



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 18, 2026 – 03:13 PM UTC

PDB ID : 3QGW / pdb_00003qgw
Title : Crystal Structure of ITK kinase bound to an inhibitor
Authors : Brown, K.; Cheetham, G.M.T.
Deposited on : 2011-01-25
Resolution : 2.10 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

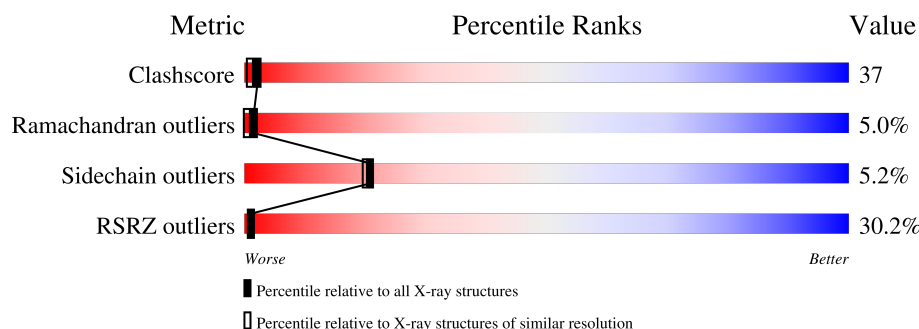
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	286	
1	B	286	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	PQC	A	1	-	X	-	-
3	L7A	B	1	-	X	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5040 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 Tyrosine-protein kinase ITK/TSK.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	244	Total	C	N	O	S	0	1	0
			1956	1251	323	365	17			
1	B	240	Total	C	N	O	S	0	0	0
			1924	1231	319	358	16			

There are 50 discrepancies between the modelled and reference sequences:

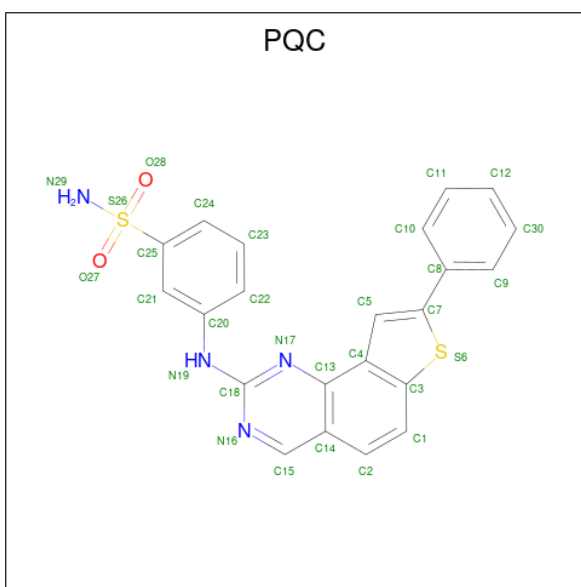
Chain	Residue	Modelled	Actual	Comment	Reference
A	335	MET	-	expression tag	UNP Q08881
A	336	GLY	-	expression tag	UNP Q08881
A	337	SER	-	expression tag	UNP Q08881
A	338	SER	-	expression tag	UNP Q08881
A	339	HIS	-	expression tag	UNP Q08881
A	340	HIS	-	expression tag	UNP Q08881
A	341	HIS	-	expression tag	UNP Q08881
A	342	HIS	-	expression tag	UNP Q08881
A	343	HIS	-	expression tag	UNP Q08881
A	344	HIS	-	expression tag	UNP Q08881
A	345	SER	-	expression tag	UNP Q08881
A	346	SER	-	expression tag	UNP Q08881
A	347	GLY	-	expression tag	UNP Q08881
A	348	LEU	-	expression tag	UNP Q08881
A	349	VAL	-	expression tag	UNP Q08881
A	350	PRO	-	expression tag	UNP Q08881
A	351	ARG	-	expression tag	UNP Q08881
A	352	GLY	-	expression tag	UNP Q08881
A	353	SER	-	expression tag	UNP Q08881
A	354	LEU	-	expression tag	UNP Q08881
A	355	HIS	-	expression tag	UNP Q08881
A	356	MET	-	expression tag	UNP Q08881
A	394	LYS	ARG	conflict	UNP Q08881
A	397	SER	ALA	conflict	UNP Q08881
A	401	ASP	GLU	conflict	UNP Q08881

