



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 09:39 PM UTC

PDB ID : 9DM9 / pdb_00009dm9
Title : HIV-RT pre-catalytic complex with MK-8527
Authors : Hayes, R.P.; Tummala, S.
Deposited on : 2024-09-12
Resolution : 2.73 Å(reported)

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

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

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

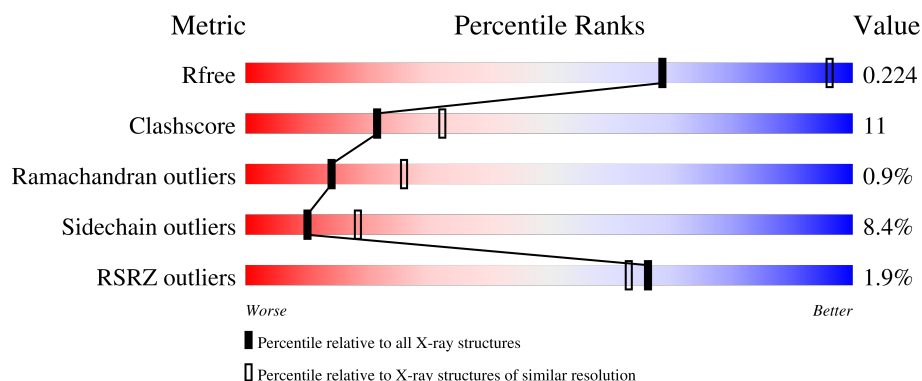
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.73 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	1819 (2.76-2.72)
Clashscore	190562	1866 (2.76-2.72)
Ramachandran outliers	187476	1830 (2.76-2.72)
Sidechain outliers	187428	1831 (2.76-2.72)
RSRZ outliers	180081	1819 (2.76-2.72)

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

Mol	Chain	Length	Quality of chain
1	A	562	<div> <div>3%</div> <div>66%</div> <div>29%</div> <div>..</div> </div>
2	B	455	<div> <div>%</div> <div>58%</div> <div>25%</div> <div>13%</div> </div>
3	P	21	<div> <div>57%</div> <div>29%</div> <div>14%</div> </div>
4	T	27	<div> <div>44%</div> <div>41%</div> <div>15%</div> </div>

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8622 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 Reverse transcriptase/ribonuclease H.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	549	Total	C	N	O	S	0	0	0
			4477	2896	749	824	8			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P04585
A	0	VAL	-	expression tag	UNP P04585
A	258	CYS	GLN	engineered mutation	UNP P04585
A	280	SER	CYS	engineered mutation	UNP P04585

- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	395	Total	C	N	O	S	0	0	0
			3263	2120	545	592	6			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-14	MET	-	expression tag	UNP P04585
B	-13	ALA	-	expression tag	UNP P04585
B	-12	HIS	-	expression tag	UNP P04585
B	-11	HIS	-	expression tag	UNP P04585
B	-10	HIS	-	expression tag	UNP P04585
B	-9	HIS	-	expression tag	UNP P04585
B	-8	HIS	-	expression tag	UNP P04585
B	-7	HIS	-	expression tag	UNP P04585
B	-6	LEU	-	expression tag	UNP P04585
B	-5	GLU	-	expression tag	UNP P04585
B	-4	VAL	-	expression tag	UNP P04585
B	-3	LEU	-	expression tag	UNP P04585

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-2	PHE	-	expression tag	UNP P04585
B	-1	GLN	-	expression tag	UNP P04585
B	0	GLY	-	expression tag	UNP P04585
B	280	SER	CYS	engineered mutation	UNP P04585

- Molecule 3 is a DNA chain called DNA Primer.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
3	P	18	Total	C	N	O	P	S	0	0	0
			370	176	64	111	18	1			

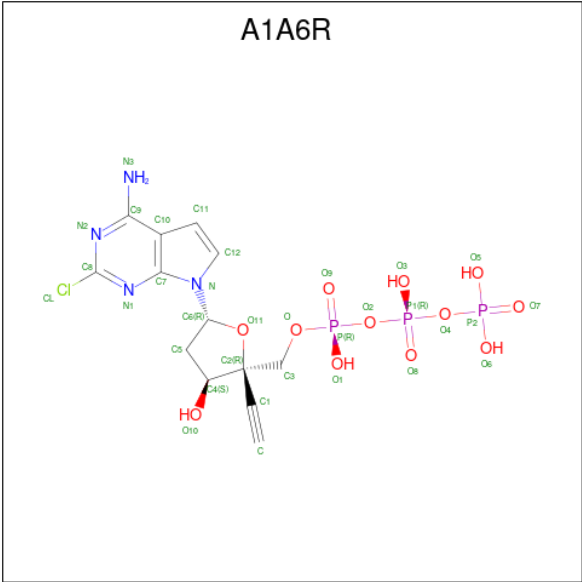
- Molecule 4 is a DNA chain called DNA Template.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	T	23	Total	C	N	O	P	0	0	0
			477	223	95	136	23			

