



Full wwPDB X-ray Structure Validation Report ⓘ

May 29, 2020 – 10:38 am BST

PDB ID : 5VQR
Title : Crystal Structure of HIV-1 Reverse Transcriptase in Complex with N-(6-cyan
o-3-(2-(2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy)phenoxy)-4-methy
lnaphthalen-1-yl)-N-methylacrylamide (JLJ684), a Non-nucleoside Inhibitor
Authors : Chan, A.H.; Anderson, K.S.
Deposited on : 2017-05-09
Resolution : 2.55 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

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

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

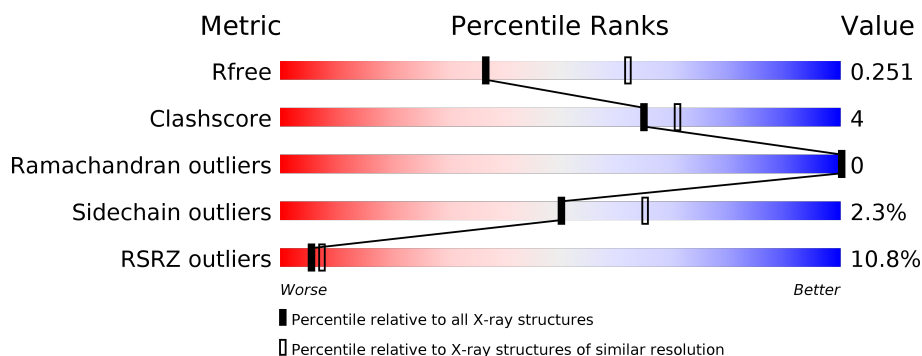
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.55 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	1284 (2.56-2.52)
Clashscore	141614	1332 (2.56-2.52)
Ramachandran outliers	138981	1315 (2.56-2.52)
Sidechain outliers	138945	1315 (2.56-2.52)
RSRZ outliers	127900	1272 (2.56-2.52)

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	557	<div> <div>10%</div> <div>85%</div> <div>12%</div> <div>..</div> </div>
2	B	428	<div> <div>11%</div> <div>82%</div> <div>11%</div> <div>7%</div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7802 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	547	Total	C	N	O	S	0	0	0
			4413	2861	726	818	8			

There are 5 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	MET	-	expression tag	UNP P03366
A	0	VAL	-	expression tag	UNP P03366
A	172	ALA	LYS	engineered mutation	UNP P03366
A	173	ALA	LYS	engineered mutation	UNP P03366
A	280	SER	CYS	engineered mutation	UNP P03366

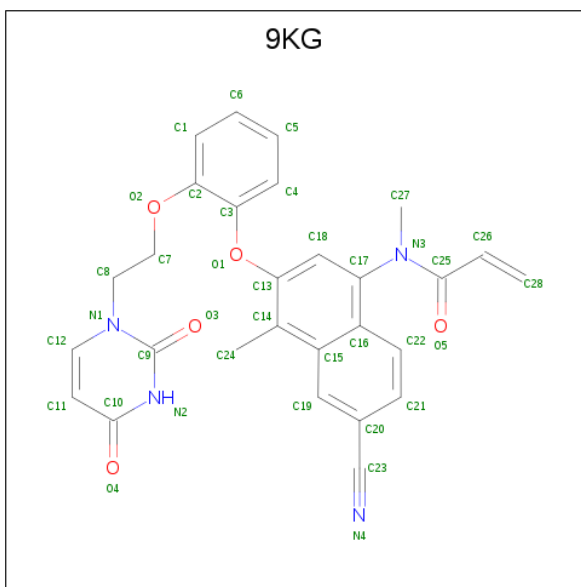
- Molecule 2 is a protein called p51 RT.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	400	Total	C	N	O	S	0	0	0
			3307	2152	547	602	6			

There is a discrepancy between the modelled and reference sequences:

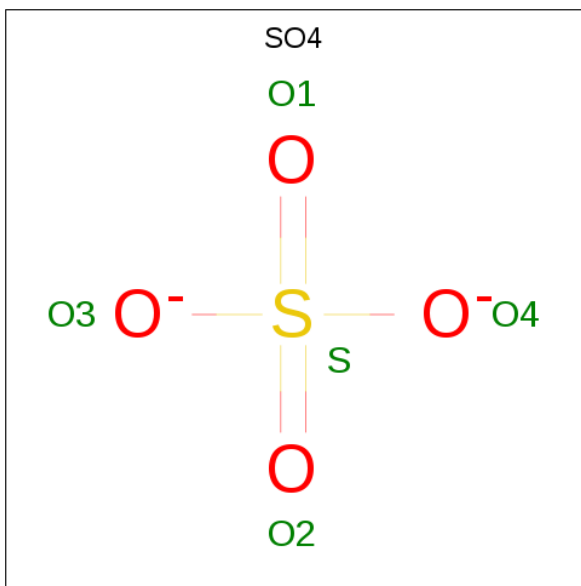
Chain	Residue	Modelled	Actual	Comment	Reference
B	280	SER	CYS	engineered mutation	UNP P03366

- Molecule 3 is N-(6-cyano-3-{2-[2-(2,4-dioxo-3,4-dihydropyrimidin-1(2H)-yl)ethoxy]phenoxy}-4-methylnaphthalen-1-yl)-N-methylprop-2-enamide (three-letter code: 9KG) (formula: C₂₈H₂₄N₄O₅).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			37	28	4	5		

- Molecule 4 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



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

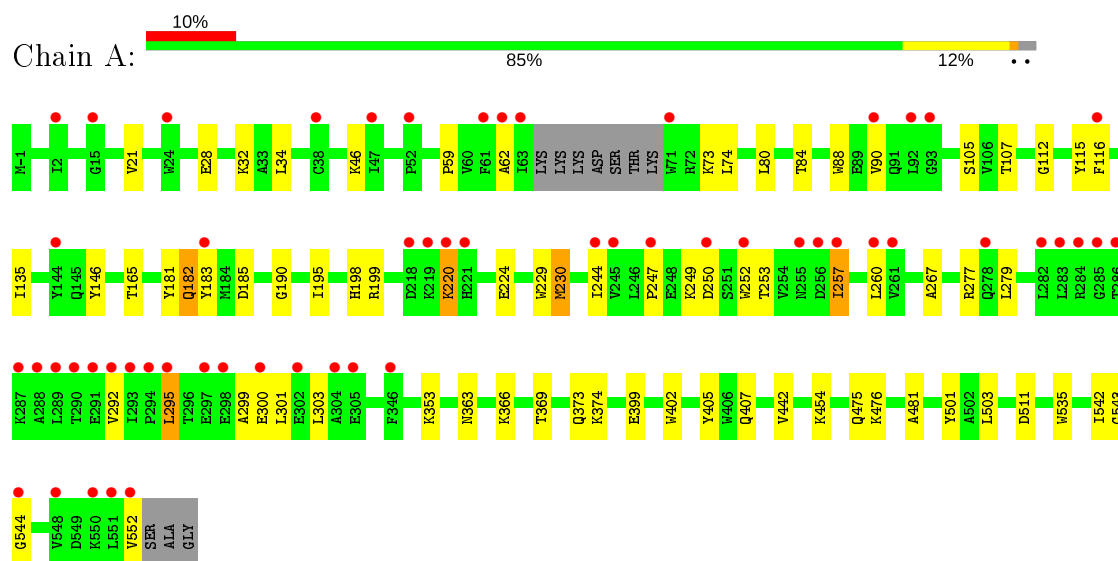
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	24	Total 24	O 24	0	0
5	B	16	Total 16	O 16	0	0

