



Full wwPDB X-ray Structure Validation Report ⓘ

May 16, 2020 – 06:13 am BST

PDB ID : 3R8F
Title : Replication initiator DnaA bound to AMPPCP and single-stranded DNA
Authors : Duderstadt, K.E.; Chuang, K.; Berger, J.M.
Deposited on : 2011-03-23
Resolution : 3.37 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

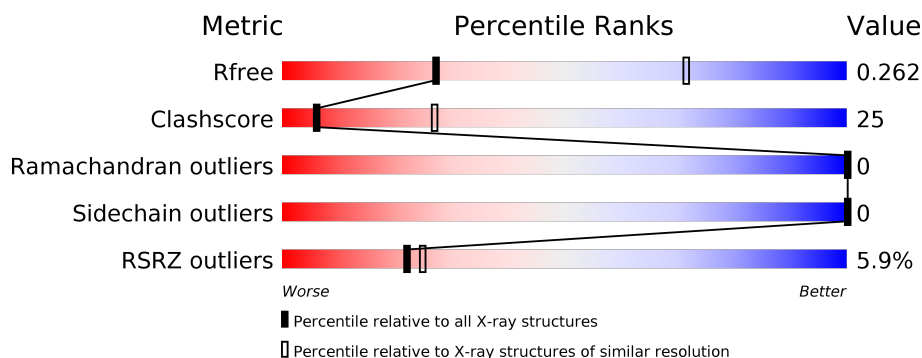
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.37 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	1558 (3.42-3.30)
Clashscore	141614	1627 (3.42-3.30)
Ramachandran outliers	138981	1599 (3.42-3.30)
Sidechain outliers	138945	1598 (3.42-3.30)
RSRZ outliers	127900	1507 (3.42-3.30)

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 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	324	<div> <div>4%</div> <div> <div></div> <div>67%</div> <div>32%</div> <div></div> </div> <div></div> </div>
1	B	324	<div> <div>3%</div> <div> <div></div> <div>65%</div> <div>33%</div> <div></div> </div> <div></div> </div>
1	C	324	<div> <div>10%</div> <div> <div></div> <div>65%</div> <div>34%</div> <div></div> </div> <div></div> </div>
1	D	324	<div> <div>6%</div> <div> <div></div> <div>67%</div> <div>31%</div> <div></div> </div> <div></div> </div>
2	E	12	<div> <div>17%</div> <div> <div></div> <div>92%</div> <div>8%</div> <div></div> </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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	ACP	A	700	-	-	X	-
4	ACP	B	700	-	-	X	-
4	ACP	C	700	-	-	X	-
4	ACP	D	700	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 10874 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 Chromosomal replication initiator protein dnaA.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	319	Total	C	N	O	S	0	0	0
			2618	1678	456	477	7			
1	B	319	Total	C	N	O	S	0	0	0
			2618	1678	456	477	7			
1	C	319	Total	C	N	O	S	0	0	0
			2618	1678	456	477	7			
1	D	319	Total	C	N	O	S	0	0	0
			2618	1678	456	477	7			

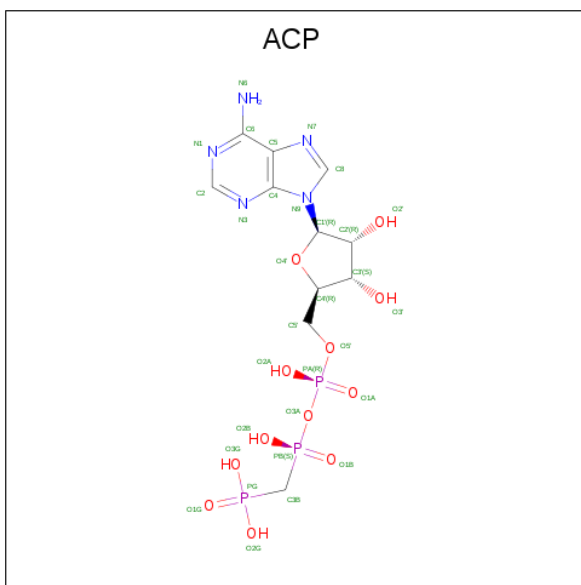
- Molecule 2 is a DNA chain called 5'-D(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	E	12	Total	C	N	O	P	0	0	0
			252	120	60	60	12			

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

- Molecule 4 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: C₁₁H₁₈N₅O₁₂P₃).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	A	1	Total 31	C 11	N 5	O 12	P 3	0	0
4	B	1	Total 31	C 11	N 5	O 12	P 3	0	0
4	C	1	Total 31	C 11	N 5	O 12	P 3	0	0
4	D	1	Total 31	C 11	N 5	O 12	P 3	0	0

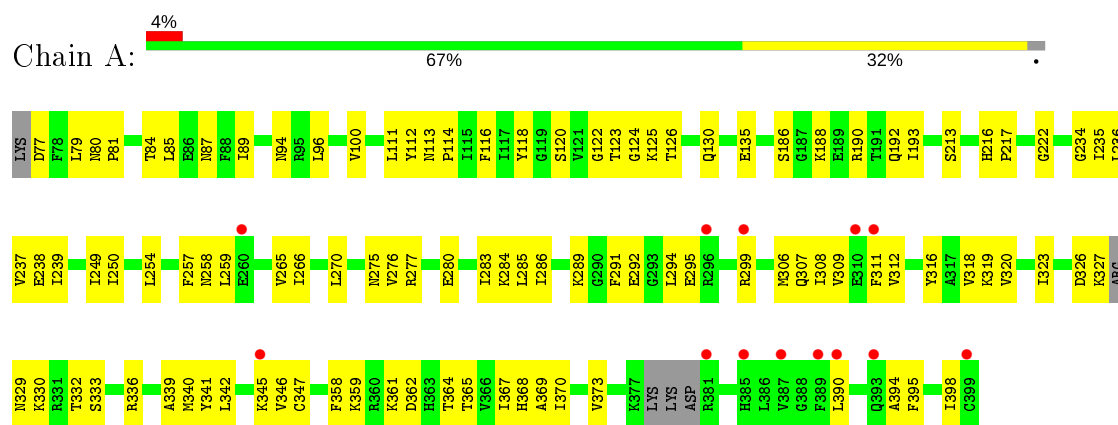
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	4	Total O 4 4	0	0
5	B	5	Total O 5 5	0	0
5	C	6	Total O 6 6	0	0
5	D	6	Total O 6 6	0	0
5	E	1	Total O 1 1	0	0

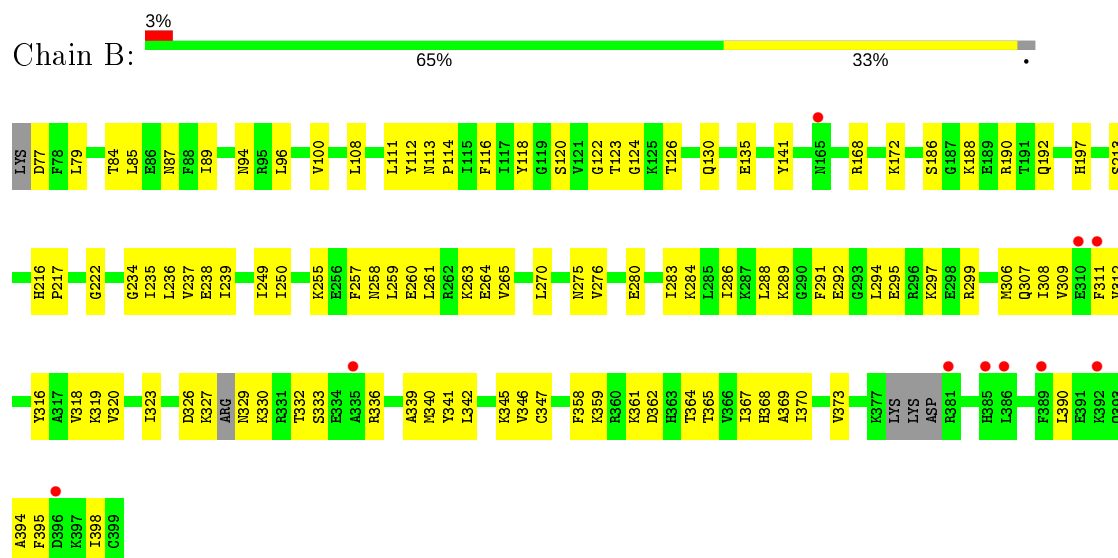
3 Residue-property plots [i](#)

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.

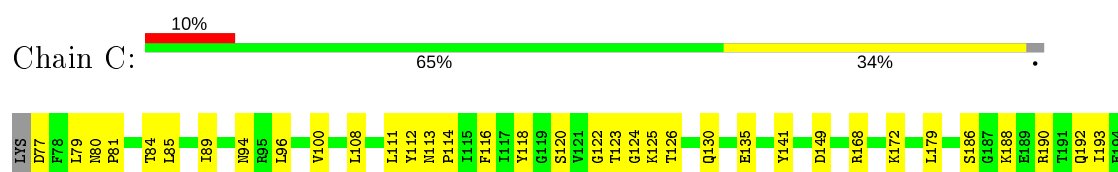
- Molecule 1: Chromosomal replication initiator protein dnaA

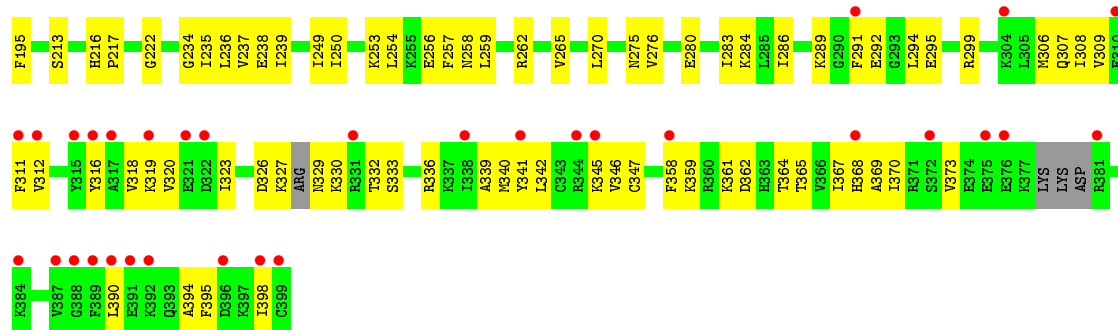


- Molecule 1: Chromosomal replication initiator protein dnaA

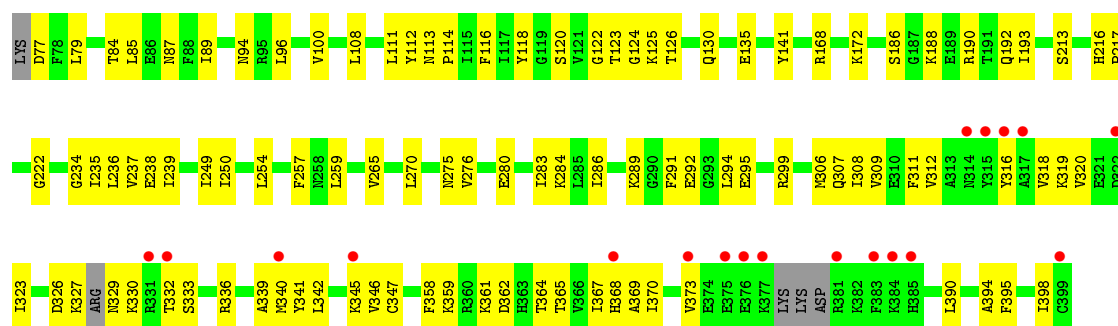


- Molecule 1: Chromosomal replication initiator protein dnaA

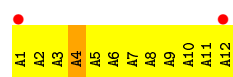
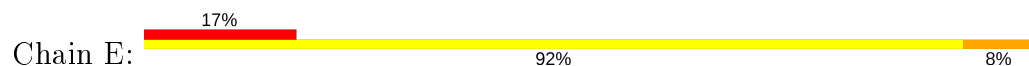