- Molecule 5 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Mg	0	0
			2	2		

- Molecule 6 is 2-chloro-7-{(4xi)-2-deoxy-4-ethynyl-5-O-[(R)-hydroxy{[(R)-hydroxy(phosphonooxy)phosphoryl]oxy}phosphoryl]-beta-D-erythro-pentofuranosyl}-7H-pyrrolo[2,3-d]pyrimidin-4-amine (CCD ID: A1A6R) (formula: C₁₃H₁₆ClN₄O₁₂P₃) (labeled as "Ligand of Interest" by depositor).

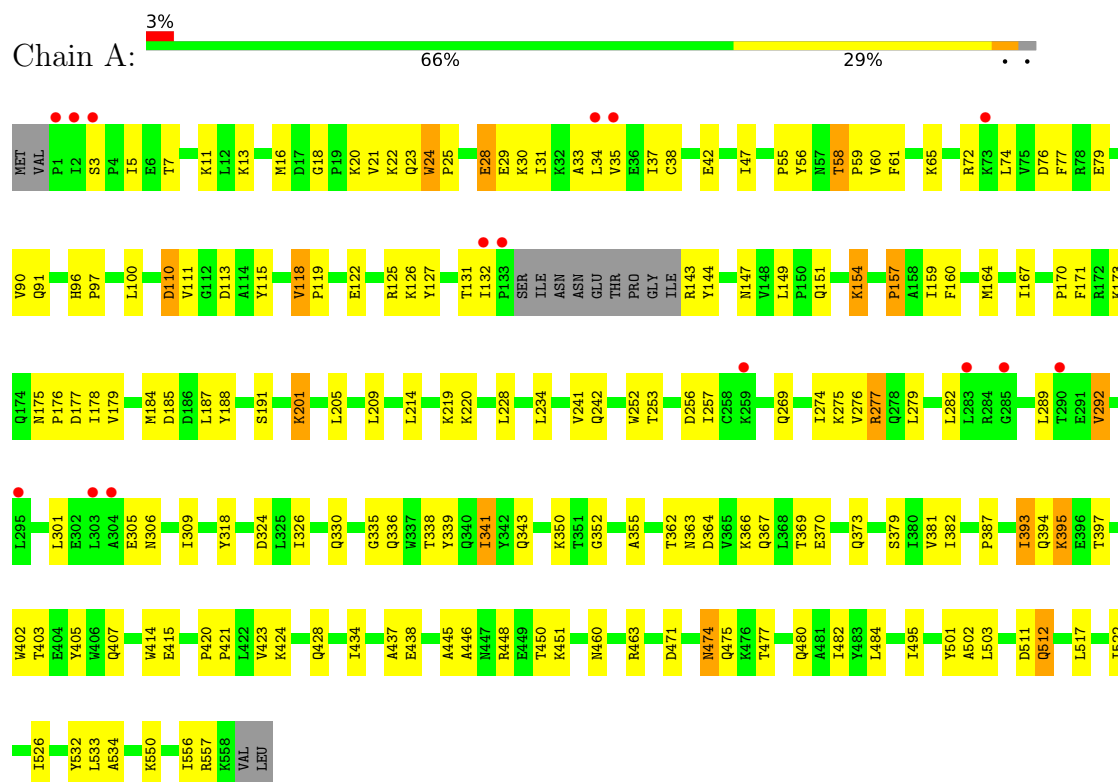


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	Cl	N	O	P		
6	A	1	33	13	1	4	12	3	0	0

