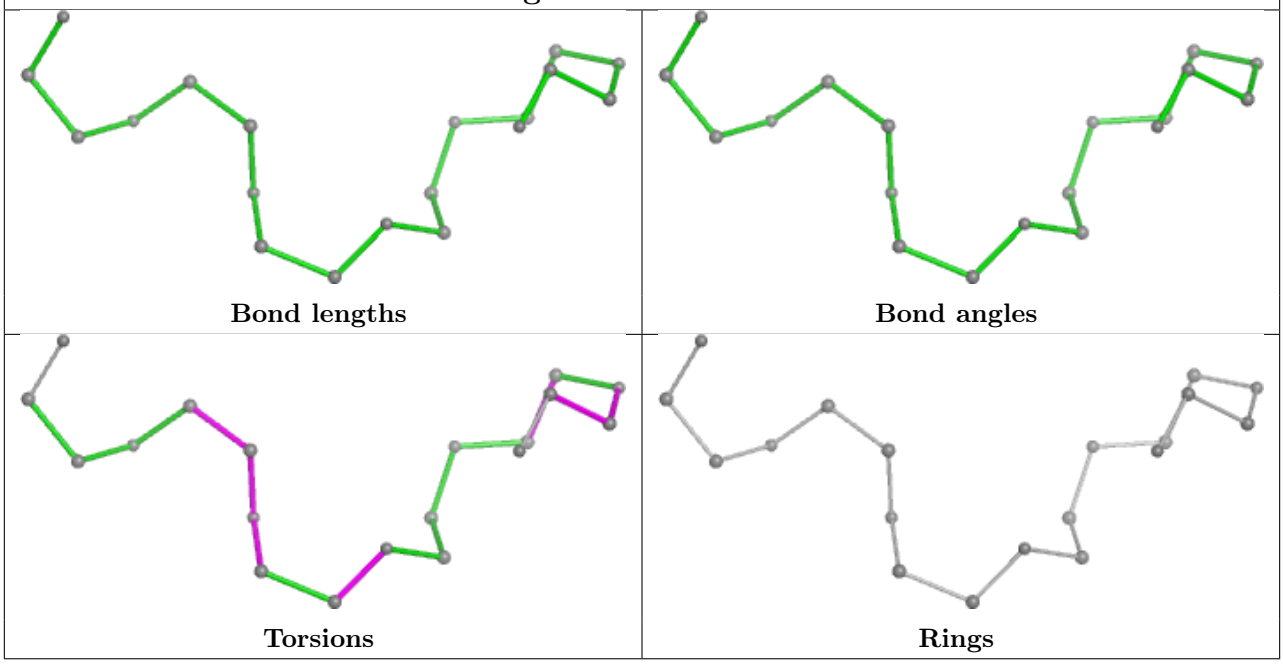
Ligand ATR C 1470 (B)



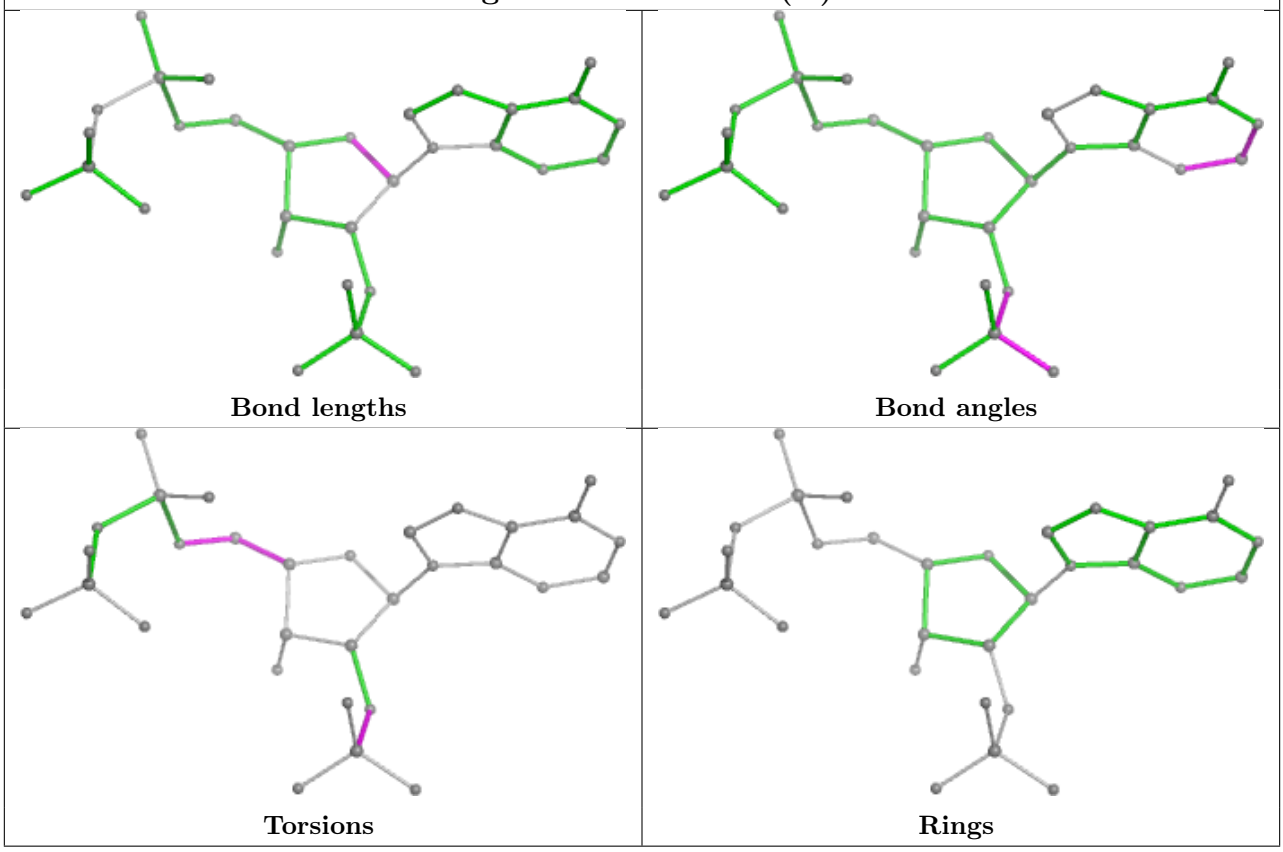
Ligand ATR B 1470 (B)