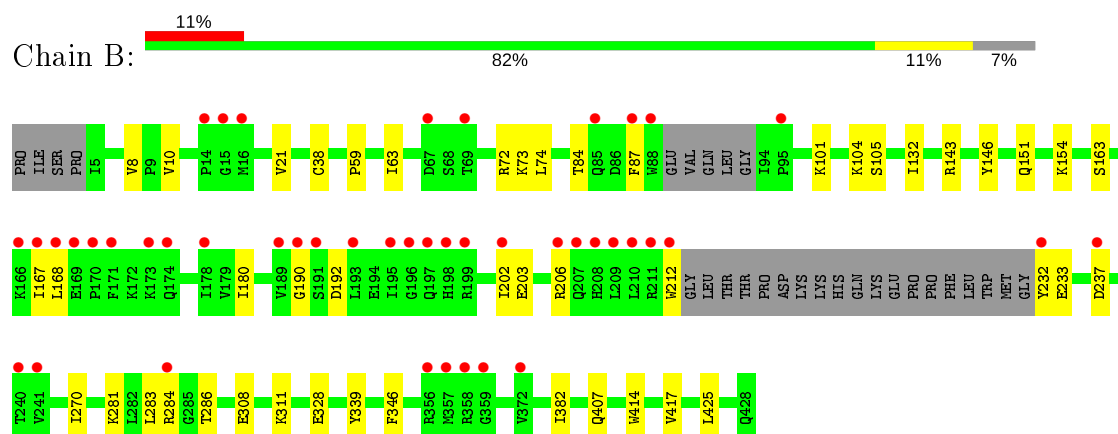
3 Residue-property plots [i](#)

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: Reverse transcriptase/ribonuclease H



- Molecule 2: p51 RT



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	162.43 Å 73.73 Å 108.35 Å 90.00° 99.69° 90.00°	Depositor
Resolution (Å)	43.23 – 2.55 43.23 – 2.55	Depositor EDS
% Data completeness (in resolution range)	99.2 (43.23-2.55) 94.5 (43.23-2.55)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.05 (at 2.54 Å)	Xtriage
Refinement program	PHENIX 1.10.1 _2155	Depositor
R, R_{free}	0.226 , 0.250 0.226 , 0.251	Depositor DCC
R_{free} test set	2000 reflections (4.87%)	wwPDB-VP
Wilson B-factor (Å ²)	56.2	Xtriage
Anisotropy	0.088	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 46.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7802	wwPDB-VP
Average B, all atoms (Å ²)	71.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.61% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 9KG, SO4

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	0.24	0/4530	0.42	0/6169
2	B	0.24	0/3401	0.41	0/4622
All	All	0.24	0/7931	0.42	0/10791

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

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	4413	0	4419	42	0
2	B	3307	0	3316	25	0
3	A	37	0	0	2	0
4	A	5	0	0	0	0
5	A	24	0	0	1	0
5	B	16	0	0	0	0
All	All	7802	0	7735	63	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 4.