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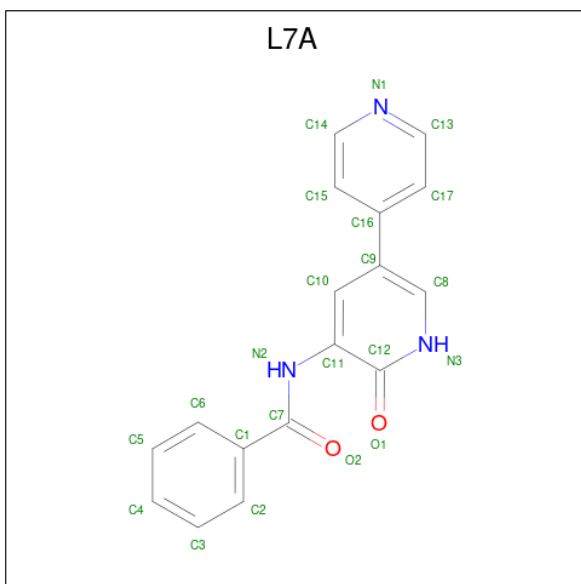
Chain	Residue	Modelled	Actual	Comment	Reference
B	335	MET	-	expression tag	UNP Q08881
B	336	GLY	-	expression tag	UNP Q08881
B	337	SER	-	expression tag	UNP Q08881
B	338	SER	-	expression tag	UNP Q08881
B	339	HIS	-	expression tag	UNP Q08881
B	340	HIS	-	expression tag	UNP Q08881
B	341	HIS	-	expression tag	UNP Q08881
B	342	HIS	-	expression tag	UNP Q08881
B	343	HIS	-	expression tag	UNP Q08881
B	344	HIS	-	expression tag	UNP Q08881
B	345	SER	-	expression tag	UNP Q08881
B	346	SER	-	expression tag	UNP Q08881
B	347	GLY	-	expression tag	UNP Q08881
B	348	LEU	-	expression tag	UNP Q08881
B	349	VAL	-	expression tag	UNP Q08881
B	350	PRO	-	expression tag	UNP Q08881
B	351	ARG	-	expression tag	UNP Q08881
B	352	GLY	-	expression tag	UNP Q08881
B	353	SER	-	expression tag	UNP Q08881
B	354	LEU	-	expression tag	UNP Q08881
B	355	HIS	-	expression tag	UNP Q08881
B	356	MET	-	expression tag	UNP Q08881
B	394	LYS	ARG	conflict	UNP Q08881
B	397	SER	ALA	conflict	UNP Q08881
B	401	ASP	GLU	conflict	UNP Q08881

- Molecule 2 is 3-[(8-phenylthieno[2,3-h]quinazolin-2-yl)amino]benzenesulfonamide (CCD ID: PQC) (formula: C₂₂H₁₆N₄O₂S₂).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			30	22	4	2	2		

- Molecule 3 is N-(6-oxo-1,6-dihydro-3,4'-bipyridin-5-yl)benzamide (CCD ID: L7A) (formula: $C_{17}H_{13}N_3O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	B	1	Total	C	N	O	0	0
			22	17	3	2		

- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	485	Total 485	O 485	0	0
4	B	623	Total 623	O 623	0	0

4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	125.86Å 74.38Å 78.83Å 90.00° 94.00° 90.00°	Depositor
Resolution (Å)	20.00 – 2.10 20.00 – 2.10	Depositor EDS
% Data completeness (in resolution range)	(Not available) (20.00-2.10) 90.9 (20.00-2.10)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.59 (at 2.09Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.245 , 0.320 0.305 , (Not available)	Depositor DCC
R_{free} test set	No test flags present.	wwPDB-VP
Wilson B-factor (Å ²)	27.4	Xtriage
Anisotropy	0.704	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 53.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.87	EDS
Total number of atoms	5040	wwPDB-VP
Average B, all atoms (Å ²)	29.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.41% 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: L7A, PQC