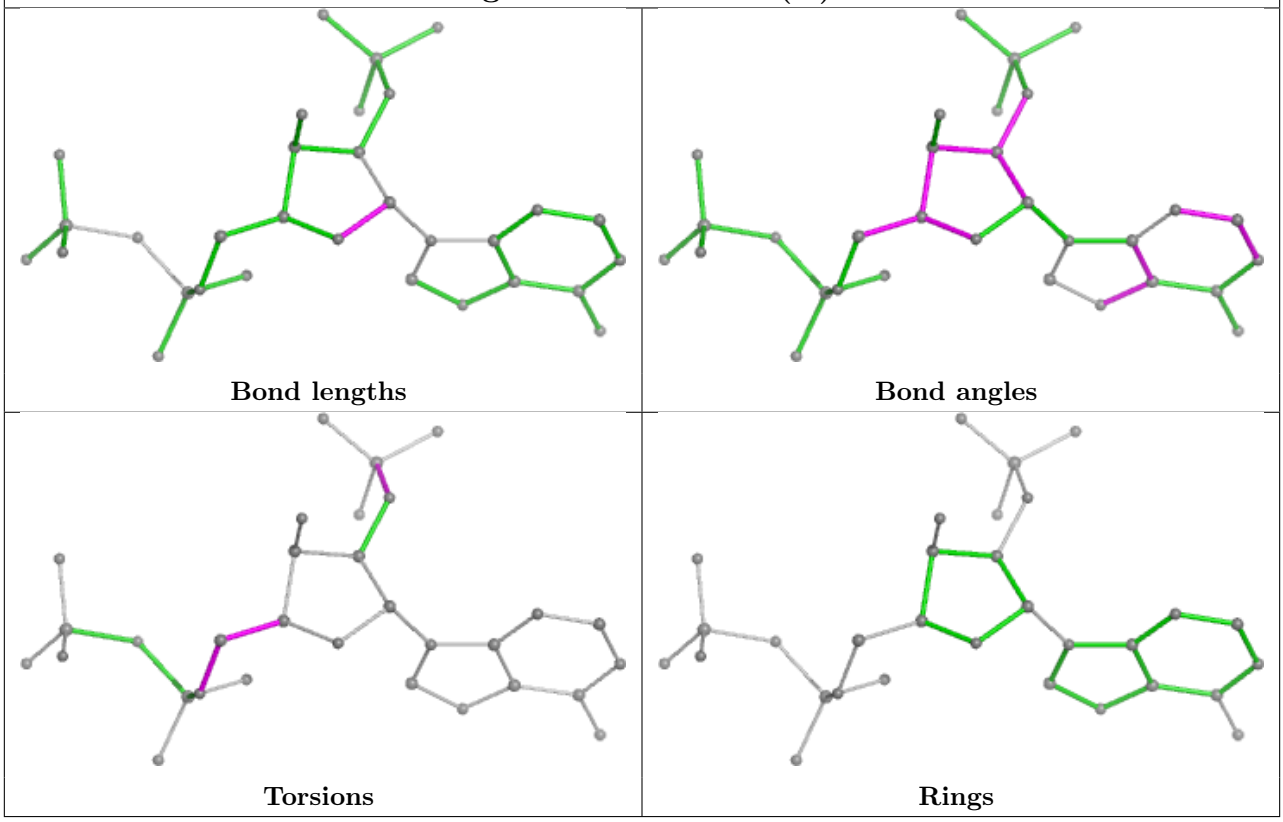
Ligand P33 C 1473



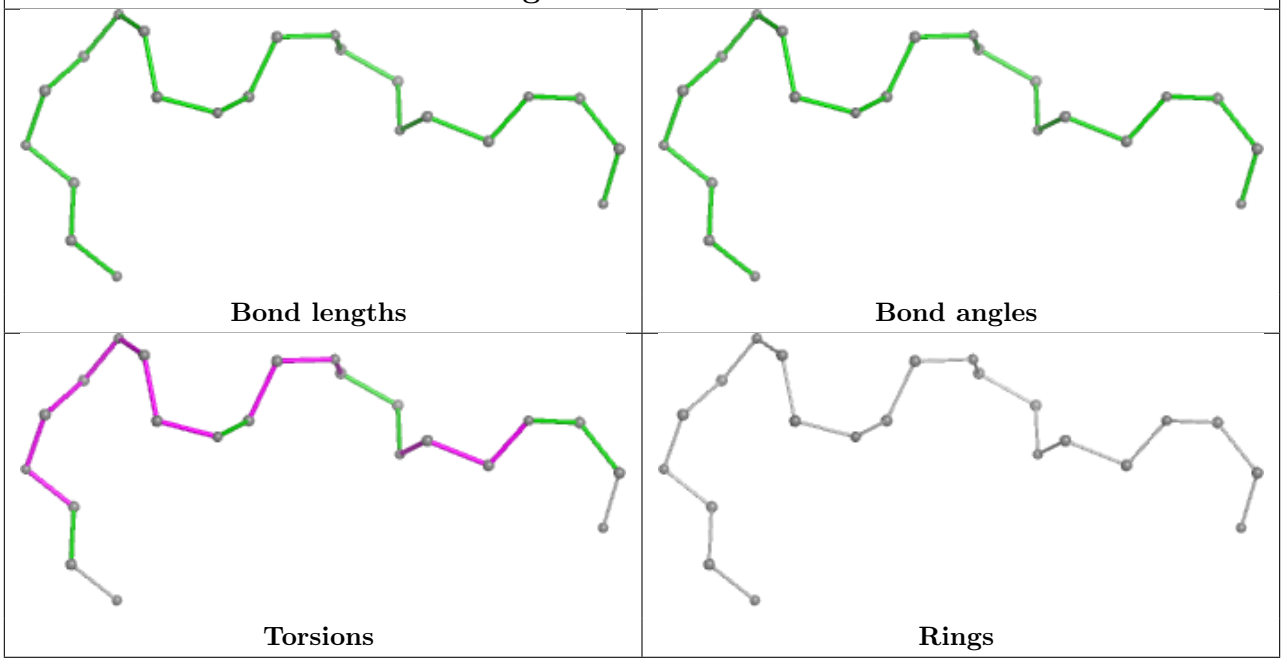
Ligand ATR A 1470 (A)



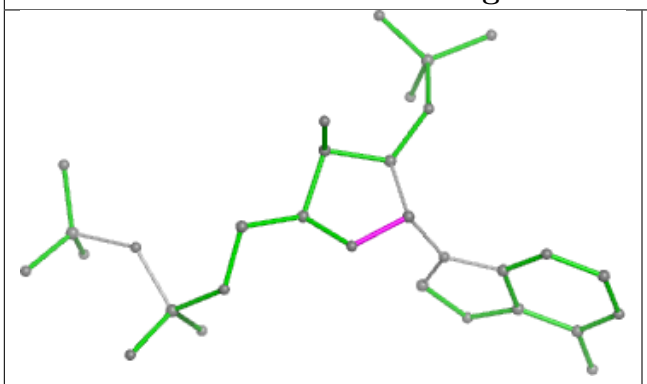
Ligand ATR C 1470 (A)