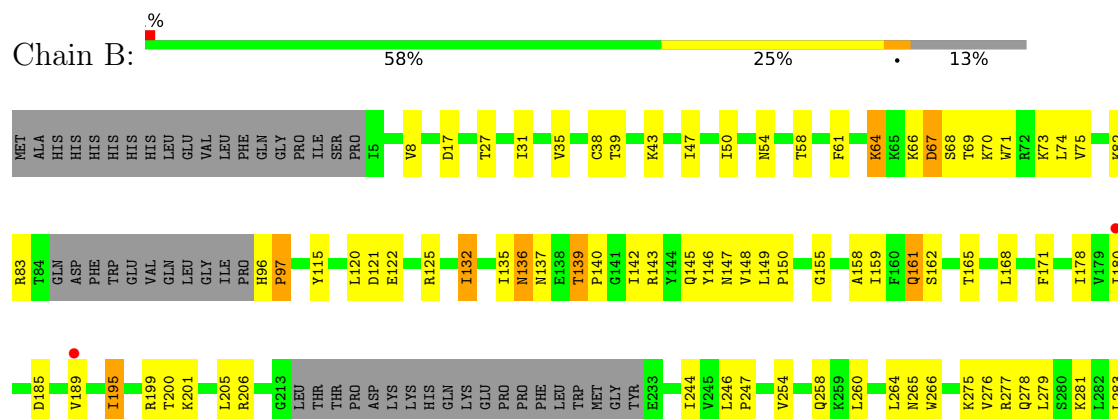
3 Residue-property plots

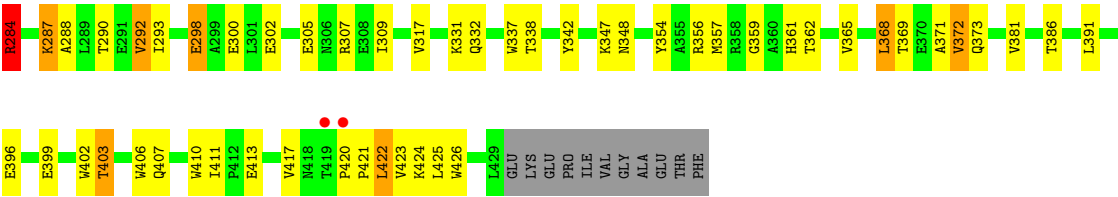
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density.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

• Molecule 1: Reverse transcriptase/ribonuclease H

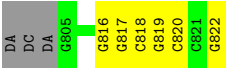


• Molecule 2: p51 RT

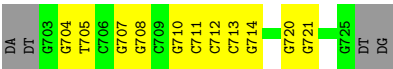




• Molecule 3: DNA Primer



• Molecule 4: DNA Template



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	163.91Å 170.81Å 101.45Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.50 – 2.73 38.50 – 2.73	Depositor EDS
% Data completeness (in resolution range)	60.9 (38.50-2.73) 60.9 (38.50-2.73)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.68 (at 2.72Å)	Xtriage
Refinement program	PHENIX (1.19.2_4158: ???)	Depositor
R, R_{free}	0.201 , 0.228 0.199 , 0.224	Depositor DCC
R_{free} test set	1110 reflections (2.92%)	wwPDB-VP
Wilson B-factor (Å ²)	67.7	Xtriage
Anisotropy	0.041	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 32.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.012 for -k,-h,-l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	8622	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.25% 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: MRG, A1A6R, 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	0.49	0/4592	0.69	0/6234
2	B	0.47	0/3352	0.66	0/4550
3	P	0.58	0/382	0.73	0/584
4	T	0.58	0/536	0.63	0/826
All	All	0.49	0/8862	0.68	0/12194

There are no bond length outliers.

There are no bond angle outliers.

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	4477	0	4536	101	0
2	B	3263	0	3305	73	0
3	P	370	0	206	9	0
4	T	477	0	256	8	0
5	A	2	0	0	0	0
6	A	33	0	0	2	0
All	All	8622	0	8303	182	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 11.