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	0.70	0/2005	1.10	15/2707 (0.6%)
1	B	0.71	0/1968	1.15	13/2657 (0.5%)
All	All	0.71	0/3973	1.12	28/5364 (0.5%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	562	ARG	N-CA-C	10.14	125.22	110.42
1	B	531	SER	N-CA-C	8.37	121.99	111.69
1	A	362	GLU	N-CA-C	-7.84	104.20	113.21
1	A	530	PHE	N-CA-C	-7.45	102.85	110.97
1	B	403	PHE	N-CA-C	-7.32	102.28	112.45
1	B	439	GLU	N-CA-C	7.14	119.97	111.33
1	B	530	PHE	CB-CA-C	-6.87	99.99	110.92
1	A	533	SER	N-CA-C	6.78	125.25	110.80
1	A	359	ASP	N-CA-C	6.73	118.12	109.65
1	B	436	GLU	N-CA-C	-6.71	101.68	110.53
1	A	440	HIS	N-CA-C	6.39	120.00	112.72
1	B	427	GLU	N-CA-C	-6.18	100.89	110.10
1	A	379	LEU	N-CA-C	-6.07	99.35	109.24
1	A	434	VAL	N-CA-C	5.93	116.35	107.51
1	B	362	GLU	N-CA-C	-5.93	106.29	112.93
1	B	539	SER	N-CA-C	-5.90	105.57	112.89
1	A	439	GLU	N-CA-C	5.87	119.26	111.75
1	A	589	GLN	N-CA-C	-5.83	104.85	111.14
1	B	553	SER	N-CA-C	-5.71	105.97	113.17
1	A	429	ALA	N-CA-C	5.62	122.24	109.81
1	A	402	ASP	N-CA-C	-5.48	104.71	111.40
1	A	493	ASN	N-CA-C	-5.46	105.92	113.18

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	431	ILE	N-CA-C	5.34	120.44	109.34
1	A	436	GLU	N-CA-C	-5.21	103.16	110.50
1	A	481	ARG	N-CA-C	5.15	121.78	110.80
1	A	553	SER	N-CA-C	-5.07	106.88	113.16
1	B	537	SER	N-CA-C	-5.06	106.37	112.54
1	B	422	TYR	N-CA-C	-5.03	106.83	113.12

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	1956	0	1908	135	1
1	B	1924	0	1885	150	2
2	A	30	0	16	4	0
3	B	22	0	13	2	0
4	A	485	0	0	37	1
4	B	623	0	0	50	2
All	All	5040	0	3822	288	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 37.

All (288) 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:493:ASN:N	1:A:493:ASN:HD22	1.54	1.04
1:B:607:ARG:HH11	1:B:610:ARG:HD2	1.27	0.98
1:B:607:ARG:NH1	1:B:610:ARG:HD2	1.85	0.91
1:B:538:LYS:HE3	4:B:947:HOH:O	1.72	0.88
1:B:430:PRO:HB2	4:B:708:HOH:O	1.73	0.88
1:B:388:VAL:HG11	1:B:434:VAL:HG13	1.56	0.87
1:B:398:MET:HE2	1:B:398:MET:HA	1.57	0.86
1:B:373:GLN:H	1:B:394:LYS:HZ2	1.26	0.83