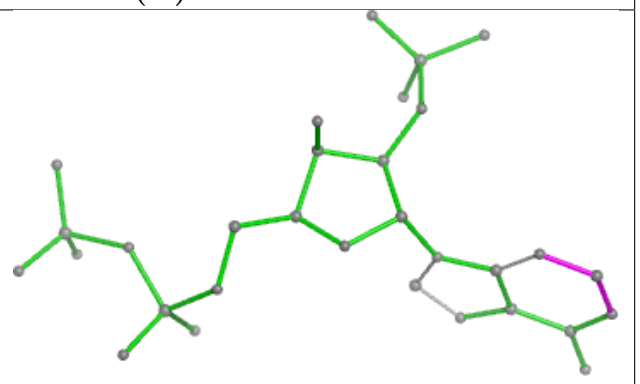
Ligand P33 A 1472



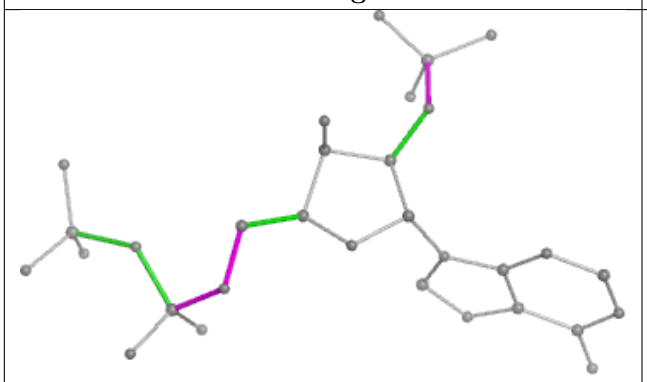
Ligand ATR B 1470 (A)