All (182) 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:277:ARG:HH12	1:A:355:ALA:HB1	1.50	0.76
3:P:816:DG:H2'	3:P:817:MRG:C8	2.15	0.76
1:A:28:GLU:O	1:A:31:ILE:N	2.21	0.74
1:A:184:MET:HG3	3:P:822:DG:H1'	1.71	0.71
2:B:305:GLU:O	2:B:309:ILE:HG13	1.92	0.70
1:A:34:LEU:HB3	1:A:132:ILE:HD12	1.74	0.69
3:P:817:MRG:H2'	3:P:818:DC:C6	2.28	0.68
2:B:247:PRO:O	2:B:307:ARG:NH2	2.26	0.68
2:B:35:VAL:O	2:B:39:THR:HG23	1.95	0.66
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.78	0.65
1:A:72:ARG:NH2	6:A:602:A1A6R:O9	2.21	0.65
1:A:111:VAL:HB	1:A:185:ASP:HB2	1.79	0.64
2:B:368:LEU:O	2:B:372:VAL:HG13	1.97	0.64
1:A:30:LYS:NZ	4:T:704:DG:O6	2.29	0.64
2:B:317:VAL:HG22	2:B:347:LYS:HG3	1.80	0.64
1:A:289:LEU:HD11	3:P:817:MRG:H4'	1.81	0.63
2:B:399:GLU:HA	2:B:402:TRP:HD1	1.64	0.62
2:B:357:MET:HE2	2:B:359:GLY:HA3	1.82	0.61
1:A:252:TRP:HD1	1:A:256:ASP:HB3	1.65	0.61
1:A:13:LYS:HB2	1:A:16:MET:HG3	1.83	0.61
2:B:421:PRO:HA	2:B:424:LYS:HB3	1.83	0.59
3:P:817:MRG:H2'	3:P:818:DC:H6	1.67	0.59
2:B:281:LYS:HB2	2:B:284:ARG:NH1	2.18	0.59
1:A:503:LEU:HD12	1:A:533:LEU:HD23	1.85	0.59
1:A:115:TYR:CD2	1:A:151:GLN:HG2	2.38	0.59
3:P:817:MRG:H8	3:P:817:MRG:O5'	2.03	0.58
2:B:64:LYS:HG3	2:B:71:TRP:CZ2	2.39	0.58
2:B:365:VAL:O	2:B:369:THR:HG23	2.04	0.58
1:A:402:TRP:CH2	2:B:362:THR:HB	2.39	0.57
1:A:96:HIS:NE2	1:A:269:GLN:OE1	2.35	0.57
2:B:54:ASN:O	2:B:143:ARG:NH2	2.38	0.57
1:A:395:LYS:HD3	1:A:414:TRP:CZ2	2.40	0.57
2:B:168:LEU:HD13	2:B:180:ILE:HG21	1.86	0.57
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.41	0.55
4:T:713:DC:H2'	4:T:714:DG:C8	2.41	0.55
2:B:50:ILE:HD13	2:B:145:GLN:HB3	1.87	0.54
2:B:354:TYR:CE2	2:B:356:ARG:HG2	2.42	0.54
1:A:339:TYR:CZ	1:A:352:GLY:HA3	2.43	0.54
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.43	0.54
1:A:394:GLN:O	1:A:397:THR:N	2.41	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:24:TRP:HB2	1:A:25:PRO:HD2	1.88	0.53
2:B:260:LEU:HD23	2:B:279:LEU:HD22	1.91	0.53
2:B:399:GLU:HA	2:B:402:TRP:CD1	2.42	0.53
2:B:17:ASP:O	2:B:83:ARG:NH1	2.42	0.53
2:B:64:LYS:HG3	2:B:71:TRP:CE2	2.43	0.53
1:A:495:ILE:HB	1:A:533:LEU:HD12	1.91	0.53
1:A:149:LEU:HD11	1:A:159:ILE:HG22	1.89	0.52
1:A:420:PRO:HA	1:A:421:PRO:C	2.34	0.52
2:B:266:TRP:CZ3	2:B:426:TRP:HB3	2.45	0.52
2:B:331:LYS:HB2	2:B:337:TRP:CZ3	2.44	0.52
1:A:175:ASN:OD1	1:A:201:LYS:HE3	2.10	0.51
1:A:382:ILE:O	2:B:136:ASN:HB2	2.10	0.51
1:A:460:ASN:ND2	2:B:288:ALA:HB2	2.26	0.51
1:A:100:LEU:O	1:A:318:TYR:HB3	2.11	0.51
1:A:277:ARG:NH1	1:A:355:ALA:HB1	2.24	0.51
2:B:246:LEU:HD11	2:B:264:LEU:HD21	1.93	0.50
1:A:20:LYS:HE2	1:A:55:PRO:HB2	1.94	0.50
2:B:275:LYS:HG3	2:B:302:GLU:HG3	1.92	0.50
1:A:279:LEU:O	1:A:282:LEU:HB2	2.11	0.50