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:579:LYS:HE2	1:B:588:TYR:HB2	1.62	0.81
1:B:494:GLN:HB3	4:B:803:HOH:O	1.82	0.80
1:A:424:VAL:HG12	1:A:433:LEU:CD1	2.12	0.80
1:A:480:HIS:O	1:A:482:ASP:N	2.15	0.79
1:B:470:MET:HE3	1:B:498:VAL:HG21	1.63	0.79
1:B:530:PHE:HD1	4:B:974:HOH:O	1.66	0.79
1:A:470:MET:HE1	1:A:473:LEU:HD12	1.63	0.78
1:B:358:ILE:HG22	4:B:736:HOH:O	1.82	0.78
1:B:452:GLY:HA3	4:B:876:HOH:O	1.84	0.78
1:B:491:GLY:C	1:B:493:ASN:H	1.92	0.78
1:A:492:GLU:C	1:A:493:ASN:HD22	1.92	0.77
1:B:450:GLN:O	1:B:451:ARG:HG3	1.84	0.77
1:A:373:GLN:HA	1:A:394:LYS:HD2	1.66	0.77
1:A:470:MET:CE	1:A:473:LEU:HD12	2.15	0.77
1:A:470:MET:HE3	1:A:498:VAL:HG11	1.65	0.76
1:A:421:LEU:HD21	1:A:433:LEU:HD11	1.65	0.76
1:A:430:PRO:HG2	1:A:431:ILE:H	1.51	0.75
1:B:402:ASP:HB3	4:B:634:HOH:O	1.86	0.75
1:B:373:GLN:H	1:B:394:LYS:NZ	1.85	0.75
1:B:600:GLU:HG2	4:B:235:HOH:O	1.86	0.74
1:B:426:LEU:HA	1:B:431:ILE:HD12	1.68	0.74
1:A:442[A]:CYS:SG	2:A:1:PQC:N29	2.60	0.74
1:B:453:LEU:HA	4:B:15:HOH:O	1.85	0.74
1:A:361:SER:C	1:A:363:LEU:H	1.96	0.73
1:A:442[B]:CYS:SG	2:A:1:PQC:N29	2.61	0.73
1:B:464:LEU:O	1:B:468:GLU:HG3	1.86	0.73
1:B:479:ILE:CD1	1:B:535:TYR:HB3	2.19	0.73
1:A:569:GLU:O	1:A:573:THR:HG23	1.89	0.72
1:B:579:LYS:HE2	1:B:588:TYR:CB	2.19	0.71
1:A:457:GLU:HG3	4:A:904:HOH:O	1.90	0.71
1:B:396:GLY:HA3	4:B:1062:HOH:O	1.91	0.70
1:A:470:MET:CE	1:A:498:VAL:HG11	2.21	0.70
1:B:429:ALA:HB2	4:B:984:HOH:O	1.92	0.70
1:B:587:VAL:HG12	1:B:591:MET:HE3	1.74	0.69
1:B:431:ILE:HG12	4:B:1067:HOH:O	1.93	0.69
1:B:398:MET:HG2	4:B:710:HOH:O	1.93	0.69
1:A:533:SER:HB3	1:A:535:TYR:CE1	2.28	0.68
1:A:600:GLU:CD	1:A:600:GLU:H	2.01	0.68
1:A:479:ILE:HG13	4:A:724:HOH:O	1.92	0.68
1:A:375:GLY:HA3	1:A:392:THR:O	1.94	0.68
1:B:493:ASN:HA	4:B:814:HOH:O	1.94	0.68