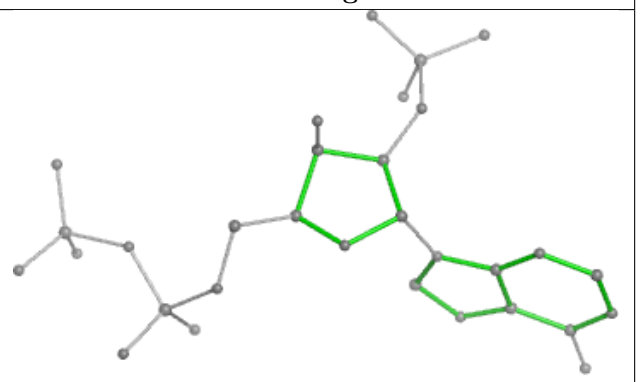
Bond lengths



Bond angles

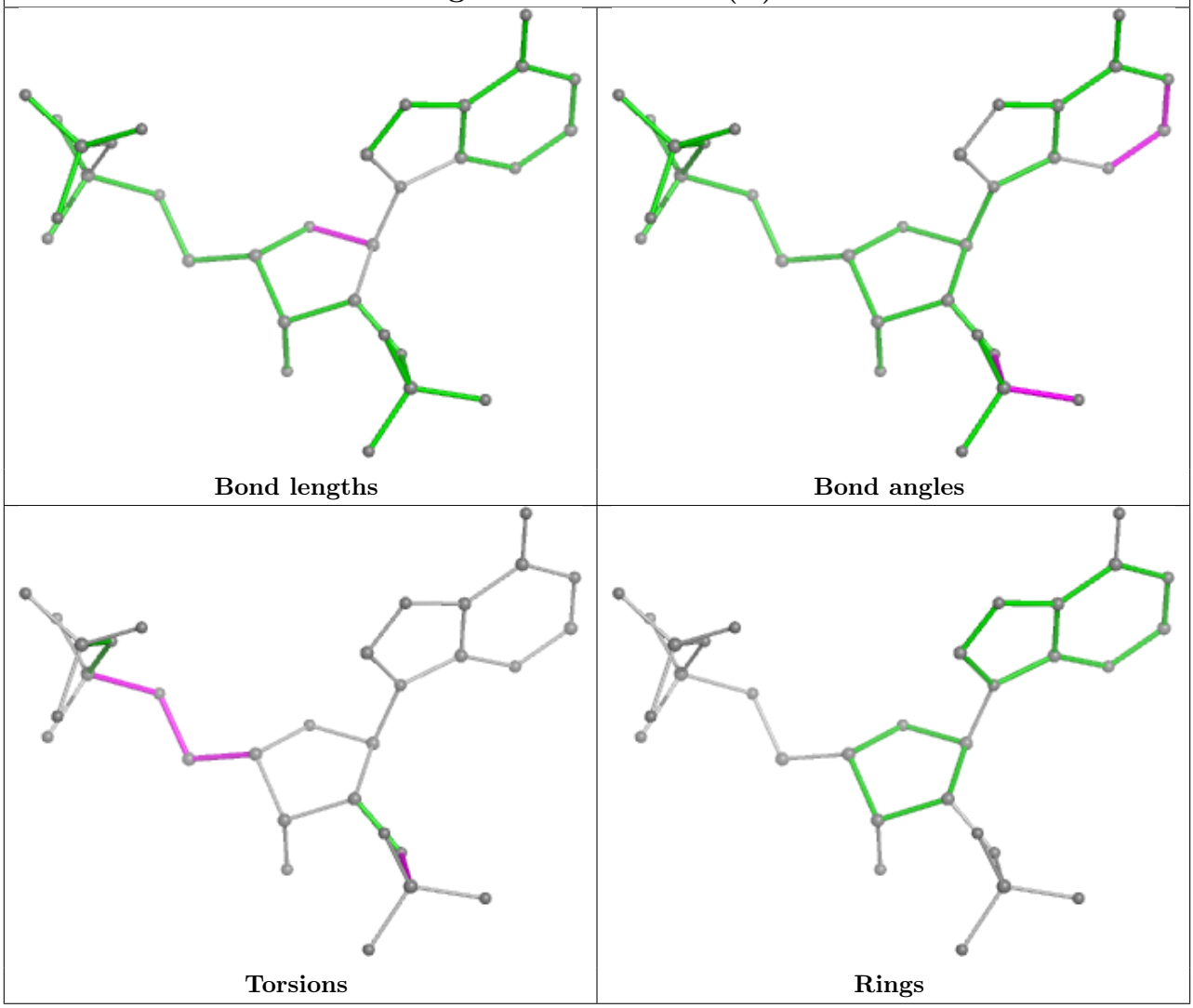


Torsions



Rings

Ligand ATR A 1470 (B)



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 (i)

6.1 Protein, DNA and RNA chains (i)

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	470/474 (99%)	-0.23	9 (1%)	66	73	12, 19, 30, 38	1 (0%)
1	B	472/474 (99%)	-0.41	4 (0%)	86	89	11, 16, 26, 43	0
1	C	469/474 (98%)	-0.49	6 (1%)	77	81	7, 12, 22, 32	0
All	All	1411/1422 (99%)	-0.38	19 (1%)	77	81	7, 16, 28, 43	1 (0%)

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1[A]	MET	4.8
1	A	470	THR	4.5
1	C	470	THR	3.5
1	A	450[A]	PHE	3.2
1	C	2	ALA	3.2
1	B	261	ASN	2.9
1	B	470	THR	2.8
1	C	469	TYR	2.7
1	A	110[A]	ARG	2.5
1	C	313	SER	2.4
1	B	-1[A]	HIS	2.2
1	B	313	SER	2.2
1	A	42	VAL	2.2
1	C	450[A]	PHE	2.2
1	A	313[A]	SER	2.2
1	A	190	ILE	2.1
1	A	2	ALA	2.1
1	A	41	GLU	2.0
1	C	311	ASP	2.0

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