1:A:393:ILE:HG13	1:A:423:VAL:HB	1.94	0.50
1:A:61:PHE:HE1	1:A:76:ASP:HB2	1.77	0.50
3:P:819:DG:H2'	3:P:820:DC:C6	2.46	0.50
4:T:710:DG:H2'	4:T:711:DC:C6	2.47	0.50
1:A:438:GLU:OE2	1:A:463:ARG:HD3	2.12	0.49
1:A:253:THR:H	1:A:256:ASP:HB2	1.76	0.49
1:A:522:ILE:O	1:A:526:ILE:HG13	2.12	0.49
1:A:38:CYS:HA	1:A:47:ILE:HD11	1.95	0.49
2:B:281:LYS:HB2	2:B:284:ARG:CZ	2.43	0.49
1:A:446:ALA:HB2	1:A:477:THR:HG21	1.96	0.48
2:B:120:LEU:HB2	2:B:148:VAL:O	2.13	0.48
2:B:195:ILE:HG23	2:B:199:ARG:NH1	2.27	0.48
1:A:362:THR:HG21	1:A:367:GLN:HE21	1.77	0.48
2:B:125:ARG:HD3	2:B:147:ASN:HA	1.95	0.48
1:A:366:LYS:O	1:A:370:GLU:HG3	2.13	0.48
1:A:324:ASP:O	1:A:343:GLN:HG2	2.14	0.48
1:A:31:ILE:O	1:A:35:VAL:HG13	2.14	0.47
1:A:125:ARG:HD3	1:A:147:ASN:HA	1.96	0.47
1:A:157:PRO:HG2	4:T:707:DG:O4'	2.14	0.47
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.14	0.47
2:B:391:LEU:O	2:B:417:VAL:HG12	2.13	0.47
1:A:451:LYS:HB3	1:A:471:ASP:HA	1.97	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:42:GLU:HG3	1:A:144:TYR:HE1	1.78	0.47
1:A:56:TYR:HE2	1:A:126:LYS:HD2	1.80	0.47
2:B:283:LEU:O	2:B:284:ARG:C	2.58	0.46
2:B:125:ARG:HD3	2:B:146:TYR:O	2.16	0.46
2:B:195:ILE:HD13	2:B:195:ILE:HA	1.62	0.46
2:B:342:TYR:HB3	2:B:348:ASN:HA	1.98	0.46
1:A:164:MET:HE2	1:A:187:LEU:HD21	1.97	0.46
1:A:115:TYR:HB3	1:A:149:LEU:O	2.15	0.46
1:A:160:PHE:CD1	1:A:160:PHE:C	2.93	0.46
1:A:511:ASP:HA	1:A:522:ILE:HD13	1.98	0.46
1:A:209:LEU:O	1:A:214:LEU:HB2	2.17	0.45
2:B:420:PRO:HB2	2:B:422:LEU:HD23	1.97	0.45
1:A:7:THR:HG22	1:A:119:PRO:HB2	1.98	0.45
2:B:64:LYS:O	2:B:407:GLN:NE2	2.37	0.45
2:B:283:LEU:HD23	2:B:283:LEU:HA	1.77	0.45
1:A:96:HIS:CG	1:A:97:PRO:HD2	2.52	0.45
2:B:292:VAL:O	2:B:293:ILE:HD13	2.17	0.45
2:B:373:GLN:HG3	2:B:406:TRP:CZ3	2.52	0.45
1:A:35:VAL:HG12	1:A:132:ILE:HG21	1.98	0.45
1:A:305:GLU:O	1:A:309:ILE:HG13	2.16	0.45
1:A:350:LYS:HB2	1:A:350:LYS:HE2	1.81	0.45
1:A:253:THR:HA	1:A:292:VAL:HA	1.99	0.45
2:B:298:GLU:H	2:B:298:GLU:CD	2.25	0.45
2:B:74:LEU:HA	2:B:74:LEU:HD23	1.66	0.45
2:B:189:VAL:HG21	2:B:205:LEU:HD23	1.98	0.45
1:A:474:ASN:O	1:A:477:THR:OG1	2.35	0.44
2:B:68:SER:C	2:B:70:LYS:H	2.25	0.44
1:A:97:PRO:HA	1:A:100:LEU:HD12	1.99	0.44
1:A:277:ARG:NH2	1:A:335:GLY:O	2.51	0.44
1:A:511:ASP:OD1	1:A:512:GLN:HG2	2.17	0.44
2:B:171:PHE:CZ	2:B:205:LEU:HB2	2.52	0.44
1:A:3:SER:HB3	1:A:5:ILE:HG22	2.00	0.44
1:A:532:TYR:CE2	1:A:534:ALA:HB2	2.53	0.44
2:B:122:GLU:HA	2:B:125:ARG:HG3	2.00	0.44
1:A:91:GLN:O	4:T:708:DG:H4'	2.17	0.44
2:B:155:GLY:O	2:B:159:ILE:HG12	2.18	0.44
1:A:167:ILE:O	1:A:170:PRO:HD2	2.18	0.43
2:B:278:GLN:O	2:B:281:LYS:HG2	2.18	0.43
1:A:379:SER:CB	1:A:387:PRO:HD3	2.48	0.43
1:A:517:LEU:HA	1:A:517:LEU:HD12	1.77	0.43