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:400:GLU:O	1:A:404:ILE:HG12	1.94	0.67
1:A:450:GLN:HB3	1:A:454:PHE:CE1	2.29	0.67
1:B:373:GLN:HA	1:B:394:LYS:HD2	1.77	0.67
1:B:407:ALA:O	1:B:411:MET:HG3	1.95	0.67
1:A:533:SER:HB3	1:A:535:TYR:HE1	1.58	0.66
1:B:360:PRO:HD2	1:B:362:GLU:CD	2.20	0.66
1:A:430:PRO:O	1:A:431:ILE:HG13	1.96	0.66
1:B:392:THR:HG23	4:B:957:HOH:O	1.94	0.66
1:B:373:GLN:N	1:B:394:LYS:HZ2	1.94	0.66
1:A:410:MET:O	4:A:145:HOH:O	2.14	0.66
1:B:360:PRO:HA	1:B:427:GLU:OE2	1.95	0.66
1:A:420:GLN:NE2	4:A:698:HOH:O	2.26	0.65
1:A:493:ASN:N	1:A:493:ASN:ND2	2.28	0.65
1:B:413:LEU:HD12	1:B:501:PHE:HE1	1.59	0.65
1:A:368:GLU:C	1:A:369:ILE:HG13	2.19	0.65
1:A:405:GLU:O	1:A:409:VAL:HG23	1.95	0.65
1:A:424:VAL:HG12	1:A:433:LEU:HD13	1.80	0.64
1:A:585:THR:HG22	4:A:295:HOH:O	1.98	0.63
1:B:361:SER:HB2	4:B:739:HOH:O	1.98	0.63
1:A:486:ARG:NH1	1:A:486:ARG:HB2	2.13	0.63
1:B:393:ILE:HD11	4:B:895:HOH:O	1.97	0.63
1:B:400:GLU:O	1:B:404:ILE:HG13	1.99	0.62
1:B:555:GLY:HA2	4:B:215:HOH:O	1.99	0.62
1:A:392:THR:HG22	1:A:432:CYS:HB3	1.80	0.62
1:B:427:GLU:O	1:B:429:ALA:N	2.33	0.62
1:B:479:ILE:HG13	1:B:481:ARG:HG3	1.82	0.62
1:A:527:PRO:HA	1:A:530:PHE:CD2	2.34	0.62
1:B:479:ILE:HD12	1:B:535:TYR:HB3	1.81	0.61
1:B:501:PHE:HA	4:B:900:HOH:O	2.00	0.61
1:A:361:SER:O	4:A:68:HOH:O	2.16	0.61
1:B:440:HIS:HD2	1:B:491:GLY:O	1.83	0.61
1:A:570:ASP:O	1:A:575:PHE:HB3	2.01	0.60
1:B:360:PRO:HG2	1:B:362:GLU:HG3	1.81	0.60
1:B:564:ASN:HB2	4:B:977:HOH:O	2.01	0.60
1:B:388:VAL:CG1	1:B:434:VAL:HG13	2.30	0.60
1:B:470:MET:HE1	1:B:473:LEU:HD12	1.83	0.60
1:B:398:MET:N	4:B:895:HOH:O	2.32	0.60
1:B:401:ASP:O	1:B:405:GLU:HB2	2.02	0.60
1:A:368:GLU:HA	1:A:378:HIS:HA	1.84	0.60
1:B:468:GLU:HG2	1:B:609:LEU:HD11	1.84	0.60
1:B:420:GLN:OE1	4:B:772:HOH:O	2.16	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:HIS:HD2	4:A:937:HOH:O	1.83	0.59
1:A:491:GLY:C	1:A:493:ASN:H	2.10	0.59
1:B:585:THR:HG22	4:B:49:HOH:O	2.03	0.59
1:B:452:GLY:O	4:B:786:HOH:O	2.17	0.59
1:B:569:GLU:O	1:B:573:THR:HG23	2.02	0.59
1:A:370:GLY:N	1:A:377:VAL:HG12	2.17	0.59
1:A:547:LEU:C	1:A:547:LEU:HD23	2.28	0.59
1:B:491:GLY:C	1:B:493:ASN:N	2.61	0.59
1:B:360:PRO:HB3	4:B:1053:HOH:O	2.01	0.59
1:A:494:GLN:HG3	4:A:84:HOH:O	2.03	0.59
1:A:400:GLU:HB2	4:A:693:HOH:O	2.03	0.58
1:A:493:ASN:HB2	1:A:495:VAL:HG23	1.85	0.58