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

6.3 Carbohydrates (i)

There are no monosaccharides in this entry.

6.4 Ligands (i)

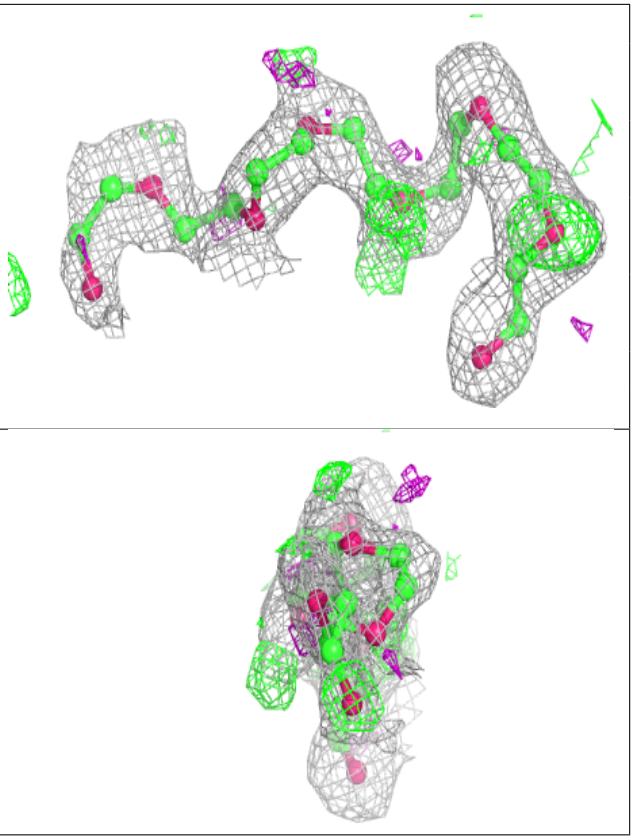
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	PEG	A	1473	7/7	0.82	0.23	41,43,43,44	0
4	P33	A	1472	22/22	0.84	0.23	12,36,42,43	0
4	P33	C	1473	19/22	0.85	0.25	30,34,42,42	0
2	ATR	B	1470[B]	31/31	0.92	0.17	24,29,38,38	11
2	ATR	C	1470[A]	31/31	0.92	0.17	22,25,38,38	11
2	ATR	C	1470[B]	31/31	0.92	0.17	22,25,40,40	11
2	ATR	A	1470[A]	31/31	0.92	0.15	33,34,40,40	11
2	ATR	A	1470[B]	31/31	0.92	0.15	33,34,38,39	11
2	ATR	B	1470[A]	31/31	0.92	0.17	24,29,35,36	11
6	CL	C	1471	1/1	0.98	0.12	19,19,19,19	0
6	CL	B	1471	1/1	0.99	0.10	20,20,20,20	0
6	CL	B	1472	1/1	0.99	0.08	17,17,17,17	0
3	RES	A	1471	14/14	0.99	0.10	16,17,18,19	1
6	CL	C	1472	1/1	0.99	0.09	11,11,11,11	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.