2:B:420:PRO:HB2	2:B:422:LEU:CD2	2.47	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:66:LYS:HG2	2:B:67:ASP:HB2	2.00	0.43
2:B:82:LYS:HD2	2:B:413:GLU:OE2	2.18	0.43
1:A:394:GLN:HB2	1:A:397:THR:OG1	2.19	0.43
1:A:434:ILE:HB	1:A:437:ALA:HB3	1.99	0.43
1:A:445:ALA:HB3	1:A:556:ILE:HD11	2.00	0.43
2:B:258:GLN:HG2	2:B:283:LEU:HD13	2.01	0.43
1:A:28:GLU:O	1:A:29:GLU:C	2.60	0.43
1:A:154:LYS:O	1:A:157:PRO:HD2	2.18	0.43
2:B:135:ILE:O	2:B:137:ASN:N	2.51	0.43
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.59	0.43
1:A:448:ARG:O	1:A:451:LYS:NZ	2.42	0.43
2:B:61:PHE:CE2	2:B:403:THR:HG22	2.53	0.43
2:B:356:ARG:HA	2:B:356:ARG:HD2	1.80	0.43
1:A:397:THR:HG21	1:A:424:LYS:HA	2.00	0.43
1:A:33:ALA:O	1:A:37:ILE:HG13	2.19	0.42
2:B:8:VAL:O	2:B:121:ASP:HB2	2.18	0.42
2:B:410:TRP:C	2:B:411:ILE:HG13	2.44	0.42
1:A:274:ILE:HA	1:A:306:ASN:OD1	2.18	0.42
1:A:482:ILE:HD12	1:A:502:ALA:HB1	2.01	0.42
1:A:18:GLY:HA3	1:A:127:TYR:HD1	1.84	0.42
3:P:819:DG:H2'	3:P:820:DC:H6	1.84	0.42
1:A:301:LEU:O	1:A:305:GLU:HG2	2.19	0.42
1:A:110:ASP:HB3	1:A:220:LYS:HB3	2.01	0.42
1:A:480:GLN:HG2	1:A:517:LEU:HD21	2.01	0.42
2:B:178:ILE:HD11	2:B:201:LYS:HG2	2.01	0.42
3:P:816:DG:H2'	3:P:817:MRG:H8	1.99	0.42
2:B:254:VAL:HG21	2:B:287:LYS:HB2	2.02	0.42
1:A:131:THR:OG1	1:A:143:ARG:HG2	2.20	0.42
4:T:711:DC:H2'	4:T:712:DC:C6	2.54	0.42
1:A:178:ILE:CD1	1:A:201:LYS:HG2	2.50	0.42
1:A:252:TRP:CD1	1:A:256:ASP:HB3	2.50	0.42
1:A:326:ILE:O	1:A:341:ILE:HA	2.19	0.42
2:B:27:THR:O	2:B:31:ILE:HG13	2.20	0.42
1:A:228:LEU:HD22	1:A:242:GLN:OE1	2.20	0.41
2:B:158:ALA:O	2:B:161:GLN:HB2	2.20	0.41
2:B:332:GLN:HE21	2:B:338:THR:HG21	1.84	0.41
1:A:176:PRO:HG2	1:A:177:ASP:OD2	2.20	0.41
1:A:364:ASP:HB3	1:A:423:VAL:HG13	2.02	0.41
2:B:96:HIS:HA	2:B:97:PRO:HD3	1.90	0.41
1:A:65:LYS:NZ	6:A:602:A1A6R:O7	2.44	0.41
2:B:139:THR:HG23	2:B:140:PRO:O	2.21	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:244:ILE:H	2:B:244:ILE:HG13	1.72	0.41
2:B:421:PRO:HB3	2:B:424:LYS:HD3	2.02	0.41
1:A:122:GLU:HG2	1:A:125:ARG:CZ	2.51	0.41
1:A:228:LEU:HD23	1:A:228:LEU:HA	1.69	0.41
1:A:450:THR:O	1:A:451:LYS:HB2	2.20	0.41
2:B:368:LEU:O	2:B:371:ALA:HB3	2.20	0.41
1:A:58:THR:HG21	1:A:77:PHE:CD1	2.56	0.41
2:B:38:CYS:O	2:B:47:ILE:HD11	2.20	0.41
1:A:253:THR:O	1:A:257:ILE:HG12	2.21	0.41
2:B:149:LEU:HA	2:B:150:PRO:HD3	1.93	0.41
4:T:720:DG:H2''	4:T:721:DG:C8	2.55	0.41
2:B:115:TYR:HB3	2:B:149:LEU:HB2	2.03	0.40
2:B:396:GLU:H	2:B:396:GLU:HG2	1.64	0.40
1:A:74:LEU:HD13	4:T:705:DT:N3	2.36	0.40
1:A:118:VAL:HG12	1:A:149:LEU:HG	2.02	0.40
1:A:171:PHE:CZ	1:A:205:LEU:HB2	2.56	0.40
1:A:126:LYS:HE2	1:A:127:TYR:CZ	2.57	0.40
1:A:277:ARG:HB3	1:A:336:GLN:CD	2.47	0.40
2:B:277:ARG:HD3	2:B:277:ARG:HA	1.86	0.40