All (63) 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:544:GLY:HA2	2:B:286:THR:HG22	1.66	0.77
1:A:28:GLU:HG3	1:A:135:ILE:HD12	1.73	0.69
1:A:247:PRO:HB2	1:A:249:LYS:HE2	1.75	0.67
1:A:253:THR:HG22	1:A:292:VAL:HG22	1.77	0.66
2:B:73:LYS:NZ	2:B:146:TYR:OH	2.29	0.65
1:A:543:GLY:HA3	2:B:284:ARG:HA	1.79	0.63
1:A:252:TRP:HB2	1:A:295:LEU:HD11	1.81	0.63
2:B:308:GLU:HA	2:B:311:LYS:HE2	1.82	0.62
2:B:72:ARG:NH2	2:B:151:GLN:OE1	2.36	0.57
2:B:104:LYS:HA	2:B:237:ASP:HB3	1.86	0.57
2:B:203:GLU:HA	2:B:206:ARG:HG2	1.88	0.56
2:B:270:ILE:HG12	2:B:346:PHE:HB3	1.90	0.53
1:A:454:LYS:HZ2	1:A:552:VAL:HB	1.76	0.51
1:A:229:TRP:CE2	1:A:230:MET:HG3	2.45	0.51
1:A:363:ASN:HD21	1:A:366:LYS:HE3	1.75	0.51
1:A:46:LYS:HE2	1:A:116:PHE:CD2	2.45	0.50
1:A:181:TYR:HB3	3:A:601:9KG:C28	2.42	0.49
1:A:363:ASN:ND2	1:A:366:LYS:HE3	2.28	0.49
2:B:328:GLU:O	2:B:339:TYR:HA	2.13	0.48
1:A:353:LYS:O	1:A:374:LYS:NZ	2.44	0.48
1:A:252:TRP:HB3	1:A:257:ILE:HD13	1.95	0.48
1:A:503:LEU:HD22	1:A:535:TRP:HB2	1.96	0.47
1:A:34:LEU:HD21	1:A:62:ALA:HB2	1.96	0.47
1:A:88:TRP:CD1	2:B:143:ARG:HD2	2.49	0.47
2:B:84:THR:HB	2:B:154:LYS:HE2	1.96	0.47
1:A:363:ASN:HA	1:A:511:ASP:OD1	2.15	0.47
1:A:28:GLU:HG2	1:A:32:LYS:HE3	1.97	0.47
2:B:105:SER:O	2:B:190:GLY:HA2	2.14	0.46
2:B:168:LEU:HD13	2:B:180:ILE:HG21	1.96	0.46
1:A:252:TRP:HD1	1:A:295:LEU:HD21	1.81	0.46
1:A:21:VAL:HB	1:A:59:PRO:HD3	1.96	0.46
1:A:183:TYR:HB2	3:A:601:9KG:C28	2.46	0.45
1:A:399:GLU:HA	1:A:402:TRP:CD1	2.50	0.45
1:A:475:GLN:HB3	1:A:501:TYR:CE2	2.52	0.45
1:A:80:LEU:O	1:A:84:THR:OG1	2.29	0.45
1:A:369:THR:O	1:A:373:GLN:HG2	2.16	0.45
1:A:476:LYS:NZ	5:A:701:HOH:O	2.50	0.44
1:A:366:LYS:HE2	1:A:405:TYR:OH	2.17	0.44
2:B:425:LEU:HD23	2:B:425:LEU:HA	1.89	0.44
1:A:112:GLY:HA2	1:A:185:ASP:HB2	1.99	0.44
1:A:244:ILE:HG13	1:A:267:ALA:HB2	1.99	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:101:LYS:HD3	2:B:382:ILE:HG23	2.00	0.43
2:B:21:VAL:HB	2:B:59:PRO:HD3	1.99	0.43
2:B:167:ILE:HG12	2:B:212:TRP:CE3	2.53	0.43
1:A:220:LYS:HB2	1:A:220:LYS:HE2	1.78	0.43
2:B:104:LYS:HB2	2:B:192:ASP:HA	2.00	0.42
1:A:195:ILE:HG13	1:A:199:ARG:HE	1.85	0.42
1:A:260:LEU:HD21	1:A:303:LEU:HD13	2.01	0.42
1:A:249:LYS:HB2	1:A:252:TRP:CE2	2.54	0.42
2:B:163:SER:O	2:B:167:ILE:HG13	2.19	0.41
1:A:442:VAL:HB	1:A:481:ALA:HB1	2.01	0.41
2:B:202:ILE:HD13	2:B:202:ILE:HA	1.89	0.41
2:B:10:VAL:HG13	2:B:87:PHE:HZ	1.86	0.41
1:A:405:TYR:CE2	1:A:407:GLN:HB2	2.56	0.41
2:B:38:CYS:SG	2:B:132:ILE:HD11	2.61	0.41
1:A:73:LYS:NZ	1:A:146:TYR:OH	2.49	0.41
1:A:105:SER:O	1:A:190:GLY:HA2	2.20	0.41
1:A:165:THR:OG1	1:A:182:GLN:NE2	2.44	0.41
1:A:107:THR:OG1	1:A:198:HIS:NE2	2.50	0.41
2:B:63:ILE:HD12	2:B:407:GLN:HA	2.02	0.40
1:A:279:LEU:HD23	1:A:299:ALA:HB1	2.03	0.40
1:A:542:ILE:HG12	2:B:283:LEU:HD12	2.03	0.40
2:B:281:LYS:HG3	2:B:284:ARG:NH1	2.37	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	543/557 (98%)	530 (98%)	13 (2%)	0	100	100
2	B	394/428 (92%)	379 (96%)	15 (4%)	0	100	100
All	All	937/985 (95%)	909 (97%)	28 (3%)	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	479/495 (97%)	466 (97%)	13 (3%)	44	59
2	B	362/390 (93%)	356 (98%)	6 (2%)	60	75
All	All	841/885 (95%)	822 (98%)	19 (2%)	50	65