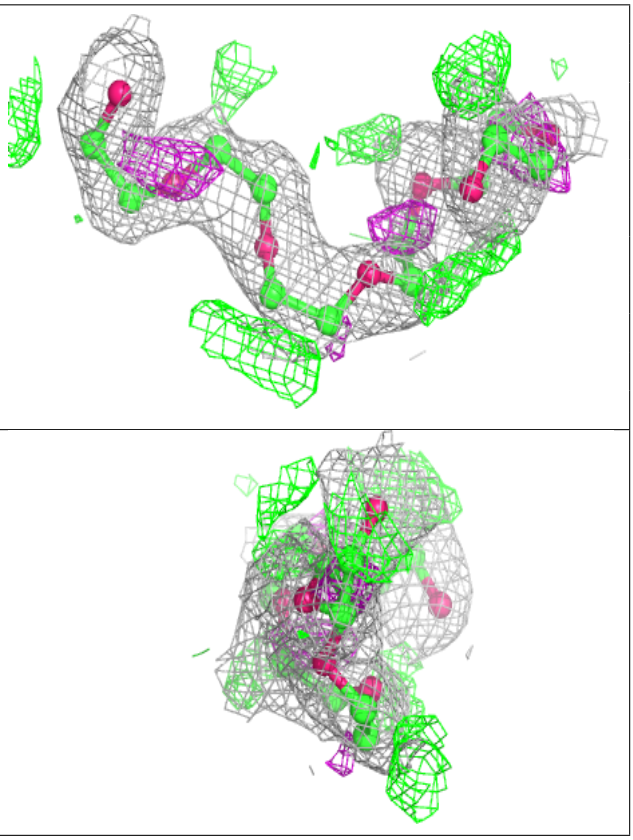
Electron density around P33 A 1472:

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



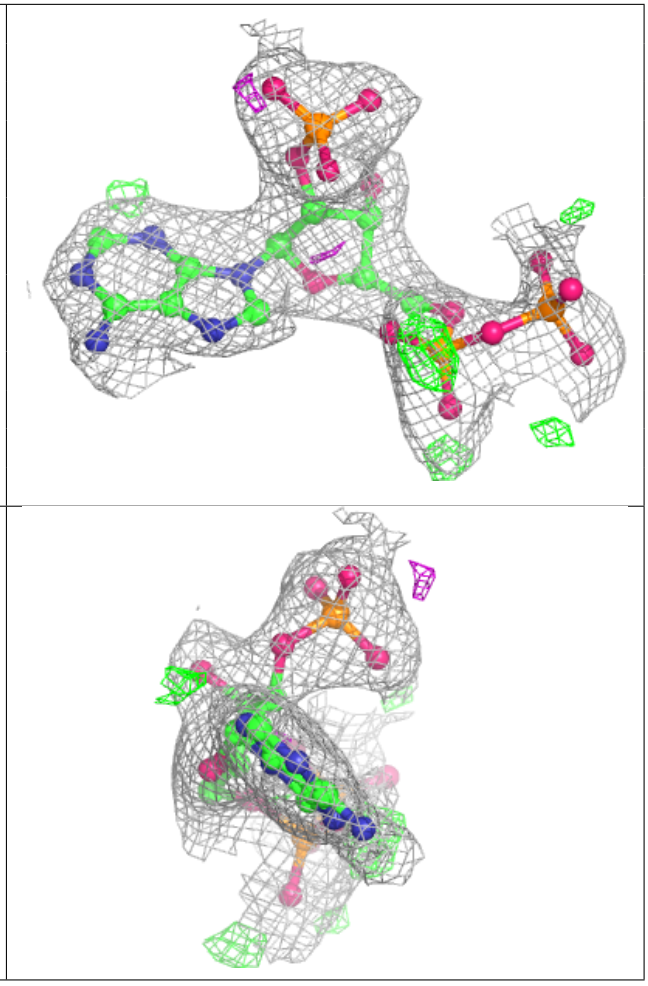
Electron density around P33 C 1473:

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



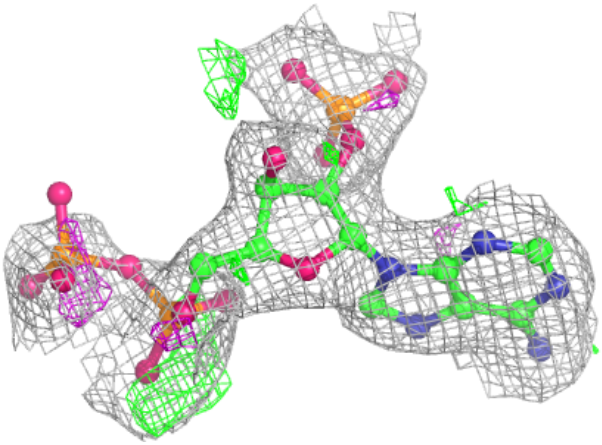
Electron density around ATR B 1470 (B):