- Molecule 1: Chromosomal replication initiator protein dnaA



- Molecule 2: 5'-D(P*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*AP*A)-3'



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.80 Å 114.22 Å 201.27 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	43.49 – 3.37 43.49 – 3.37	Depositor EDS
% Data completeness (in resolution range)	98.5 (43.49-3.37) 98.1 (43.49-3.37)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.09	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 3.40 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.249 , 0.268 0.243 , 0.262	Depositor DCC
R_{free} test set	1663 reflections (5.07%)	wwPDB-VP
Wilson B-factor (Å ²)	85.6	Xtriage
Anisotropy	0.444	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 90.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	10874	wwPDB-VP
Average B, all atoms (Å ²)	108.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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: MG, ACP

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	0.25	0/2655	0.41	0/3548
1	B	0.24	0/2655	0.39	0/3548
1	C	0.24	0/2655	0.41	0/3548
1	D	0.24	0/2655	0.41	0/3548
2	E	0.45	0/287	0.97	1/440 (0.2%)
All	All	0.25	0/10907	0.43	1/14632 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	E	4	DA	C4'-C3'-C2'	-5.15	98.47	103.10

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	2618	0	2706	125	3
1	B	2618	0	2706	129	3
1	C	2618	0	2706	127	0
1	D	2618	0	2706	134	0
2	E	252	0	133	29	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
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
4	A	31	0	14	13	0
4	B	31	0	14	13	0
4	C	31	0	14	10	0
4	D	31	0	14	13	0
5	A	4	0	0	0	0
5	B	5	0	0	1	0
5	C	6	0	0	0	0
5	D	6	0	0	0	0
5	E	1	0	0	0	0
All	All	10874	0	11013	538	3

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 25.

All (538) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:254:LEU:HD23	1:D:259:LEU:HD13	1.26	1.15
1:D:254:LEU:HD23	1:D:259:LEU:CD1	1.79	1.11
1:D:254:LEU:HA	1:D:259:LEU:HD12	1.09	1.08
1:B:124:GLY:HA2	4:B:700:ACP:O2A	1.61	1.00
1:D:340:MET:HG3	1:D:358:PHE:HE2	1.26	0.99
1:B:122:GLY:H	4:B:700:ACP:H3B1	1.26	0.98
1:B:124:GLY:CA	4:B:700:ACP:O2A	2.11	0.97
1:B:340:MET:HG3	1:B:358:PHE:HE2	1.26	0.97
1:A:340:MET:HG3	1:A:358:PHE:HE2	1.26	0.96
1:C:340:MET:HG3	1:C:358:PHE:HE2	1.26	0.96
1:D:254:LEU:CD2	1:D:259:LEU:HD13	1.97	0.95
2:E:4:DA:H2''	2:E:5:DA:H5''	1.47	0.94
1:B:340:MET:CG	1:B:358:PHE:CE2	2.52	0.93
1:A:340:MET:CG	1:A:358:PHE:CE2	2.52	0.92
1:C:340:MET:CG	1:C:358:PHE:CE2	2.52	0.92
1:B:188:LYS:O	1:B:192:GLN:HG3	1.69	0.92
1:C:188:LYS:O	1:C:192:GLN:HG3	1.70	0.92
1:D:340:MET:CG	1:D:358:PHE:CE2	2.52	0.92
1:C:111:LEU:CD1	1:C:112:TYR:CD2	2.53	0.92
2:E:7:DA:H2''	2:E:8:DA:H5''	1.52	0.91

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:111:LEU:CD1	1:B:112:TYR:CD2	2.53	0.91
2:E:10:DA:H2"	2:E:11:DA:H5"	1.52	0.91
1:D:111:LEU:CD1	1:D:112:TYR:CD2	2.53	0.91
1:D:188:LYS:O	1:D:192:GLN:HG3	1.70	0.91
1:A:111:LEU:CD1	1:A:112:TYR:CD2	2.53	0.91
1:A:188:LYS:O	1:A:192:GLN:HG3	1.70	0.90
1:A:122:GLY:H	4:A:700:ACP:H3B2	1.36	0.90
1:C:329:ASN:N	1:C:333:SER:HG	1.70	0.89
1:D:257:PHE:CD1	1:D:283:ILE:HG21	2.07	0.89
1:B:340:MET:HG2	1:B:358:PHE:CE2	2.08	0.88
1:C:340:MET:HG2	1:C:358:PHE:CE2	2.08	0.88
1:D:340:MET:HG2	1:D:358:PHE:CE2	2.08	0.88
1:A:340:MET:HG2	1:A:358:PHE:CE2	2.08	0.87
1:D:340:MET:HG3	1:D:358:PHE:CE2	2.10	0.87
1:C:122:GLY:H	4:C:700:ACP:H3B2	1.38	0.86
1:B:340:MET:HG3	1:B:358:PHE:CE2	2.10	0.85
1:D:122:GLY:H	4:D:700:ACP:H3B2	1.41	0.85
1:A:329:ASN:N	1:A:333:SER:HG	1.75	0.84
1:D:394:ALA:O	1:D:398:ILE:HB	1.78	0.84
1:B:394:ALA:O	1:B:398:ILE:HB	1.78	0.83
1:C:394:ALA:O	1:C:398:ILE:HB	1.78	0.83
1:C:340:MET:HG3	1:C:358:PHE:CE2	2.10	0.83
1:A:340:MET:HG3	1:A:358:PHE:CE2	2.10	0.83
1:B:259:LEU:HD21	1:B:286:ILE:HG21	1.61	0.83
1:B:329:ASN:N	1:B:333:SER:HG	1.77	0.83
1:D:340:MET:CG	1:D:358:PHE:HE2	1.90	0.83
1:A:394:ALA:O	1:A:398:ILE:HB	1.78	0.82
1:C:340:MET:CG	1:C:358:PHE:HE2	1.89	0.82
1:B:260:GLU:HG2	1:B:261:LEU:HG	1.61	0.82
1:B:340:MET:CG	1:B:358:PHE:HE2	1.90	0.81
1:B:122:GLY:H	4:B:700:ACP:C3B	1.94	0.81
1:D:329:ASN:N	1:D:333:SER:HG	1.78	0.80
1:D:254:LEU:CA	1:D:259:LEU:HD12	2.03	0.80
2:E:1:DA:H2"	2:E:2:DA:H5"	1.62	0.80
1:A:340:MET:CG	1:A:358:PHE:HE2	1.90	0.78
1:C:329:ASN:O	1:C:330:LYS:HB3	1.82	0.78
1:B:329:ASN:O	1:B:330:LYS:HB3	1.82	0.78
1:A:329:ASN:O	1:A:330:LYS:HB3	1.82	0.77
1:D:257:PHE:CD1	1:D:283:ILE:CG2	2.67	0.77
1:D:329:ASN:O	1:D:330:LYS:HB3	1.82	0.77
1:D:114:PRO:HG2	1:D:234:GLY:HA3	1.67	0.76