1:B:481:ARG:HD2	4:B:810:HOH:O	2.02	0.58
1:A:446:TYR:O	1:A:450:GLN:HB2	2.03	0.58
1:B:581:ARG:NH2	4:B:325:HOH:O	2.36	0.58
3:B:1:L7A:H10	3:B:1:L7A:O2	2.03	0.58
1:A:538:LYS:HD2	1:A:602:ARG:HB2	1.85	0.58
1:A:427:GLU:O	1:A:428:GLN:HB2	2.03	0.57
1:A:421:LEU:HD21	1:A:433:LEU:CD1	2.34	0.57
1:B:449:THR:HG21	4:B:641:HOH:O	2.04	0.57
1:B:449:THR:O	1:B:451:ARG:N	2.37	0.57
1:B:388:VAL:HG12	1:B:390:ILE:HG13	1.87	0.56
1:A:596:LYS:HE2	4:A:980:HOH:O	2.04	0.56
1:B:427:GLU:O	1:B:428:GLN:C	2.48	0.56
1:A:480:HIS:O	1:A:480:HIS:ND1	2.38	0.56
1:A:360:PRO:HG2	1:A:361:SER:H	1.71	0.56
1:B:360:PRO:CB	4:B:1053:HOH:O	2.53	0.56
1:A:617:GLU:O	1:A:618:SER:HB2	2.06	0.55
1:A:493:ASN:O	1:A:494:GLN:CB	2.55	0.55
1:B:579:LYS:NZ	1:B:585:THR:HA	2.21	0.55
1:B:431:ILE:HD13	1:B:431:ILE:N	2.22	0.55
1:B:579:LYS:NZ	1:B:585:THR:HG22	2.22	0.55
1:A:410:MET:HG3	1:A:502:GLY:HA3	1.88	0.55
1:A:421:LEU:HD11	1:A:433:LEU:HG	1.89	0.55
1:A:586:HIS:HB3	1:A:615:ILE:HD12	1.89	0.55
1:B:412:LYS:HE2	4:B:711:HOH:O	2.06	0.55
1:B:413:LEU:HD12	1:B:501:PHE:CE1	2.41	0.55
1:A:427:GLU:O	1:A:428:GLN:CB	2.55	0.55
1:B:596:LYS:HD2	4:B:283:HOH:O	2.07	0.55
1:B:450:GLN:O	1:B:450:GLN:HG3	2.06	0.54
1:A:470:MET:HE2	1:A:470:MET:HA	1.88	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:358:ILE:HG13	4:A:756:HOH:O	2.07	0.54
1:A:458:THR:HG23	1:A:494:GLN:NE2	2.22	0.54
1:A:425:CYS:HB2	1:A:432:CYS:SG	2.48	0.54
1:A:617:GLU:O	1:A:618:SER:CB	2.56	0.54
1:B:438:MET:N	3:B:1:L7A:O1	2.31	0.54
1:A:521:PRO:HA	4:A:646:HOH:O	2.08	0.54
1:A:500:ASP:HB2	4:A:651:HOH:O	2.07	0.54
1:B:358:ILE:O	1:B:424:VAL:O	2.25	0.54
1:B:470:MET:HA	1:B:470:MET:HE2	1.88	0.54
1:B:480:HIS:O	1:B:481:ARG:HB2	2.08	0.54
1:B:392:THR:HG22	1:B:432:CYS:HB3	1.90	0.54
1:A:492:GLU:C	1:A:493:ASN:ND2	2.65	0.53
1:B:392:THR:HG22	1:B:432:CYS:CB	2.39	0.53
1:A:370:GLY:CA	1:A:377:VAL:HG12	2.38	0.53
1:B:394:LYS:C	1:B:396:GLY:H	2.16	0.53
2:A:1:PQC:H21	2:A:1:PQC:N17	2.23	0.53
1:B:378:HIS:HD2	4:B:957:HOH:O	1.92	0.53
1:B:547:LEU:C	1:B:547:LEU:HD23	2.33	0.53
1:B:547:LEU:HD23	1:B:547:LEU:O	2.08	0.53
1:B:387:LYS:HD3	1:B:437:PHE:CD2	2.44	0.53
1:A:492:GLU:O	1:A:492:GLU:HG2	2.09	0.53
1:A:439:GLU:HB2	4:A:758:HOH:O	2.08	0.52
1:A:470:MET:HE3	1:A:498:VAL:HG21	1.91	0.52
1:A:618:SER:HB2	4:A:740:HOH:O	2.08	0.52
1:A:520:PHE:HD2	4:A:1097:HOH:O	1.92	0.52