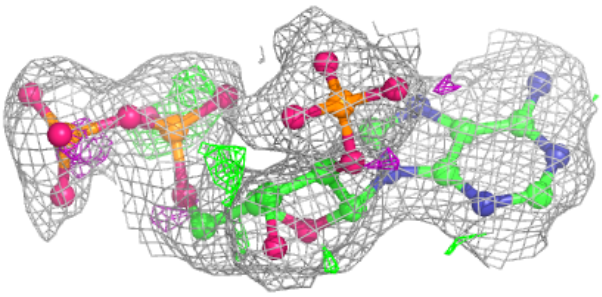
$2mF_o$-DF_c (at 0.7 rmsd) in gray
mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

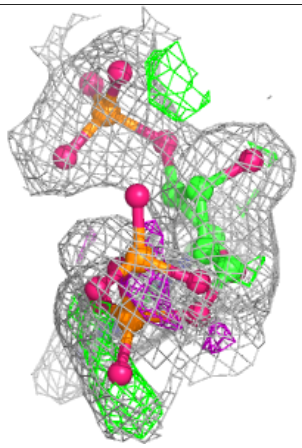


Electron density around ATR C 1470 (A):

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

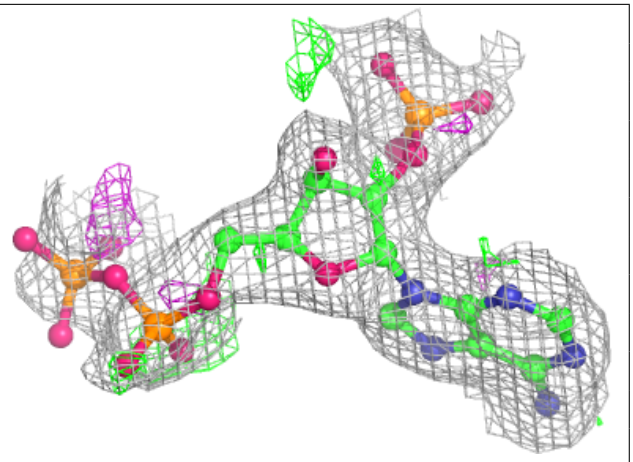


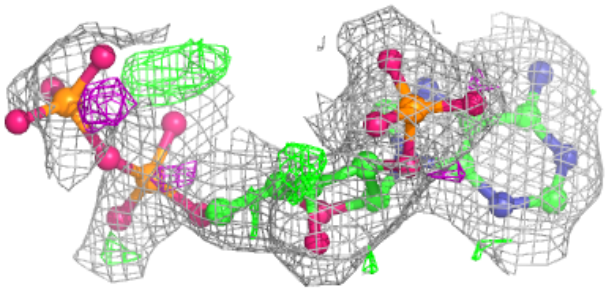


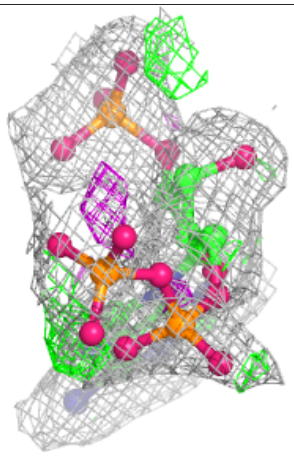


Electron density around ATR C 1470 (B):