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:114:PRO:HG2	1:C:234:GLY:HA3	1.67	0.76
1:C:122:GLY:H	4:C:700:ACP:C3B	1.99	0.75
1:D:257:PHE:HD1	1:D:283:ILE:HG21	1.49	0.75
1:A:114:PRO:HG2	1:A:234:GLY:HA3	1.67	0.75
1:C:361:LYS:O	1:C:362:ASP:HB2	1.87	0.75
1:A:361:LYS:O	1:A:362:ASP:HB2	1.87	0.74
1:A:122:GLY:H	4:A:700:ACP:C3B	2.00	0.74
1:D:361:LYS:O	1:D:362:ASP:HB2	1.87	0.74
1:B:361:LYS:O	1:B:362:ASP:HB2	1.87	0.73
1:A:254:LEU:HD23	1:A:259:LEU:HD12	1.70	0.73
1:B:114:PRO:HG2	1:B:234:GLY:HA3	1.67	0.73
1:D:276:VAL:HG11	4:D:700:ACP:C8	2.18	0.73
1:C:190:ARG:HB3	2:E:5:DA:OP2	1.87	0.73
1:C:276:VAL:HG11	4:C:700:ACP:N9	2.04	0.73
1:D:113:ASN:HB3	1:D:114:PRO:HD3	1.72	0.72
1:B:323:ILE:HG12	1:B:336:ARG:HG2	1.72	0.72
1:D:323:ILE:HG12	1:D:336:ARG:HG2	1.72	0.72
1:A:122:GLY:N	4:A:700:ACP:H3B2	2.04	0.71
1:B:113:ASN:HB3	1:B:114:PRO:HD3	1.72	0.71
1:C:113:ASN:HB3	1:C:114:PRO:HD3	1.72	0.71
1:A:113:ASN:HB3	1:A:114:PRO:HD3	1.72	0.71
1:D:276:VAL:HG11	4:D:700:ACP:N9	2.06	0.71
1:D:122:GLY:H	4:D:700:ACP:C3B	2.04	0.70
1:C:122:GLY:N	4:C:700:ACP:H3B2	2.06	0.70
1:D:254:LEU:HD23	1:D:259:LEU:HD12	1.69	0.70
1:A:323:ILE:HG12	1:A:336:ARG:HG2	1.72	0.70
1:C:323:ILE:HG12	1:C:336:ARG:HG2	1.72	0.70
1:A:111:LEU:HD13	1:A:112:TYR:CD2	2.28	0.69
1:A:276:VAL:HG11	4:A:700:ACP:C8	2.23	0.68
1:D:124:GLY:HA2	4:D:700:ACP:O2A	1.93	0.68
1:B:111:LEU:HD13	1:B:112:TYR:CD2	2.28	0.68
1:D:265:VAL:HG22	1:D:291:PHE:CD1	2.29	0.68
1:B:255:LYS:HA	1:B:260:GLU:OE1	1.94	0.67
1:C:111:LEU:HD13	1:C:112:TYR:CD2	2.28	0.67
1:D:190:ARG:HB3	2:E:2:DA:OP2	1.93	0.67
1:B:111:LEU:HD13	1:B:112:TYR:CE2	2.30	0.66
1:D:111:LEU:HD13	1:D:112:TYR:CD2	2.28	0.66
1:A:111:LEU:HD13	1:A:112:TYR:CE2	2.30	0.66
1:B:111:LEU:HD12	1:B:112:TYR:CD2	2.30	0.66
1:C:111:LEU:HD13	1:C:112:TYR:CE2	2.30	0.66
1:D:340:MET:CE	1:D:358:PHE:HD2	2.08	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:111:LEU:HD12	1:C:112:TYR:CD2	2.30	0.66
1:C:340:MET:CE	1:C:358:PHE:HD2	2.08	0.66
1:D:250:ILE:HD12	1:D:270:LEU:HD23	1.78	0.66
1:B:216:HIS:CD2	1:B:236:LEU:HD21	2.31	0.66
1:C:394:ALA:HB1	1:C:398:ILE:HD12	1.78	0.66
1:D:111:LEU:HD12	1:D:112:TYR:CD2	2.30	0.66
1:D:216:HIS:CD2	1:D:236:LEU:HD21	2.31	0.66
1:A:340:MET:CE	1:A:358:PHE:HD2	2.08	0.66
1:B:340:MET:CE	1:B:358:PHE:HD2	2.08	0.66
1:D:254:LEU:CD2	1:D:259:LEU:CD1	2.64	0.66
1:D:122:GLY:N	4:D:700:ACP:H3B2	2.10	0.66
1:C:250:ILE:HD12	1:C:270:LEU:HD23	1.78	0.66
1:D:111:LEU:HD13	1:D:112:TYR:CE2	2.30	0.66
1:D:116:PHE:CE1	1:D:217:PRO:HD3	2.31	0.66
1:A:358:PHE:O	1:A:359:LYS:HB2	1.97	0.65
1:A:216:HIS:HD2	1:A:217:PRO:HD2	1.62	0.65
1:A:216:HIS:CD2	1:A:236:LEU:HD21	2.31	0.65
1:B:116:PHE:CE1	1:B:217:PRO:HD3	2.31	0.65
1:A:116:PHE:CE1	1:A:217:PRO:HD3	2.31	0.65
1:D:216:HIS:HD2	1:D:217:PRO:HD2	1.62	0.65
1:C:116:PHE:CE1	1:C:217:PRO:HD3	2.31	0.65
1:A:250:ILE:HD12	1:A:270:LEU:HD23	1.78	0.65
1:D:358:PHE:O	1:D:359:LYS:HB2	1.97	0.65
1:B:394:ALA:HB1	1:B:398:ILE:HD12	1.78	0.65
1:C:216:HIS:HD2	1:C:217:PRO:HD2	1.62	0.65
1:A:394:ALA:HB1	1:A:398:ILE:HD12	1.78	0.64
1:C:216:HIS:CD2	1:C:236:LEU:HD21	2.31	0.64
1:B:358:PHE:O	1:B:359:LYS:HB2	1.97	0.64
1:D:394:ALA:HB1	1:D:398:ILE:HD12	1.78	0.64
1:C:358:PHE:O	1:C:359:LYS:HB2	1.97	0.64
1:D:254:LEU:O	1:D:259:LEU:HB2	1.97	0.64
1:D:125:LYS:N	4:D:700:ACP:O2B	2.30	0.64
1:B:250:ILE:HD12	1:B:270:LEU:HD23	1.78	0.64
1:A:111:LEU:HD12	1:A:112:TYR:CD2	2.30	0.63
1:B:216:HIS:HD2	1:B:217:PRO:HD2	1.62	0.63
1:B:276:VAL:HG11	4:B:700:ACP:C8	2.28	0.63
1:D:113:ASN:HB3	1:D:114:PRO:CD	2.29	0.63
1:A:113:ASN:HB3	1:A:114:PRO:CD	2.29	0.62
1:D:257:PHE:HB2	1:D:259:LEU:HG	1.80	0.62
1:B:276:VAL:HG11	4:B:700:ACP:N9	2.14	0.62
1:C:257:PHE:CD1	1:C:283:ILE:CG2	2.82	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:341:TYR:HB2	1:B:373:VAL:HG11	1.82	0.62
1:C:113:ASN:HB3	1:C:114:PRO:CD	2.29	0.61
1:C:276:VAL:HG11	4:C:700:ACP:C8	2.30	0.61
1:C:341:TYR:HB2	1:C:373:VAL:HG11	1.82	0.61
1:B:113:ASN:HB3	1:B:114:PRO:CD	2.29	0.61
1:A:265:VAL:HG22	1:A:291:PHE:CD1	2.35	0.61
1:A:340:MET:HE3	1:A:358:PHE:HD2	1.65	0.61
1:A:341:TYR:HB2	1:A:373:VAL:HG11	1.82	0.61
1:B:190:ARG:HB3	2:E:8:DA:OP2	2.00	0.61
1:C:257:PHE:O	1:C:258:ASN:HB2	2.00	0.60
1:D:341:TYR:HB2	1:D:373:VAL:HG11	1.82	0.60
1:C:257:PHE:CE1	1:C:283:ILE:CG2	2.85	0.60
1:B:260:GLU:O	1:B:261:LEU:HB2	2.02	0.59
1:C:318:VAL:CG2	1:C:332:THR:HG22	2.32	0.59
1:B:124:GLY:C	4:B:700:ACP:O2A	2.40	0.59
1:A:318:VAL:CG2	1:A:332:THR:HG22	2.32	0.59
1:D:318:VAL:CG2	1:D:332:THR:HG22	2.32	0.59
1:B:318:VAL:CG2	1:B:332:THR:HG22	2.32	0.59
1:B:340:MET:HE3	1:B:358:PHE:HD2	1.68	0.59
1:A:276:VAL:HG11	4:A:700:ACP:N9	2.18	0.59
2:E:11:DA:H4'	2:E:11:DA:OP1	2.03	0.58
1:B:111:LEU:CD1	1:B:112:TYR:CE2	2.87	0.58
4:B:700:ACP:O2'	5:B:9:HOH:O	2.17	0.58
1:D:309:VAL:HG23	1:D:320:VAL:HG21	1.86	0.58
1:C:309:VAL:HG23	1:C:320:VAL:HG21	1.86	0.58
1:A:111:LEU:CD1	1:A:112:TYR:CE2	2.87	0.58
1:C:111:LEU:CD1	1:C:112:TYR:CE2	2.87	0.58
2:E:5:DA:H4'	2:E:5:DA:OP1	2.04	0.57
1:B:309:VAL:HG23	1:B:320:VAL:HG21	1.86	0.57
1:D:361:LYS:O	1:D:362:ASP:CB	2.52	0.57
1:A:309:VAL:HG23	1:A:320:VAL:HG21	1.86	0.57
1:C:257:PHE:CD1	1:C:283:ILE:HG21	2.39	0.57
1:C:318:VAL:HG12	1:C:319:LYS:N	2.19	0.57
1:B:361:LYS:O	1:B:362:ASP:CB	2.52	0.57
1:A:254:LEU:O	1:A:257:PHE:O	2.23	0.57
1:C:253:LYS:O	1:C:256:GLU:HB2	2.05	0.57
1:B:259:LEU:HD21	1:B:286:ILE:CG2	2.32	0.57
1:B:308:ILE:HG13	1:B:309:VAL:N	2.20	0.57
1:C:308:ILE:HG13	1:C:309:VAL:N	2.20	0.57
1:C:361:LYS:O	1:C:362:ASP:CB	2.52	0.57
1:D:123:THR:HG21	1:D:239:ILE:HB	1.87	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:123:THR:HG21	1:B:239:ILE:HB	1.87	0.56
1:A:341:TYR:CE2	1:A:345:LYS:HG3	2.40	0.56
1:A:361:LYS:O	1:A:362:ASP:CB	2.52	0.56
1:B:341:TYR:CE2	1:B:345:LYS:HG3	2.40	0.56
1:D:318:VAL:HG12	1:D:319:LYS:N	2.19	0.56
1:A:190:ARG:HB3	2:E:11:DA:OP2	2.04	0.56
1:B:122:GLY:N	4:B:700:ACP:H3B1	2.10	0.56
1:A:308:ILE:HG13	1:A:309:VAL:N	2.20	0.56
1:A:318:VAL:HG12	1:A:319:LYS:N	2.19	0.56
1:D:341:TYR:CE2	1:D:345:LYS:HG3	2.41	0.56
1:C:341:TYR:CE2	1:C:345:LYS:HG3	2.41	0.56
1:B:318:VAL:HG12	1:B:319:LYS:N	2.19	0.56
1:C:257:PHE:CE1	1:C:283:ILE:HG22	2.41	0.56
1:D:308:ILE:HG13	1:D:309:VAL:N	2.20	0.56
1:A:123:THR:HG21	1:A:239:ILE:HB	1.87	0.55
1:D:111:LEU:CD1	1:D:112:TYR:CE2	2.87	0.55
1:C:340:MET:HE3	1:C:358:PHE:HD2	1.71	0.55
1:A:125:LYS:N	4:A:700:ACP:O1B	2.39	0.55
1:C:123:THR:HG21	1:C:239:ILE:HB	1.87	0.55
1:D:340:MET:HE3	1:D:358:PHE:HD2	1.72	0.55
2:E:8:DA:H4'	2:E:8:DA:OP1	2.07	0.54
1:A:87:ASN:O	4:A:700:ACP:H2	2.07	0.54
1:A:265:VAL:HG12	1:A:266:ILE:N	2.22	0.54
1:A:364:THR:O	1:A:367:ILE:HG22	2.08	0.54
1:C:364:THR:O	1:C:367:ILE:HG22	2.08	0.54
1:C:77:ASP:OD2	1:C:79:LEU:HB2	2.08	0.54
1:C:318:VAL:CG1	1:C:319:LYS:N	2.71	0.54
1:B:364:THR:O	1:B:367:ILE:HG22	2.08	0.53
1:B:77:ASP:OD2	1:B:79:LEU:HB2	2.08	0.53
1:D:259:LEU:HD11	1:D:283:ILE:HG23	1.89	0.53
1:A:394:ALA:CB	1:A:398:ILE:HD12	2.38	0.53
1:D:364:THR:O	1:D:367:ILE:HG22	2.08	0.53
1:B:318:VAL:CG1	1:B:319:LYS:N	2.71	0.53
1:D:394:ALA:CB	1:D:398:ILE:HD12	2.39	0.53
1:C:394:ALA:CB	1:C:398:ILE:HD12	2.39	0.53