There are no symmetry-related clashes.

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	545/562 (97%)	503 (92%)	39 (7%)	3 (1%)	21	36
2	B	389/455 (86%)	352 (90%)	32 (8%)	5 (1%)	9	16
All	All	934/1017 (92%)	855 (92%)	71 (8%)	8 (1%)	14	26

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	B	284	ARG
2	B	136	ASN
2	B	69	THR
1	A	395	LYS
1	A	403	THR
2	B	161	GLN
2	B	97	PRO
1	A	157	PRO

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	490/502 (98%)	451 (92%)	39 (8%)	11	20
2	B	359/413 (87%)	327 (91%)	32 (9%)	9	17
All	All	849/915 (93%)	778 (92%)	71 (8%)	10	18

All (71) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	11	LYS
1	A	22	LYS
1	A	23	GLN
1	A	24	TRP
1	A	28	GLU
1	A	58	THR
1	A	60	VAL
1	A	79	GLU
1	A	90	VAL
1	A	110	ASP
1	A	113	ASP
1	A	118	VAL
1	A	154	LYS
1	A	173	LYS
1	A	179	VAL
1	A	188	TYR

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Mol	Chain	Res	Type
1	A	191	SER
1	A	201	LYS
1	A	219	LYS
1	A	234	LEU
1	A	241	VAL
1	A	275	LYS
1	A	276	VAL
1	A	277	ARG
1	A	292	VAL
1	A	330	GLN
1	A	338	THR
1	A	341	ILE
1	A	369	THR
1	A	373	GLN
1	A	381	VAL
1	A	393	ILE
1	A	415	GLU
1	A	428	GLN
1	A	474	ASN
1	A	484	LEU
1	A	512	GLN
1	A	550	LYS
1	A	557	ARG
2	B	43	LYS
2	B	58	THR
2	B	64	LYS
2	B	67	ASP
2	B	73	LYS
2	B	75	VAL
2	B	132	ILE
2	B	139	THR
2	B	142	ILE
2	B	162	SER
2	B	165	THR
2	B	185	ASP
2	B	195	ILE
2	B	200	THR
2	B	206	ARG
2	B	265	ASN
2	B	276	VAL
2	B	284	ARG
2	B	287	LYS

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Mol	Chain	Res	Type
2	B	290	THR
2	B	292	VAL
2	B	298	GLU
2	B	300	GLU
2	B	361	HIS
2	B	368	LEU
2	B	372	VAL
2	B	381	VAL
2	B	386	THR
2	B	403	THR
2	B	422	LEU
2	B	423	VAL
2	B	425	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (8) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	145	GLN
1	A	334	GLN
1	A	500	GLN
1	A	545	ASN
2	B	137	ASN
2	B	235	HIS
2	B	255	ASN
2	B	258	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	MRG	P	817	4,3	25,28,29	0.21	0	32,39,42	0.38	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
3	MRG	P	817	4,3	-	3/12/26/27	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	P	817	MRG	N2-C21-C22-C23
3	P	817	MRG	N3-C2-N2-C21
3	P	817	MRG	N1-C2-N2-C21

There are no ring outliers.

1 monomer is involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	P	817	MRG	6	0

5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 3 ligands modelled in this entry, 2 are monoatomic - leaving 1 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	$\# Z > 2$
6	A1A6R	A	602	5	31,35,35	0.29	0	37,56,56	0.38	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
6	A1A6R	A	602	5	-	5/23/41/41	0/3/3/3

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	A	602	A1A6R	P1-O4-P2-O5
6	A	602	A1A6R	P-O2-P1-O3
6	A	602	A1A6R	P1-O4-P2-O7
6	A	602	A1A6R	P1-O4-P2-O6
6	A	602	A1A6R	P-O2-P1-O8

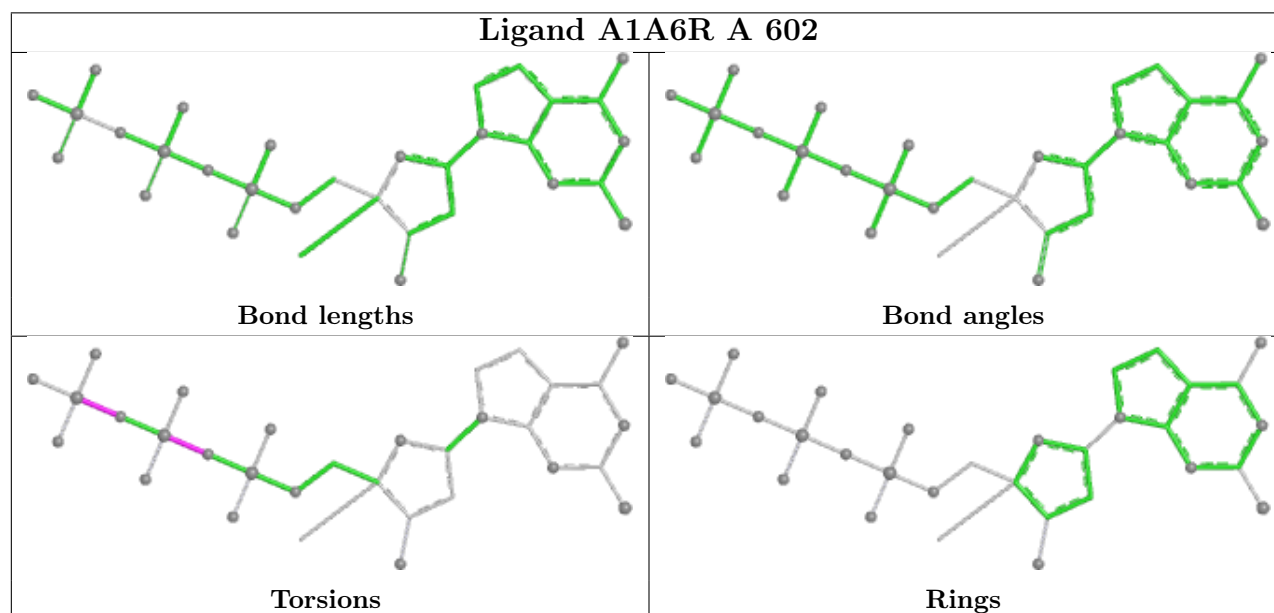
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	602	A1A6R	2	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier.