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	74	LEU
1	A	90	VAL
1	A	115	TYR
1	A	182	GLN
1	A	220	LYS
1	A	224	GLU
1	A	230	MET
1	A	250	ASP
1	A	257	ILE
1	A	277	ARG
1	A	295	LEU
1	A	300	GLU
1	A	301	LEU
2	B	8	VAL
2	B	74	LEU
2	B	232	TYR
2	B	233	GLU
2	B	414	TRP
2	B	417	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

2 ligands are 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	9KG	A	601	-	36,40,40	0.79	1 (2%)	45,56,56	1.67	10 (22%)
4	SO4	A	602	-	4,4,4	0.14	0	6,6,6	0.07	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	9KG	A	601	-	-	3/22/22/22	0/4/4/4

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	601	9KG	C10-N2	2.22	1.36	1.33

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	601	9KG	C3-O1-C13	4.81	129.48	118.04
3	A	601	9KG	C11-C10-N2	-4.61	113.17	123.31
3	A	601	9KG	O2-C2-C3	3.74	123.45	115.73
3	A	601	9KG	O2-C2-C1	-3.49	116.43	123.97
3	A	601	9KG	C11-C12-N1	3.32	123.93	121.28
3	A	601	9KG	C16-C17-N3	2.80	121.60	118.97
3	A	601	9KG	C8-N1-C12	2.52	122.75	118.11
3	A	601	9KG	C7-O2-C2	2.18	123.01	117.69
3	A	601	9KG	O1-C3-C4	2.12	126.39	120.73
3	A	601	9KG	C27-N3-C25	2.10	122.42	118.51

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	601	9KG	C3-C2-O2-C7
3	A	601	9KG	C1-C2-O2-C7
3	A	601	9KG	C8-C7-O2-C2

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	601	9KG	2	0

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	547/557 (98%)	0.68	57 (10%) 6 8	35, 71, 119, 152	0
2	B	400/428 (93%)	0.78	45 (11%) 5 6	40, 65, 120, 133	0
All	All	947/985 (96%)	0.72	102 (10%) 5 7	35, 68, 120, 152	0

All (102) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	289	LEU	10.0
1	A	290	THR	8.2
2	B	358	ARG	7.2
1	A	286	THR	6.4
1	A	548	VAL	6.2
2	B	241	VAL	6.2
1	A	285	GLY	6.0
1	A	221	HIS	6.0
1	A	260	LEU	5.8
2	B	207	GLN	5.7
2	B	195	ILE	5.6
1	A	288	ALA	5.5
2	B	212	TRP	5.3
1	A	219	LYS	5.1
1	A	24	TRP	5.0
2	B	357	MET	4.9
2	B	168	LEU	4.8
1	A	256	ASP	4.7
2	B	359	GLY	4.7
1	A	292	VAL	4.7
2	B	210	LEU	4.6
2	B	67	ASP	4.4
2	B	209	LEU	4.4
1	A	287	LYS	4.4