1:D:276:VAL:HG21	4:D:700:ACP:N7	2.24	0.53
1:A:77:ASP:OD2	1:A:79:LEU:HB2	2.08	0.53
1:A:318:VAL:CG1	1:A:319:LYS:N	2.71	0.53
1:C:125:LYS:N	4:C:700:ACP:O2B	2.42	0.53
1:A:254:LEU:O	1:A:259:LEU:HB2	2.08	0.53
1:D:318:VAL:CG1	1:D:319:LYS:N	2.71	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:394:ALA:CB	1:B:398:ILE:HD12	2.39	0.53
1:D:340:MET:HE2	1:D:358:PHE:HD2	1.74	0.53
1:A:340:MET:CE	1:A:358:PHE:CD2	2.91	0.52
1:C:257:PHE:CE1	1:C:283:ILE:HG21	2.44	0.52
1:D:124:GLY:CA	4:D:700:ACP:O2A	2.57	0.52
1:B:318:VAL:HG12	1:B:319:LYS:O	2.09	0.52
1:C:318:VAL:HG12	1:C:319:LYS:O	2.09	0.52
1:A:118:TYR:CZ	1:A:238:GLU:HB2	2.45	0.52
1:A:318:VAL:HG12	1:A:319:LYS:O	2.09	0.52
1:A:326:ASP:O	1:A:327:LYS:CB	2.58	0.52
1:D:77:ASP:OD2	1:D:79:LEU:HB2	2.08	0.52
2:E:8:DA:H5"	2:E:8:DA:C8	2.45	0.52
1:D:118:TYR:CZ	1:D:238:GLU:HB2	2.45	0.52
1:D:318:VAL:HG12	1:D:319:LYS:O	2.09	0.52
1:A:277:ARG:NH2	4:A:700:ACP:O1G	2.42	0.52
1:B:260:GLU:O	1:B:261:LEU:CB	2.57	0.52
1:B:329:ASN:O	1:B:330:LYS:CB	2.56	0.52
1:B:118:TYR:CZ	1:B:238:GLU:HB2	2.45	0.52
1:A:307:GLN:NE2	1:A:342:LEU:HB3	2.25	0.52
1:B:326:ASP:O	1:B:327:LYS:CB	2.58	0.52
1:D:326:ASP:O	1:D:327:LYS:CB	2.58	0.52
1:D:362:ASP:O	1:D:364:THR:HG23	2.10	0.52
1:B:318:VAL:HG21	1:B:332:THR:HG22	1.92	0.52
1:C:362:ASP:O	1:C:364:THR:HG23	2.10	0.52
1:D:89:ILE:HG21	1:D:249:ILE:HA	1.92	0.52
1:C:89:ILE:HG21	1:C:249:ILE:HA	1.92	0.51
1:C:340:MET:CE	1:C:358:PHE:CD2	2.92	0.51
1:D:318:VAL:HG21	1:D:332:THR:HG22	1.92	0.51
1:C:118:TYR:CZ	1:C:238:GLU:HB2	2.45	0.51
1:B:362:ASP:O	1:B:364:THR:HG23	2.10	0.51
1:D:307:GLN:NE2	1:D:342:LEU:HB3	2.25	0.51
1:B:307:GLN:NE2	1:B:342:LEU:HB3	2.25	0.51
1:A:362:ASP:O	1:A:364:THR:HG23	2.10	0.51
1:A:79:LEU:HA	1:A:130:GLN:HE22	1.75	0.51
1:D:340:MET:CE	1:D:358:PHE:CD2	2.92	0.51
1:C:329:ASN:O	1:C:330:LYS:CB	2.56	0.51
1:C:79:LEU:HA	1:C:130:GLN:HE22	1.75	0.51
1:D:340:MET:HE2	1:D:358:PHE:CD2	2.46	0.51
1:C:340:MET:HE2	1:C:358:PHE:HD2	1.75	0.51
1:C:307:GLN:NE2	1:C:342:LEU:HB3	2.25	0.51
1:C:318:VAL:HG21	1:C:332:THR:HG22	1.92	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:89:ILE:HG21	1:A:249:ILE:HA	1.92	0.50
1:B:118:TYR:HA	1:B:213:SER:O	2.12	0.50
4:C:700:ACP:O3G	4:C:700:ACP:O1B	2.30	0.50
1:A:122:GLY:CA	4:A:700:ACP:H3B2	2.42	0.50
1:B:79:LEU:HA	1:B:130:GLN:HE22	1.75	0.50
1:B:89:ILE:HG21	1:B:249:ILE:HA	1.92	0.50
1:D:79:LEU:HA	1:D:130:GLN:HE22	1.75	0.50
1:A:318:VAL:HG21	1:A:332:THR:HG22	1.92	0.50
1:B:308:ILE:HG22	1:B:339:ALA:HB1	1.94	0.50
1:C:118:TYR:HA	1:C:213:SER:O	2.12	0.50
1:C:326:ASP:O	1:C:327:LYS:CB	2.58	0.50
1:B:190:ARG:N	2:E:8:DA:OP2	2.45	0.50
1:A:118:TYR:HA	1:A:213:SER:O	2.12	0.50
1:B:85:LEU:HD12	1:B:135:GLU:HG3	1.94	0.50
1:A:308:ILE:HG22	1:A:339:ALA:HB1	1.94	0.50
2:E:11:DA:C8	2:E:11:DA:H5"	2.47	0.49
1:C:254:LEU:CD2	1:C:259:LEU:HD11	2.42	0.49
1:B:340:MET:CE	1:B:358:PHE:CD2	2.91	0.49
1:C:85:LEU:HD12	1:C:135:GLU:HG3	1.94	0.49
1:C:308:ILE:HG22	1:C:339:ALA:HB1	1.94	0.49
1:C:340:MET:HE2	1:C:358:PHE:CD2	2.48	0.49
1:A:120:SER:O	1:A:123:THR:OG1	2.22	0.49
1:A:295:GLU:O	1:A:299:ARG:HG3	2.13	0.49
1:A:307:GLN:OE1	1:A:398:ILE:HD13	2.13	0.49
1:C:295:GLU:O	1:C:299:ARG:HG3	2.13	0.49
1:D:85:LEU:HD12	1:D:135:GLU:HG3	1.94	0.49
1:B:257:PHE:O	1:B:258:ASN:HB2	2.12	0.49
1:D:118:TYR:HA	1:D:213:SER:O	2.12	0.49
2:E:5:DA:C8	2:E:5:DA:H5"	2.46	0.49
1:D:295:GLU:O	1:D:299:ARG:HG3	2.13	0.49
1:C:122:GLY:CA	4:C:700:ACP:H3B2	2.43	0.49
4:D:700:ACP:O3G	4:D:700:ACP:O1B	2.31	0.49
1:A:257:PHE:CD1	1:A:283:ILE:HG21	2.48	0.49
1:B:188:LYS:HB3	2:E:8:DA:OP1	2.12	0.49
4:B:700:ACP:O1B	4:B:700:ACP:O1G	2.31	0.48
1:D:308:ILE:HG22	1:D:339:ALA:HB1	1.94	0.48
1:B:307:GLN:OE1	1:B:398:ILE:HD13	2.13	0.48
1:D:186:SER:HA	1:D:222:GLY:O	2.14	0.48
1:B:295:GLU:O	1:B:299:ARG:HG3	2.13	0.48
1:C:342:LEU:O	1:C:346:VAL:HG12	2.14	0.48
1:D:329:ASN:O	1:D:330:LYS:CB	2.56	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85:LEU:HD12	1:A:135:GLU:HG3	1.94	0.48
1:C:307:GLN:OE1	1:C:398:ILE:HD13	2.13	0.48
1:D:342:LEU:O	1:D:346:VAL:HG12	2.13	0.48
2:E:2:DA:H4'	2:E:2:DA:OP1	2.13	0.48
1:D:257:PHE:HB2	1:D:259:LEU:CG	2.43	0.48
1:A:280:GLU:O	1:A:284:LYS:HG3	2.14	0.48
1:B:323:ILE:O	1:B:336:ARG:HD3	2.14	0.48
1:C:265:VAL:HA	1:C:291:PHE:CE1	2.49	0.48
2:E:7:DA:H2''	2:E:8:DA:C8	2.49	0.48
1:C:280:GLU:O	1:C:284:LYS:HG3	2.14	0.47
1:D:307:GLN:OE1	1:D:398:ILE:HD13	2.13	0.47
2:E:11:DA:H8	2:E:11:DA:H5''	1.79	0.47
1:A:186:SER:HA	1:A:222:GLY:O	2.14	0.47
1:A:323:ILE:O	1:A:336:ARG:HD3	2.14	0.47
1:A:342:LEU:O	1:A:346:VAL:HG12	2.14	0.47
1:C:186:SER:HA	1:C:222:GLY:O	2.14	0.47
1:D:323:ILE:O	1:D:336:ARG:HD3	2.14	0.47
1:D:330:LYS:O	1:D:330:LYS:HG3	2.15	0.47
1:A:330:LYS:O	1:A:330:LYS:HG3	2.15	0.47
1:B:123:THR:HG22	1:B:239:ILE:HG21	1.96	0.47
1:B:342:LEU:O	1:B:346:VAL:HG12	2.14	0.47
1:C:323:ILE:O	1:C:336:ARG:HD3	2.14	0.47
1:B:280:GLU:O	1:B:284:LYS:HG3	2.14	0.47
1:B:346:VAL:HG23	1:B:395:PHE:CE1	2.50	0.47
1:D:217:PRO:HG2	1:D:236:LEU:HD11	1.97	0.47
1:D:286:ILE:HD12	1:D:294:LEU:HD22	1.97	0.47
1:C:330:LYS:HG3	1:C:330:LYS:O	2.15	0.47
1:C:346:VAL:HG23	1:C:395:PHE:CE1	2.50	0.47
1:D:346:VAL:HG23	1:D:395:PHE:CE1	2.50	0.47
1:A:277:ARG:NH1	4:A:700:ACP:O1G	2.47	0.47
1:C:286:ILE:HD12	1:C:294:LEU:HD22	1.97	0.47
1:B:120:SER:O	1:B:123:THR:OG1	2.22	0.47
1:B:326:ASP:O	1:B:327:LYS:HB3	2.15	0.47
1:D:280:GLU:O	1:D:284:LYS:HG3	2.14	0.47
2:E:8:DA:H2''	2:E:9:DA:O5'	2.15	0.47
1:A:286:ILE:HD12	1:A:294:LEU:HD22	1.97	0.47
1:C:265:VAL:HG22	1:C:291:PHE:CD1	2.49	0.47
4:A:700:ACP:O3G	4:A:700:ACP:O2B	2.32	0.46
1:B:87:ASN:O	4:B:700:ACP:H2	2.14	0.46
1:C:123:THR:HG22	1:C:239:ILE:HG21	1.96	0.46
1:A:346:VAL:HG23	1:A:395:PHE:CE1	2.50	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:330:LYS:HG3	1:B:330:LYS:O	2.15	0.46
1:A:292:GLU:H	1:A:292:GLU:CD	2.19	0.46
1:A:96:LEU:HD23	1:A:100:VAL:HG23	1.98	0.46
1:B:286:ILE:HD12	1:B:294:LEU:HD22	1.97	0.46
2:E:10:DA:H2''	2:E:11:DA:C8	2.51	0.46
1:A:123:THR:HG22	1:A:239:ILE:HG21	1.96	0.46
1:A:326:ASP:O	1:A:327:LYS:HB3	2.15	0.46
1:B:340:MET:HE2	1:B:358:PHE:CD2	2.51	0.46
1:C:111:LEU:HD12	1:C:112:TYR:CG	2.51	0.46
1:C:217:PRO:HG2	1:C:236:LEU:HD11	1.97	0.46
1:C:123:THR:CG2	1:C:239:ILE:CG2	2.94	0.46
1:D:265:VAL:HA	1:D:291:PHE:CE1	2.51	0.46
1:A:217:PRO:HG2	1:A:236:LEU:HD11	1.97	0.46
1:A:123:THR:CG2	1:A:239:ILE:CG2	2.94	0.46
1:B:292:GLU:CD	1:B:292:GLU:H	2.19	0.46
1:D:326:ASP:O	1:D:327:LYS:HB3	2.15	0.46
2:E:5:DA:H2''	2:E:6:DA:O5'	2.14	0.46
1:B:217:PRO:HG2	1:B:236:LEU:HD11	1.97	0.46
1:B:186:SER:HA	1:B:222:GLY:O	2.16	0.46
1:C:94:ASN:HB3	1:C:239:ILE:HG23	1.98	0.45
1:D:111:LEU:HD12	1:D:112:TYR:CG	2.51	0.45
1:D:123:THR:HG22	1:D:239:ILE:HG21	1.96	0.45
1:B:96:LEU:HD23	1:B:100:VAL:HG23	1.98	0.45
1:B:260:GLU:HG2	1:B:261:LEU:CG	2.41	0.45
1:C:292:GLU:H	1:C:292:GLU:CD	2.19	0.45
1:A:257:PHE:HD1	1:A:283:ILE:HG21	1.81	0.45
1:A:289:LYS:HE2	1:A:294:LEU:HD12	1.99	0.45
1:B:111:LEU:HD12	1:B:112:TYR:CG	2.51	0.45
1:C:326:ASP:O	1:C:327:LYS:HB3	2.15	0.45
1:D:94:ASN:HB3	1:D:239:ILE:HG23	1.98	0.45
1:D:276:VAL:CG1	4:D:700:ACP:C8	2.90	0.45