The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.



5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

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

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	549/562 (97%)	0.09	15 (2%) 56 53	22, 49, 95, 116	0
2	B	395/455 (86%)	-0.09	4 (1%) 79 79	26, 50, 86, 106	0
3	P	17/21 (80%)	-0.55	0 100 100	39, 56, 70, 72	0
4	T	23/27 (85%)	-0.38	0 100 100	32, 60, 89, 134	0
All	All	984/1065 (92%)	-0.00	19 (1%) 66 63	22, 50, 92, 134	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	2	ILE	5.0
1	A	283	LEU	2.9
2	B	420	PRO	2.9
1	A	1	PRO	2.9
1	A	73	LYS	2.7
1	A	132	ILE	2.6
1	A	290	THR	2.5
1	A	303	LEU	2.5
1	A	3	SER	2.4
1	A	34	LEU	2.3
1	A	295	LEU	2.3
1	A	35	VAL	2.3
1	A	304	ALA	2.2
2	B	180	ILE	2.2
2	B	419	THR	2.2
1	A	285	GLY	2.1
1	A	133	PRO	2.1
1	A	259	LYS	2.0
2	B	189	VAL	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [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
3	MRG	P	817	26/27	0.89	0.11	58,69,74,88	0

6.3 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

6.4 Ligands [i](#)

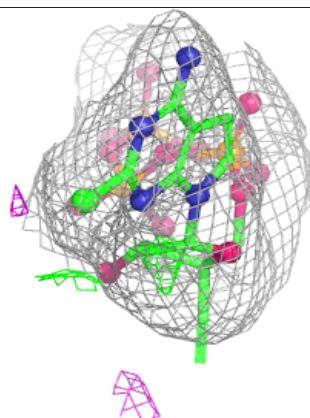
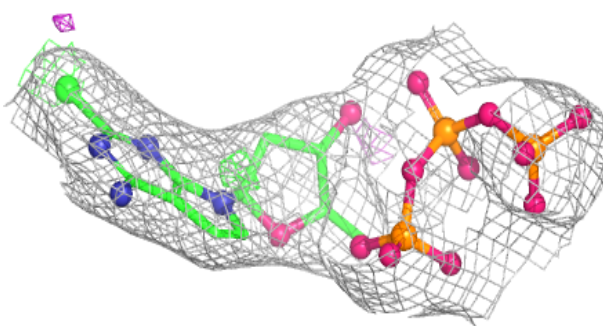
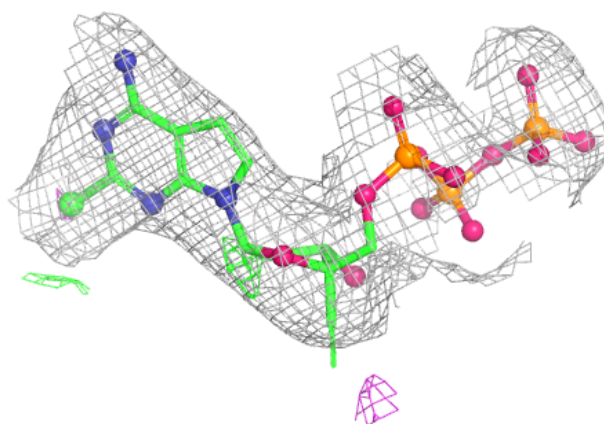
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	MG	A	601	1/1	0.83	0.26	46,46,46,46	0
6	A1A6R	A	602	33/33	0.93	0.09	34,47,60,62	0
5	MG	A	603	1/1	0.98	0.11	44,44,44,44	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 A1A6R A 602:

$2mF_o-DF_c$ (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.