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Mol	Chain	Res	Type	RSRZ
1	A	295	LEU	4.4
2	B	232	TYR	4.2
1	A	552	VAL	4.0
1	A	245	VAL	3.9
1	A	218	ASP	3.8
1	A	93	GLY	3.7
2	B	166	LYS	3.7
2	B	206	ARG	3.6
1	A	62	ALA	3.6
2	B	202	ILE	3.6
1	A	252	TRP	3.6
1	A	284	ARG	3.5
2	B	208	HIS	3.5
1	A	116	PHE	3.5
1	A	544	GLY	3.5
2	B	88	TRP	3.4
2	B	189	VAL	3.4
2	B	95	PRO	3.4
2	B	87	PHE	3.3
1	A	250	ASP	3.3
1	A	255	ASN	3.3
2	B	198	HIS	3.3
2	B	196	GLY	3.2
1	A	244	ILE	3.1
1	A	282	LEU	3.1
1	A	257	ILE	3.1
2	B	284	ARG	3.1
1	A	291	GLU	3.1
1	A	551	LEU	3.0
1	A	305	GLU	3.0
1	A	90	VAL	3.0
1	A	38	CYS	3.0
2	B	174	GLN	2.9
1	A	2	ILE	2.9
1	A	63	ILE	2.9
1	A	294	PRO	2.9
1	A	297	GLU	2.8
1	A	261	VAL	2.7
2	B	199	ARG	2.7
1	A	61	PHE	2.7
1	A	15	GLY	2.7
1	A	302	GLU	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	247	PRO	2.7
2	B	15	GLY	2.6
2	B	69	THR	2.6
2	B	190	GLY	2.6
2	B	14	PRO	2.6
1	A	278	GLN	2.6
2	B	356	ARG	2.6
1	A	71	TRP	2.6
2	B	173	LYS	2.6
2	B	240	THR	2.6
2	B	169	GLU	2.5
2	B	171	PHE	2.5
2	B	237	ASP	2.5
2	B	191	SER	2.5
1	A	550	LYS	2.4
1	A	293	ILE	2.4
1	A	283	LEU	2.4
1	A	52	PRO	2.4
1	A	144	TYR	2.4
2	B	197	GLN	2.4
1	A	298	GLU	2.4
2	B	170	PRO	2.4
2	B	16	MET	2.3
1	A	304	ALA	2.3
2	B	211	ARG	2.3
1	A	92	LEU	2.3
2	B	372	VAL	2.2
1	A	346	PHE	2.2
2	B	85	GLN	2.2
1	A	300	GLU	2.1
1	A	47	ILE	2.1
2	B	193	LEU	2.1
2	B	178	ILE	2.1
1	A	220	LYS	2.1
1	A	183	TYR	2.0
2	B	167	ILE	2.0

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

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

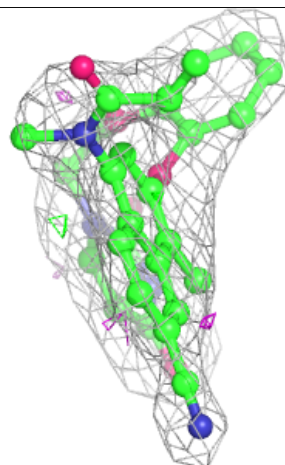
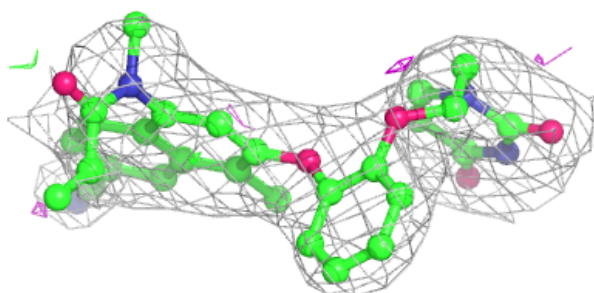
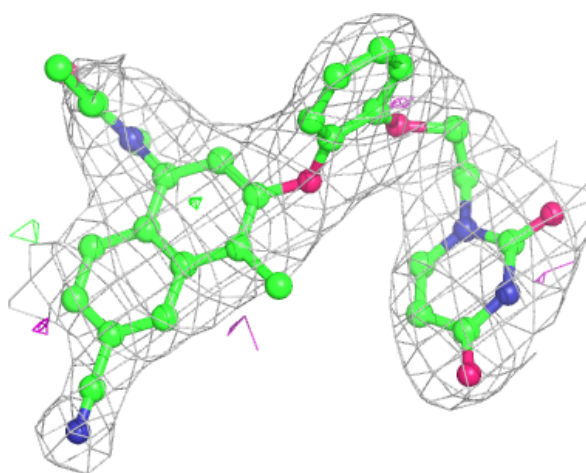
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	9KG	A	601	37/37	0.93	0.20	54,68,82,92	0
4	SO4	A	602	5/5	0.96	0.10	89,94,100,108	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 9KG A 601:

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.