1:B:123:THR:CG2	1:B:239:ILE:CG2	2.94	0.45
1:D:292:GLU:H	1:D:292:GLU:CD	2.19	0.45
1:D:87:ASN:O	4:D:700:ACP:H2	2.17	0.45
1:A:398:ILE:CG2	1:A:398:ILE:O	2.65	0.45
1:C:289:LYS:HE2	1:C:294:LEU:HD12	1.99	0.45
2:E:2:DA:H2''	2:E:3:DA:O5'	2.17	0.45
2:E:4:DA:H2''	2:E:5:DA:C8	2.52	0.45
1:B:250:ILE:CD1	1:B:270:LEU:HD23	2.47	0.45
1:D:123:THR:CG2	1:D:239:ILE:CG2	2.94	0.45
1:A:111:LEU:HD12	1:A:112:TYR:CG	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:289:LYS:HE2	1:B:294:LEU:HD12	1.99	0.44
1:B:320:VAL:O	1:B:323:ILE:HG22	2.17	0.44
1:C:96:LEU:HD23	1:C:100:VAL:HG23	1.98	0.44
1:A:306:MET:HG3	1:A:309:VAL:HG12	1.99	0.44
1:B:340:MET:HE2	1:B:358:PHE:HD2	1.78	0.44
1:B:94:ASN:HB3	1:B:239:ILE:HG23	1.98	0.44
2:E:8:DA:H5''	2:E:8:DA:H8	1.81	0.44
1:A:250:ILE:CD1	1:A:270:LEU:HD23	2.47	0.44
1:C:259:LEU:C	1:C:259:LEU:HD12	2.38	0.44
1:D:190:ARG:HA	1:D:193:ILE:HD12	1.99	0.44
1:A:216:HIS:HD2	1:A:217:PRO:CD	2.30	0.44
1:D:111:LEU:CD1	1:D:112:TYR:CG	3.01	0.44
1:D:286:ILE:CD1	1:D:294:LEU:HD22	2.47	0.44
1:C:124:GLY:HA2	4:C:700:ACP:O2A	2.18	0.44
1:C:306:MET:HG3	1:C:309:VAL:HG12	1.99	0.44
1:D:96:LEU:HD23	1:D:100:VAL:HG23	1.98	0.44
1:D:257:PHE:CD1	1:D:283:ILE:HG22	2.48	0.44
1:D:309:VAL:HG23	1:D:320:VAL:CG2	2.48	0.44
1:C:286:ILE:CD1	1:C:294:LEU:HD22	2.48	0.44
1:C:320:VAL:O	1:C:323:ILE:HG22	2.17	0.44
1:A:84:THR:HG22	1:A:85:LEU:N	2.33	0.44
1:C:111:LEU:CD1	1:C:112:TYR:CG	3.01	0.44
1:D:306:MET:HG3	1:D:309:VAL:HG12	1.99	0.44
1:A:94:ASN:HB3	1:A:239:ILE:HG23	1.98	0.44
1:A:286:ILE:CD1	1:A:294:LEU:HD22	2.48	0.44
1:D:320:VAL:O	1:D:323:ILE:HG22	2.17	0.44
1:D:398:ILE:O	1:D:398:ILE:CG2	2.65	0.44
1:A:111:LEU:CD1	1:A:112:TYR:CG	3.01	0.43
1:A:311:PHE:CE1	1:A:390:LEU:HD22	2.53	0.43
1:B:398:ILE:CG2	1:B:398:ILE:O	2.65	0.43
1:B:84:THR:HG22	1:B:85:LEU:N	2.33	0.43
1:C:120:SER:O	1:C:123:THR:OG1	2.22	0.43
1:C:190:ARG:HA	1:C:193:ILE:HD12	2.00	0.43
1:B:286:ILE:CD1	1:B:294:LEU:HD22	2.48	0.43
1:B:306:MET:HG3	1:B:309:VAL:HG12	1.99	0.43
1:C:311:PHE:CE1	1:C:390:LEU:HD22	2.53	0.43
1:D:254:LEU:O	1:D:259:LEU:CB	2.66	0.43
1:A:320:VAL:O	1:A:323:ILE:HG22	2.17	0.43
1:A:340:MET:HE2	1:A:358:PHE:HD2	1.81	0.43
1:B:365:THR:O	1:B:369:ALA:HB2	2.19	0.43
1:D:257:PHE:CE1	1:D:283:ILE:HG21	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:289:LYS:HE2	1:D:294:LEU:HD12	1.99	0.43
1:A:365:THR:O	1:A:369:ALA:HB2	2.18	0.43
1:B:126:THR:O	1:B:130:GLN:HG2	2.19	0.43
1:C:126:THR:O	1:C:130:GLN:HG2	2.19	0.43
1:C:250:ILE:CD1	1:C:270:LEU:HD23	2.47	0.43
1:D:122:GLY:O	1:D:275:ASN:HB2	2.19	0.43
1:A:329:ASN:O	1:A:330:LYS:CB	2.56	0.43
1:D:120:SER:O	1:D:123:THR:OG1	2.22	0.43
2:E:1:DA:H2''	2:E:2:DA:C8	2.53	0.43
1:A:126:THR:O	1:A:130:GLN:HG2	2.19	0.43
1:B:122:GLY:O	1:B:275:ASN:HB2	2.19	0.43
1:B:124:GLY:N	4:B:700:ACP:O2A	2.51	0.43
1:C:122:GLY:HA2	4:C:700:ACP:H3B2	2.00	0.43
1:C:84:THR:HG22	1:C:85:LEU:N	2.33	0.43
1:A:122:GLY:O	1:A:275:ASN:HB2	2.19	0.43
1:A:312:VAL:O	1:A:316:TYR:HB2	2.19	0.43
1:B:311:PHE:CE1	1:B:390:LEU:HD22	2.53	0.43
1:B:197:HIS:CE1	1:C:149:ASP:OD2	2.71	0.43
1:C:398:ILE:O	1:C:398:ILE:CG2	2.65	0.43
1:D:84:THR:HG22	1:D:85:LEU:N	2.33	0.43
2:E:11:DA:H2''	2:E:12:DA:O5'	2.19	0.43
1:A:122:GLY:HA2	4:A:700:ACP:H3B2	2.00	0.43
1:C:262:ARG:HB2	1:C:265:VAL:HB	2.01	0.43
1:C:398:ILE:O	1:C:398:ILE:HG22	2.19	0.43
1:C:122:GLY:O	1:C:275:ASN:HB2	2.19	0.42
1:C:309:VAL:HG23	1:C:320:VAL:CG2	2.48	0.42
1:C:346:VAL:HG13	1:C:347:CYS:N	2.34	0.42
1:C:312:VAL:O	1:C:316:TYR:HB2	2.19	0.42
1:C:365:THR:O	1:C:369:ALA:HB2	2.19	0.42
1:D:365:THR:O	1:D:369:ALA:HB2	2.18	0.42
1:D:346:VAL:HG13	1:D:347:CYS:N	2.34	0.42
1:C:367:ILE:HG23	1:C:368:HIS:N	2.34	0.42
1:B:340:MET:HG2	1:B:358:PHE:CD2	2.53	0.42
1:C:235:ILE:HG22	1:C:237:VAL:HG13	2.02	0.42
1:D:126:THR:O	1:D:130:GLN:HG2	2.19	0.42
1:D:370:ILE:O	1:D:373:VAL:HG12	2.20	0.42
1:A:370:ILE:O	1:A:373:VAL:HG12	2.20	0.42
1:D:312:VAL:O	1:D:316:TYR:HB2	2.19	0.42
1:B:346:VAL:HG13	1:B:347:CYS:N	2.34	0.42
1:B:398:ILE:HG22	1:B:398:ILE:O	2.19	0.42
1:A:190:ARG:HA	1:A:193:ILE:HD12	2.00	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:309:VAL:HG23	1:A:320:VAL:CG2	2.48	0.42
1:A:398:ILE:O	1:A:398:ILE:HG22	2.19	0.42
1:A:96:LEU:HD21	1:B:288:LEU:HD23	2.02	0.42
1:B:235:ILE:HG22	1:B:237:VAL:HG13	2.02	0.42
1:B:312:VAL:O	1:B:316:TYR:HB2	2.19	0.42
1:C:257:PHE:CD1	1:C:283:ILE:HG22	2.55	0.42
1:D:367:ILE:HG23	1:D:368:HIS:N	2.35	0.42
1:D:398:ILE:O	1:D:398:ILE:HG22	2.19	0.42
1:D:122:GLY:CA	4:D:700:ACP:H3B2	2.48	0.42
1:B:346:VAL:HG23	1:B:395:PHE:CD1	2.55	0.42
1:B:394:ALA:CA	1:B:398:ILE:HD12	2.50	0.42
1:D:311:PHE:CE1	1:D:390:LEU:HD22	2.53	0.42
1:C:394:ALA:CA	1:C:398:ILE:HD12	2.50	0.41
1:D:346:VAL:HG23	1:D:395:PHE:CD1	2.55	0.41
1:B:111:LEU:CD1	1:B:112:TYR:CG	3.01	0.41
1:D:216:HIS:HD2	1:D:217:PRO:CD	2.30	0.41
1:A:340:MET:HE2	1:A:358:PHE:CD2	2.54	0.41
1:B:108:LEU:HD22	1:B:141:TYR:CD2	2.56	0.41
1:B:257:PHE:CE1	1:B:283:ILE:HG22	2.55	0.41
1:D:108:LEU:HD22	1:D:141:TYR:CD2	2.56	0.41
1:A:190:ARG:NH1	2:E:9:DA:H4'	2.36	0.41
1:A:257:PHE:CD1	1:A:283:ILE:CG2	3.04	0.41
1:A:346:VAL:HG13	1:A:347:CYS:N	2.34	0.41
1:B:370:ILE:O	1:B:373:VAL:HG12	2.20	0.41
1:C:108:LEU:HD22	1:C:141:TYR:CD2	2.56	0.41
1:C:254:LEU:HD22	1:C:259:LEU:HD11	2.02	0.41
1:B:367:ILE:HG23	1:B:368:HIS:N	2.34	0.41
1:C:346:VAL:HG23	1:C:395:PHE:CD1	2.55	0.41
1:D:394:ALA:CA	1:D:398:ILE:HD12	2.50	0.41
1:A:235:ILE:HG22	1:A:237:VAL:HG13	2.02	0.41
1:A:340:MET:HG2	1:A:358:PHE:CD2	2.54	0.41
1:A:394:ALA:CA	1:A:398:ILE:HD12	2.50	0.41
1:B:122:GLY:N	4:B:700:ACP:C3B	2.71	0.41
1:D:250:ILE:CD1	1:D:270:LEU:HD23	2.47	0.41
1:A:111:LEU:HD12	1:A:111:LEU:C	2.41	0.41
1:A:367:ILE:HG23	1:A:368:HIS:N	2.35	0.41
1:A:96:LEU:HD22	1:A:237:VAL:CG1	2.51	0.41
1:C:96:LEU:HD22	1:C:237:VAL:CG1	2.51	0.41
1:A:254:LEU:HD23	1:A:259:LEU:CD1	2.46	0.41
1:B:96:LEU:HD22	1:B:237:VAL:CG1	2.51	0.41
1:B:264:GLU:N	1:B:264:GLU:OE1	2.54	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:111:LEU:C	1:C:111:LEU:HD12	2.41	0.41
1:C:370:ILE:O	1:C:373:VAL:HG12	2.20	0.41
1:D:168:ARG:O	1:D:172:LYS:HG3	2.21	0.41
1:D:235:ILE:HG22	1:D:237:VAL:HG13	2.02	0.41
1:A:346:VAL:HG23	1:A:395:PHE:CD1	2.55	0.41
1:C:80:ASN:HA	1:C:81:PRO:HD3	1.88	0.41
1:D:123:THR:HG22	1:D:239:ILE:CG2	2.51	0.41
1:B:265:VAL:HA	1:B:291:PHE:CE1	2.56	0.40
1:B:264:GLU:HG2	1:B:265:VAL:N	2.36	0.40
1:B:309:VAL:HG23	1:B:320:VAL:CG2	2.48	0.40
1:D:257:PHE:HB2	1:D:259:LEU:CD1	2.50	0.40
1:B:111:LEU:C	1:B:111:LEU:HD12	2.42	0.40
1:B:123:THR:HG22	1:B:239:ILE:CG2	2.52	0.40
1:A:238:GLU:OE1	1:B:297:LYS:HE3	2.21	0.40
1:A:285:LEU:HA	1:A:285:LEU:HD12	1.97	0.40
1:A:80:ASN:HA	1:A:81:PRO:HD3	1.88	0.40
1:C:216:HIS:HD2	1:C:217:PRO:CD	2.30	0.40
1:D:111:LEU:C	1:D:111:LEU:HD12	2.41	0.40
1:A:124:GLY:HA2	4:A:700:ACP:O1A	2.20	0.40
1:B:168:ARG:O	1:B:172:LYS:HG3	2.21	0.40
1:B:190:ARG:HD3	2:E:7:DA:OP1	2.21	0.40
1:C:123:THR:HG22	1:C:239:ILE:CG2	2.52	0.40
1:D:96:LEU:HD22	1:D:237:VAL:CG1	2.51	0.40
1:C:168:ARG:O	1:C:172:LYS:HG3	2.21	0.40
1:C:179:LEU:HD22	1:C:195:PHE:CE1	2.57	0.40
1:D:323:ILE:HG12	1:D:336:ARG:CG	2.48	0.40