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

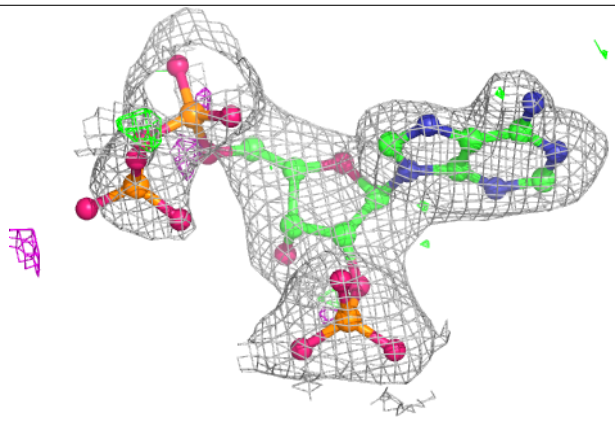


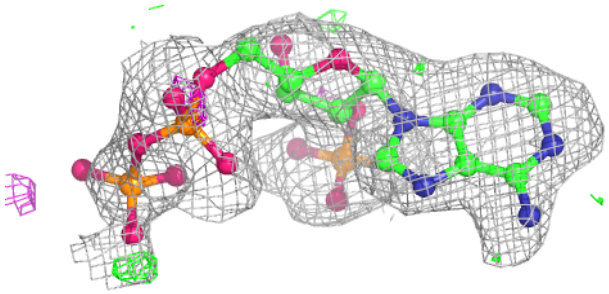


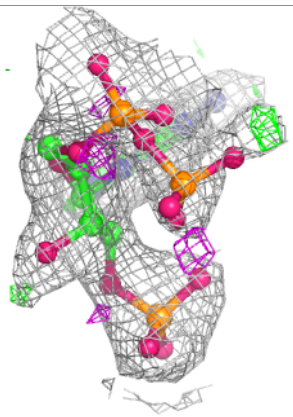


Electron density around ATR A 1470 (A):

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

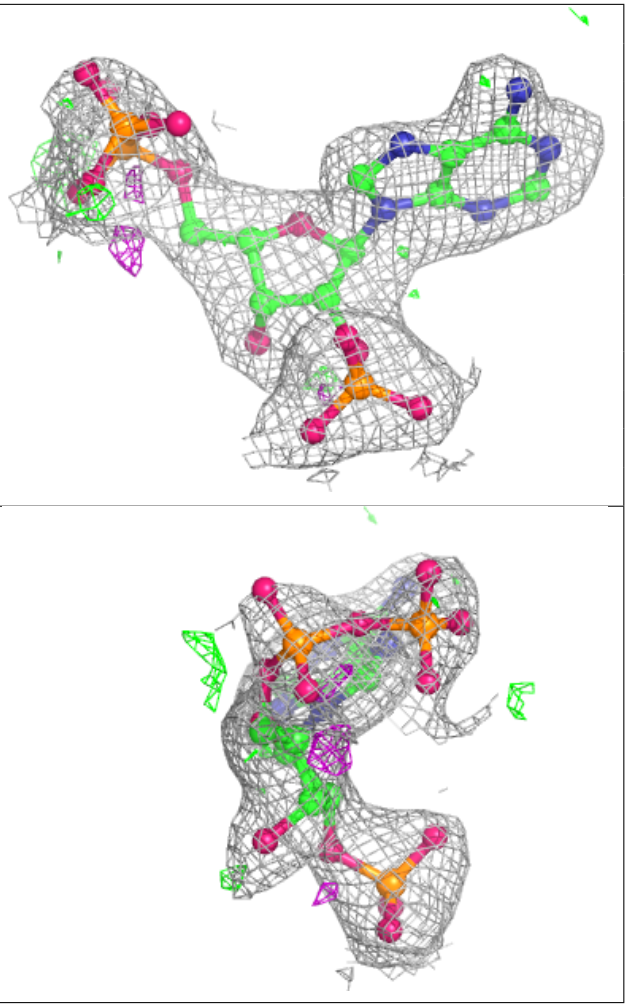






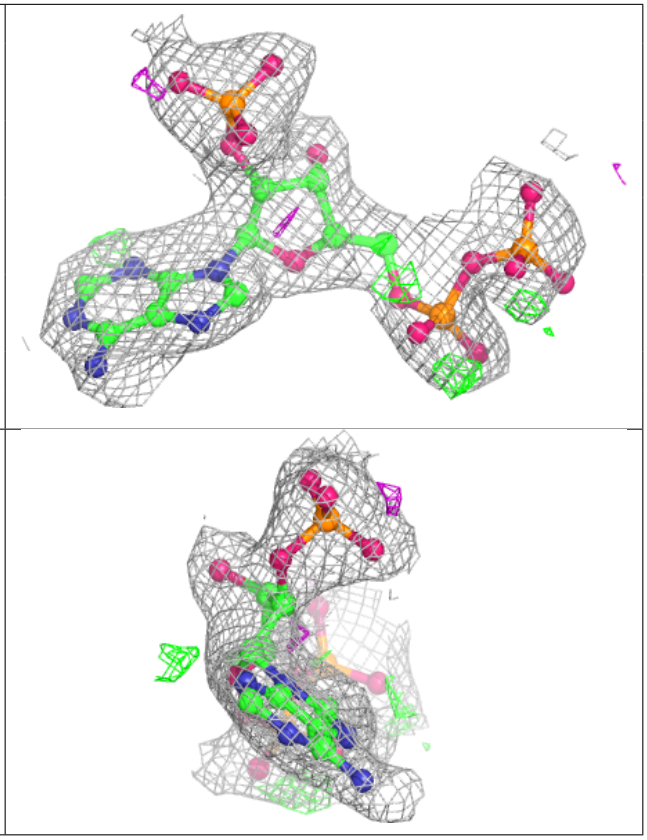
Electron density around ATR A 1470 (B):

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



Electron density around ATR B 1470 (A):

$2mF_o$-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.