1:B:398:MET:HA	1:B:398:MET:CE	2.33	0.52
1:A:585:THR:O	1:A:589:GLN:HG3	2.09	0.52
1:B:404:ILE:C	1:B:406:GLU:H	2.16	0.52
1:B:450:GLN:O	1:B:451:ARG:CG	2.54	0.52
1:A:362:GLU:HA	4:A:68:HOH:O	2.10	0.51
1:A:378:HIS:HE1	4:A:897:HOH:O	1.91	0.51
1:B:449:THR:HG23	4:B:745:HOH:O	2.11	0.51
1:A:373:GLN:NE2	1:A:397:SER:HA	2.26	0.51
1:B:456:ALA:HB1	4:B:796:HOH:O	2.10	0.51
1:B:431:ILE:HD13	1:B:431:ILE:H	1.76	0.51
1:A:486:ARG:CB	1:A:486:ARG:HH11	2.25	0.50
1:A:523:LYS:HD3	1:A:558:PRO:O	2.11	0.50
1:A:589:GLN:NE2	4:A:703:HOH:O	2.43	0.50
1:B:379:LEU:HD23	1:B:380:GLY:N	2.27	0.50
1:B:493:ASN:O	1:B:494:GLN:HB2	2.12	0.50
1:A:373:GLN:HE21	1:A:397:SER:HA	1.77	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:486:ARG:NH1	1:A:486:ARG:CB	2.75	0.49
1:B:607:ARG:HH11	1:B:610:ARG:HH11	1.60	0.49
1:A:470:MET:HE2	1:A:473:LEU:HD12	1.93	0.49
1:B:373:GLN:HE21	1:B:373:GLN:C	2.19	0.49
1:B:481:ARG:HG2	1:B:535:TYR:CD2	2.48	0.49
1:A:392:THR:HG23	4:A:937:HOH:O	2.13	0.49
1:A:611:GLN:O	1:A:615:ILE:HG12	2.13	0.49
1:B:470:MET:CE	1:B:473:LEU:HD12	2.42	0.49
1:A:361:SER:C	1:A:363:LEU:N	2.66	0.49
1:A:480:HIS:C	1:A:482:ASP:H	2.19	0.49
1:A:360:PRO:HB3	4:A:929:HOH:O	2.12	0.49
1:A:360:PRO:HD2	1:A:362:GLU:HG3	1.95	0.49
1:B:393:ILE:HG13	4:B:917:HOH:O	2.13	0.48
1:B:537:SER:O	1:B:541:VAL:HG23	2.14	0.48
1:B:565:SER:N	4:B:977:HOH:O	2.41	0.48
1:A:410:MET:CG	1:A:502:GLY:HA3	2.43	0.48
1:A:572:SER:HA	4:A:882:HOH:O	2.13	0.48
1:A:578:TYR:HB3	4:A:294:HOH:O	2.13	0.48
1:B:584:SER:OG	1:B:587:VAL:HG23	2.14	0.48
1:B:585:THR:O	1:B:589:GLN:HG3	2.14	0.48
1:A:368:GLU:HB3	1:A:378:HIS:CE1	2.49	0.48
1:A:547:LEU:O	1:A:551:VAL:HG23	2.14	0.48
1:A:445:ASP:O	1:A:449:THR:HG23	2.14	0.47
1:A:450:GLN:HB3	1:A:454:PHE:CZ	2.49	0.47
1:B:373:GLN:O	1:B:373:GLN:NE2	2.47	0.47
1:B:598:ARG:HB2	1:B:601:ASP:OD2	2.14	0.47
1:B:426:LEU:CD2	1:B:431:ILE:HG23	2.44	0.47
1:A:360:PRO:HG2	1:A:362:GLU:HG3	1.97	0.47
1:A:379:LEU:HD12	1:A:380:GLY:N	2.29	0.47
1:B:394:LYS:O	1:B:396:GLY:N	2.48	0.47
1:B:579:LYS:HZ3	1:B:585:THR:HA	1.80	0.47
1:B:448:ARG:HG2	1:B:555:GLY:HA3	1.96	0.47
1:A:368:GLU:C	1:A:369:ILE:CG1	2.88	0.46
1:B:579:LYS:HD3	1:B:583:ALA:O	2.16	0.46
1:A:362:GLU:HB2	1:A:382:TRP:CD1	2.51	0.46
1:A:613:ALA:HB3	4:A:1109:HOH:O	2.16	0.46
1:B:525:ALA:O	1:B:530:PHE:CE2	2.68	0.46
1:B:444:SER:O	1:B:448:ARG:HG3	2.16	0.46
1:B:576:ARG:HE	1:B:595:TRP:HB3	1.79	0.46