All (3) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:292:GLU:OE2	1:B:258:ASN:OD1[4_545]	1.78	0.42
1:A:292:GLU:OE1	1:B:260:GLU:OE2[4_545]	2.11	0.09
1:A:258:ASN:OD1	1:B:263:LYS:CB[4_545]	2.14	0.06

5.3 Torsion angles

5.3.1 Protein backbone

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	313/324 (97%)	298 (95%)	15 (5%)	0	100	100
1	B	313/324 (97%)	297 (95%)	16 (5%)	0	100	100
1	C	313/324 (97%)	297 (95%)	16 (5%)	0	100	100
1	D	313/324 (97%)	296 (95%)	17 (5%)	0	100	100
All	All	1252/1296 (97%)	1188 (95%)	64 (5%)	0	100	100

There are no Ramachandran outliers to report.

5.3.2 Protein sidechains

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

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

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	284/289 (98%)	284 (100%)	0	100	100
1	B	284/289 (98%)	284 (100%)	0	100	100
1	C	284/289 (98%)	284 (100%)	0	100	100
1	D	284/289 (98%)	284 (100%)	0	100	100
All	All	1136/1156 (98%)	1136 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	130	GLN
1	A	197	HIS
1	A	216	HIS
1	A	218	GLN
1	B	130	GLN
1	B	197	HIS
1	B	216	HIS
1	B	218	GLN
1	C	87	ASN
1	C	130	GLN
1	C	216	HIS
1	C	218	GLN
1	D	130	GLN
1	D	216	HIS
1	D	218	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 4 are monoatomic - leaving 4 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
4	ACP	A	700	3	27,33,33	1.66	9 (33%)	32,52,52	1.45	3 (9%)
4	ACP	D	700	3	27,33,33	1.66	9 (33%)	32,52,52	1.44	3 (9%)
4	ACP	B	700	3	27,33,33	1.66	9 (33%)	32,52,52	1.45	3 (9%)
4	ACP	C	700	3	27,33,33	1.66	9 (33%)	32,52,52	1.44	3 (9%)

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	ACP	A	700	3	-	5/15/38/38	0/3/3/3
4	ACP	D	700	3	-	4/15/38/38	0/3/3/3
4	ACP	B	700	3	-	5/15/38/38	0/3/3/3
4	ACP	C	700	3	-	5/15/38/38	0/3/3/3

All (36) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	C	700	ACP	C2'-C1'	-3.39	1.48	1.53
4	A	700	ACP	C2'-C1'	-3.32	1.48	1.53
4	D	700	ACP	C2'-C1'	-3.31	1.48	1.53
4	B	700	ACP	C2'-C1'	-3.26	1.48	1.53
4	A	700	ACP	PB-O2B	-2.68	1.50	1.56
4	D	700	ACP	PB-O2B	-2.66	1.50	1.56
4	C	700	ACP	PB-O2B	-2.64	1.50	1.56
4	B	700	ACP	O4'-C4'	-2.64	1.39	1.45
4	B	700	ACP	PB-O2B	-2.64	1.50	1.56
4	D	700	ACP	O4'-C4'	-2.63	1.39	1.45
4	A	700	ACP	O4'-C4'	-2.62	1.39	1.45
4	C	700	ACP	O4'-C4'	-2.60	1.39	1.45
4	B	700	ACP	C6-N6	2.57	1.43	1.34
4	D	700	ACP	C6-N6	2.55	1.43	1.34
4	C	700	ACP	C6-N6	2.54	1.43	1.34
4	A	700	ACP	C6-N6	2.53	1.43	1.34
4	B	700	ACP	O2'-C2'	-2.16	1.37	1.43
4	A	700	ACP	PG-O3G	-2.16	1.50	1.54
4	C	700	ACP	PG-O3G	-2.15	1.50	1.54
4	C	700	ACP	O3'-C3'	-2.14	1.37	1.43
4	B	700	ACP	O3'-C3'	-2.14	1.37	1.43

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	700	ACP	C2'-C3'	-2.14	1.47	1.53
4	A	700	ACP	O2'-C2'	-2.13	1.37	1.43
4	D	700	ACP	PG-O3G	-2.13	1.50	1.54
4	A	700	ACP	O3'-C3'	-2.13	1.38	1.43
4	D	700	ACP	C2'-C3'	-2.13	1.47	1.53
4	D	700	ACP	O2'-C2'	-2.13	1.38	1.43
4	C	700	ACP	C2'-C3'	-2.13	1.47	1.53
4	C	700	ACP	O2'-C2'	-2.12	1.38	1.43
4	C	700	ACP	PG-O2G	-2.10	1.50	1.54
4	B	700	ACP	PG-O2G	-2.10	1.50	1.54
4	B	700	ACP	C2'-C3'	-2.10	1.47	1.53
4	D	700	ACP	O3'-C3'	-2.09	1.38	1.43
4	B	700	ACP	PG-O3G	-2.08	1.50	1.54
4	A	700	ACP	PG-O2G	-2.08	1.50	1.54
4	D	700	ACP	PG-O2G	-2.07	1.50	1.54

All (12) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	700	ACP	N3-C2-N1	-4.42	121.78	128.68
4	B	700	ACP	N3-C2-N1	-4.39	121.81	128.68
4	D	700	ACP	N3-C2-N1	-4.38	121.83	128.68
4	C	700	ACP	N3-C2-N1	-4.36	121.86	128.68
4	D	700	ACP	PA-O3A-PB	-4.13	119.47	132.56
4	A	700	ACP	PA-O3A-PB	-4.13	119.48	132.56
4	B	700	ACP	PA-O3A-PB	-4.12	119.49	132.56
4	C	700	ACP	PA-O3A-PB	-4.11	119.53	132.56
4	B	700	ACP	C3'-C2'-C1'	3.02	105.53	100.98
4	A	700	ACP	C3'-C2'-C1'	3.00	105.50	100.98
4	C	700	ACP	C3'-C2'-C1'	2.96	105.44	100.98
4	D	700	ACP	C3'-C2'-C1'	2.89	105.33	100.98

There are no chirality outliers.

All (19) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	A	700	ACP	PB-C3B-PG-O1G
4	A	700	ACP	PG-C3B-PB-O1B
4	D	700	ACP	PB-C3B-PG-O1G
4	D	700	ACP	PG-C3B-PB-O1B
4	D	700	ACP	PG-C3B-PB-O2B
4	B	700	ACP	PB-C3B-PG-O2G

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Mol	Chain	Res	Type	Atoms
4	B	700	ACP	PG-C3B-PB-O1B
4	B	700	ACP	PG-C3B-PB-O2B
4	B	700	ACP	PG-C3B-PB-O3A
4	C	700	ACP	PB-C3B-PG-O1G
4	C	700	ACP	PB-C3B-PG-O2G
4	C	700	ACP	PG-C3B-PB-O2B
4	A	700	ACP	PB-C3B-PG-O2G
4	A	700	ACP	PG-C3B-PB-O2B
4	D	700	ACP	PB-C3B-PG-O2G
4	B	700	ACP	PB-C3B-PG-O3G
4	C	700	ACP	PB-C3B-PG-O3G
4	A	700	ACP	PG-C3B-PB-O3A
4	C	700	ACP	PG-C3B-PB-O1B

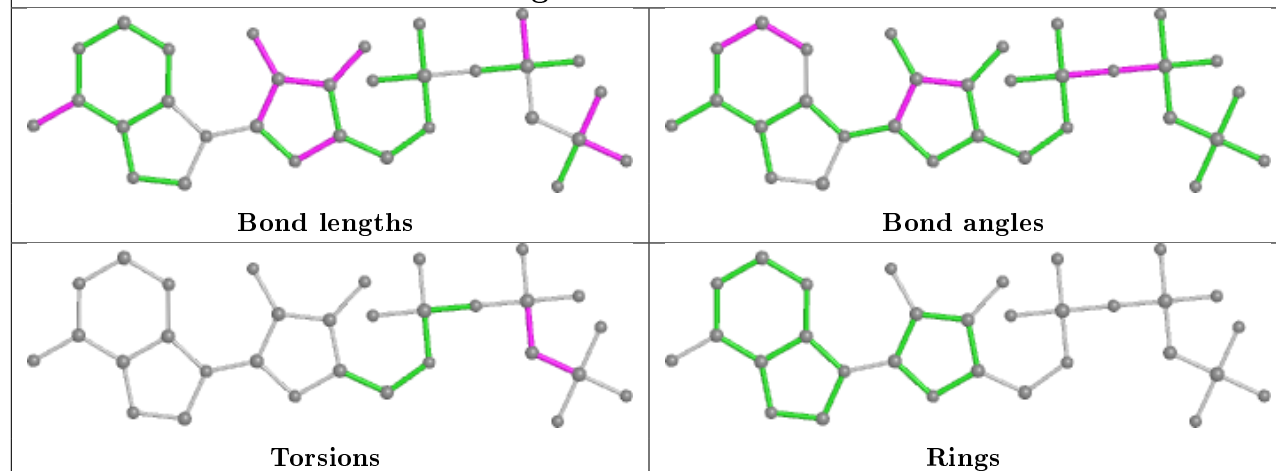
There are no ring outliers.

4 monomers are involved in 49 short contacts:

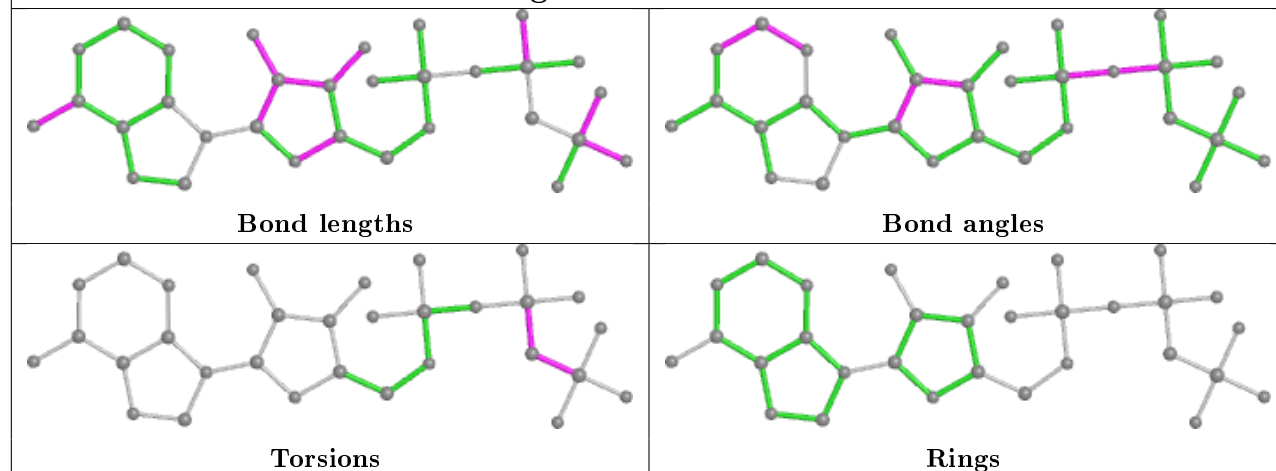
Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	700	ACP	13	0
4	D	700	ACP	13	0
4	B	700	ACP	13	0
4	C	700	ACP	10	0

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.

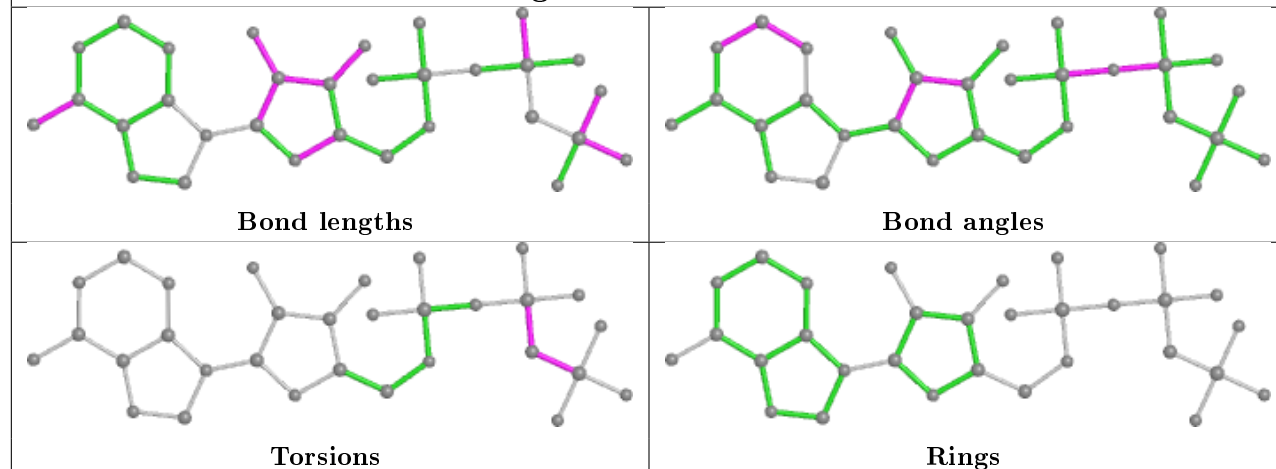
Ligand ACP A 700

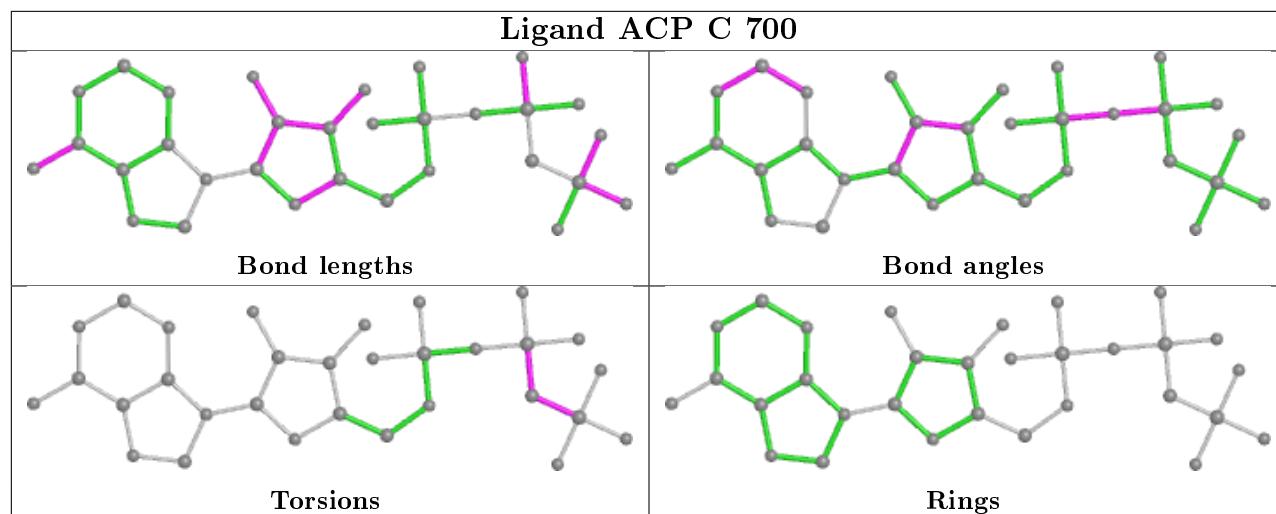


Ligand ACP D 700



Ligand ACP B 700





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	319/324 (98%)	0.11	13 (4%) 37 39	42, 84, 203, 303	0
1	B	319/324 (98%)	0.09	10 (3%) 49 52	41, 89, 189, 391	0
1	C	319/324 (98%)	0.29	32 (10%) 7 8	47, 96, 210, 359	0
1	D	319/324 (98%)	0.19	19 (5%) 21 24	42, 90, 215, 341	0
2	E	12/12 (100%)	1.50	2 (16%) 1 2	101, 125, 183, 202	0
All	All	1288/1308 (98%)	0.18	76 (5%) 22 25	41, 90, 208, 391	0

All (76) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	311	PHE	6.1
1	D	381	ARG	5.2
1	C	375	GLU	4.6
1	A	296	ARG	4.1
1	D	368	HIS	4.0
1	C	331	ARG	3.9
1	C	316	TYR	3.8
1	B	311	PHE	3.7
1	C	310	GLU	3.6
1	A	389	PHE	3.6
1	C	315	TYR	3.5
1	B	335	ALA	3.5
1	C	345	LYS	3.4
1	D	383	PHE	3.4
1	C	389	PHE	3.3
1	C	388	GLY	3.3
1	B	310	GLU	3.1
1	D	322	ASP	3.1
1	D	373	VAL	3.0
1	A	260	GLU	3.0

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Mol	Chain	Res	Type	RSRZ
1	A	387	VAL	3.0
1	B	385	HIS	2.9
1	D	399	CYS	2.9
1	A	310	GLU	2.9
1	C	322	ASP	2.9
1	C	387	VAL	2.9
1	A	385	HIS	2.8
1	C	312	VAL	2.8
1	D	315	TYR	2.8
1	D	385	HIS	2.7
1	D	375	GLU	2.7
1	D	314	ASN	2.7
1	D	316	TYR	2.7
1	C	376	GLU	2.7
1	A	345	LYS	2.7
1	C	384	LYS	2.6
1	A	399	CYS	2.6
1	B	389	PHE	2.5
1	C	391	GLU	2.5
1	A	381	ARG	2.5
1	C	399	CYS	2.5
1	C	338	ILE	2.5
1	C	341	TYR	2.5
1	C	291	PHE	2.5
1	C	317	ALA	2.4
1	D	340	MET	2.4
1	D	377	LYS	2.4
1	B	386	LEU	2.4
1	C	321	GLU	2.4
1	C	368	HIS	2.4
2	E	12	DA	2.4
1	A	311	PHE	2.4
1	D	331	ARG	2.4
1	C	396	ASP	2.3
1	C	390	LEU	2.3
1	B	392	LYS	2.3
1	C	319	LYS	2.3
1	B	165	ASN	2.3
1	D	317	ALA	2.3
1	D	384	LYS	2.3
1	C	372	SER	2.3
1	B	381	ARG	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	393	GLN	2.2
1	D	376	GLU	2.2
1	C	304	LYS	2.2
1	A	299	ARG	2.1
1	D	345	LYS	2.1
1	C	392	LYS	2.1
1	D	332	THR	2.1
1	C	344	ARG	2.1
1	A	390	LEU	2.0
1	C	398	ILE	2.0
1	C	381	ARG	2.0
2	E	1	DA	2.0
1	B	396	ASP	2.0
1	C	358	PHE	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](#)

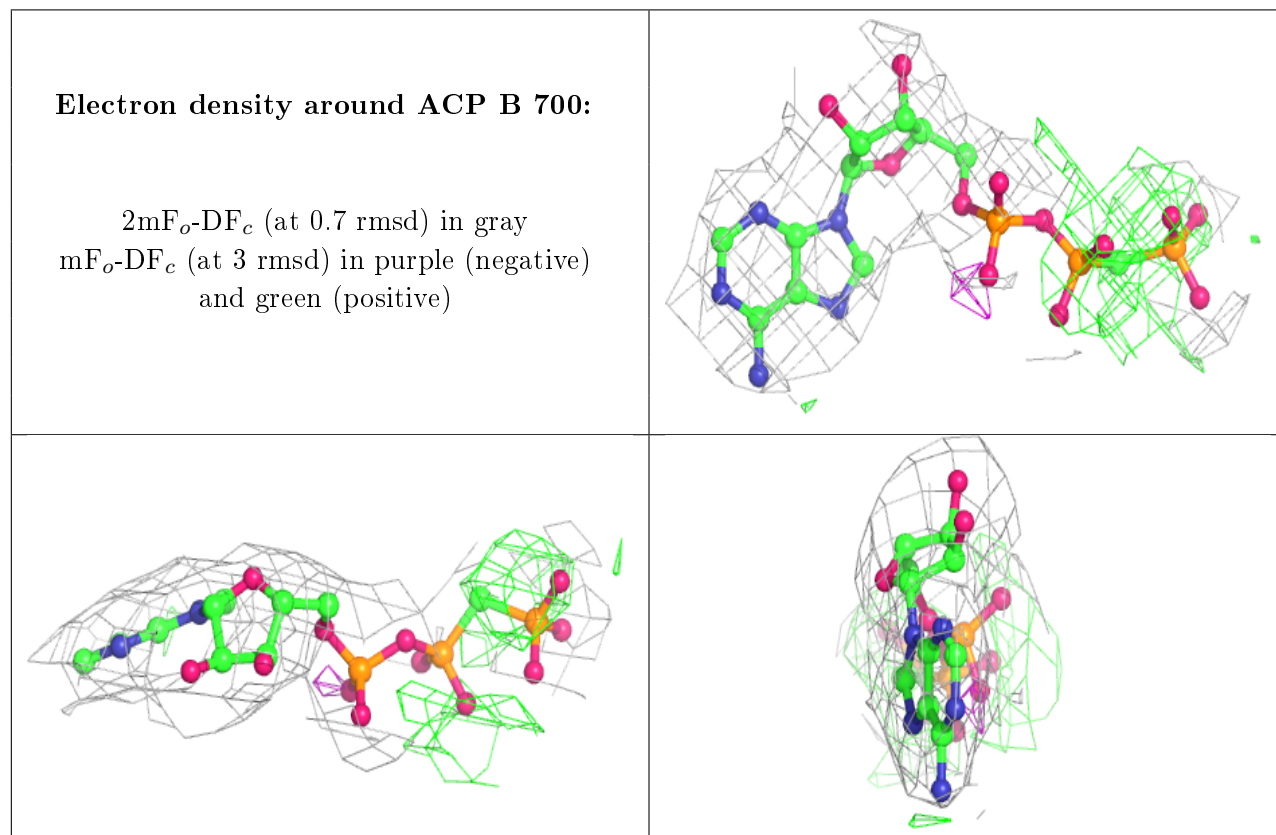
There are no carbohydrates in this entry.

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.

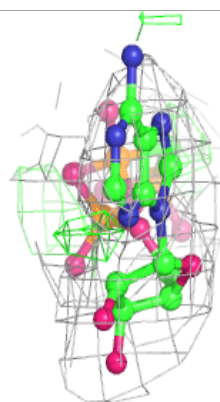
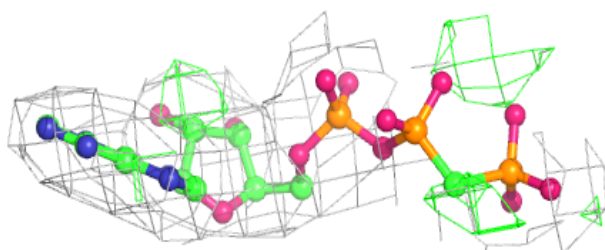
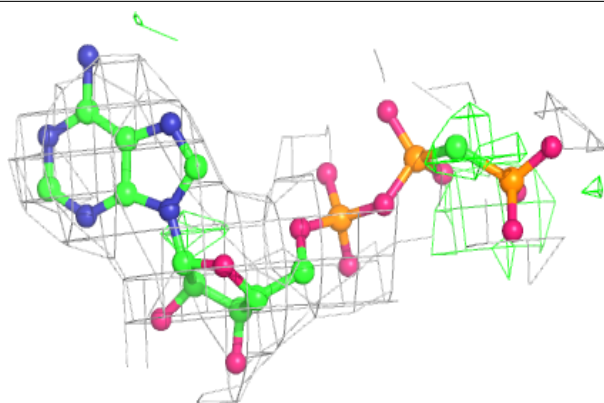
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MG	C	401	1/1	0.89	0.46	67,67,67,67	0
3	MG	B	401	1/1	0.90	0.55	48,48,48,48	0
4	ACP	B	700	31/31	0.92	0.25	42,68,82,88	0
4	ACP	C	700	31/31	0.93	0.27	55,69,85,90	0
4	ACP	A	700	31/31	0.95	0.22	33,66,83,85	0
4	ACP	D	700	31/31	0.95	0.23	43,73,84,93	0
3	MG	A	401	1/1	0.95	0.33	65,65,65,65	0
3	MG	D	401	1/1	0.96	0.29	50,50,50,50	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.

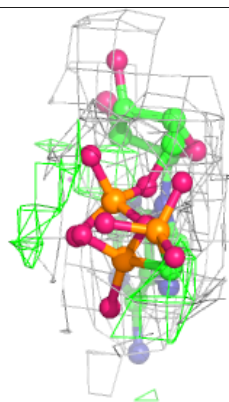
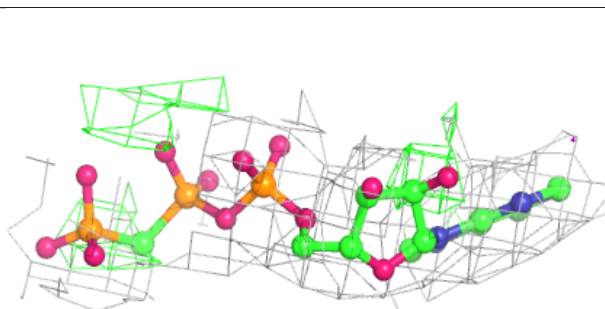
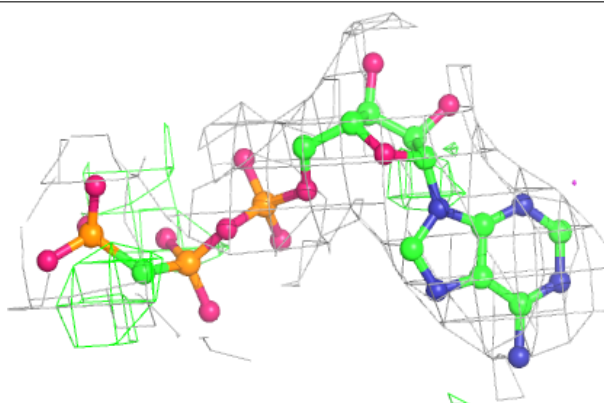


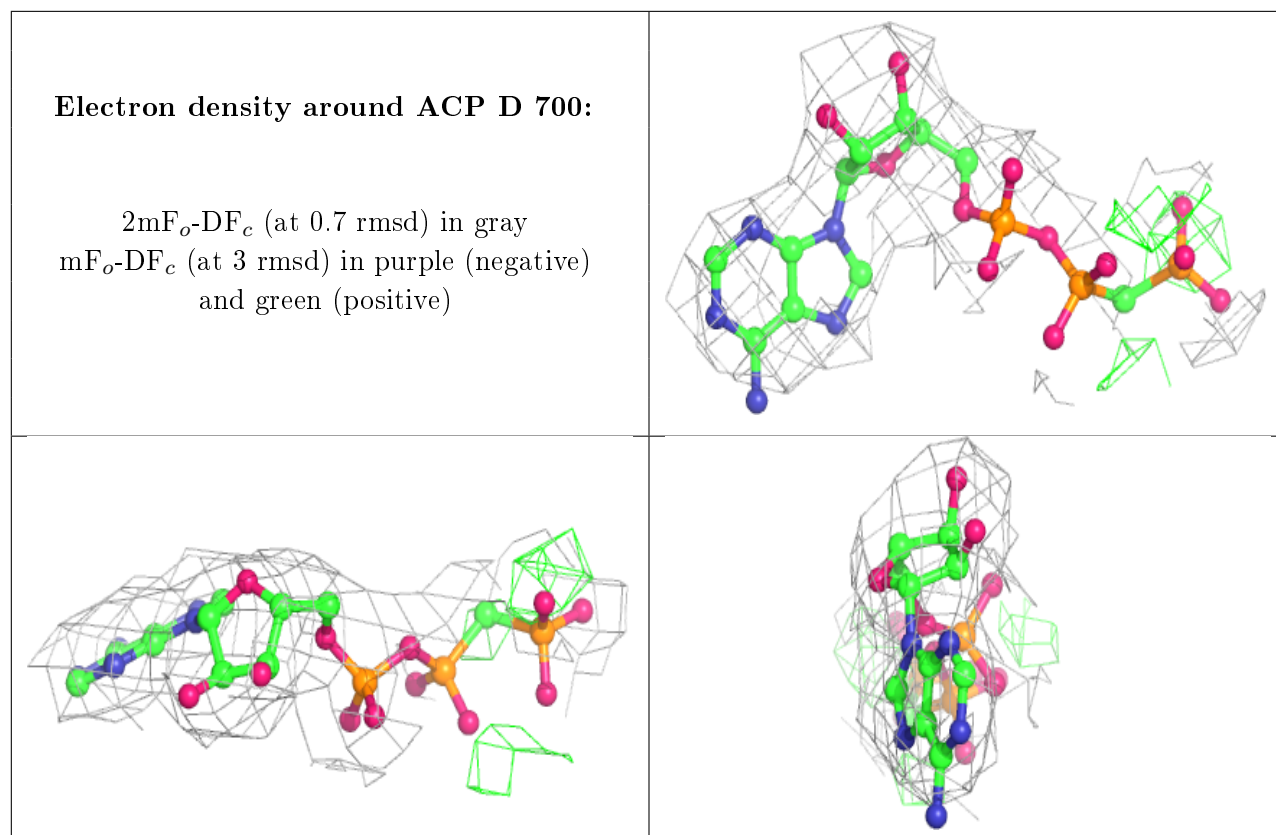
Electron density around ACP C 700:

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

**Electron density around ACP A 700:**

$2mF_o-DF_c$ (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.