1:B:523:LYS:HD3	1:B:558:PRO:O	2.16	0.46
1:A:359:ASP:N	1:A:424:VAL:O	2.47	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:388:VAL:HG13	1:B:389:ALA:N	2.31	0.46
1:B:409:VAL:CG1	4:B:998:HOH:O	2.65	0.45
1:B:589:GLN:HA	4:B:55:HOH:O	2.17	0.45
1:B:557:ILE:HB	1:B:560:GLU:HG3	1.98	0.45
1:A:494:GLN:HB3	4:A:86:HOH:O	2.15	0.45
1:B:443:LEU:HB3	1:B:485:ALA:O	2.16	0.45
1:A:358:ILE:HG12	1:A:424:VAL:HG22	1.99	0.45
1:A:486:ARG:HB2	1:A:486:ARG:CZ	2.47	0.45
1:B:373:GLN:CA	1:B:394:LYS:HD2	2.47	0.45
1:B:428:GLN:O	1:B:429:ALA:C	2.59	0.45
1:B:587:VAL:HG21	4:B:941:HOH:O	2.17	0.45
1:A:581:ARG:HD2	4:A:900:HOH:O	2.17	0.45
1:B:388:VAL:CG1	1:B:389:ALA:N	2.80	0.45
1:A:611:GLN:NE2	4:A:982:HOH:O	2.41	0.45
1:A:448:ARG:NH2	4:A:808:HOH:O	2.47	0.44
1:B:481:ARG:NH1	4:B:1071:HOH:O	2.49	0.44
1:A:482:ASP:OD2	4:A:639:HOH:O	2.21	0.44
1:A:491:GLY:C	1:A:493:ASN:N	2.75	0.44
1:B:465:ASP:HB2	1:B:496:ILE:HB	1.99	0.44
1:B:361:SER:HB3	4:B:133:HOH:O	2.17	0.44
1:B:449:THR:HB	1:B:450:GLN:H	1.46	0.44
1:A:607:ARG:NH1	4:A:173:HOH:O	2.44	0.44
1:A:411:MET:CG	1:A:421:LEU:HD23	2.48	0.44
1:A:440:HIS:HB2	1:A:490:VAL:HB	2.01	0.43
1:B:479:ILE:CG1	1:B:481:ARG:HG3	2.47	0.43
1:B:495:VAL:HB	4:B:718:HOH:O	2.18	0.43
1:A:369:ILE:C	1:A:377:VAL:HG12	2.42	0.43
1:B:427:GLU:CD	4:B:1053:HOH:O	2.61	0.43
1:B:404:ILE:C	1:B:406:GLU:N	2.77	0.43
1:B:500:ASP:HB3	4:B:928:HOH:O	2.18	0.43
1:B:450:GLN:O	1:B:451:ARG:CB	2.66	0.43
1:B:470:MET:HE1	1:B:473:LEU:CD1	2.48	0.43
1:B:491:GLY:O	1:B:493:ASN:N	2.43	0.43
1:A:440:HIS:CD2	1:A:492:GLU:HA	2.54	0.43
1:A:450:GLN:NE2	4:A:762:HOH:O	2.52	0.42
1:A:575:PHE:HD1	4:A:784:HOH:O	2.02	0.42
1:B:538:LYS:HA	1:B:538:LYS:HD3	1.79	0.42
1:B:470:MET:CE	1:B:498:VAL:HG11	2.49	0.42
1:B:538:LYS:CE	4:B:947:HOH:O	2.46	0.42
1:A:439:GLU:CB	1:A:492:GLU:HB2	2.50	0.42
1:A:382:TRP:O	1:A:383:LEU:HB2	2.18	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:451:ARG:HG2	4:B:10:HOH:O	2.19	0.42
1:B:426:LEU:HD23	1:B:431:ILE:HG23	2.02	0.42
1:B:448:ARG:HD2	4:B:785:HOH:O	2.19	0.42
1:A:369:ILE:C	1:A:377:VAL:CG1	2.93	0.41
1:A:439:GLU:HB3	1:A:492:GLU:HB2	2.02	0.41
1:A:617:GLU:CD	4:A:181:HOH:O	2.63	0.41
1:A:373:GLN:O	1:A:374:PHE:CB	2.67	0.41
1:A:426:LEU:C	1:A:428:GLN:H	2.28	0.41
1:A:501:PHE:N	4:A:1096:HOH:O	2.52	0.41
1:B:380:GLY:O	1:B:388:VAL:N	2.45	0.41
1:B:444:SER:HA	4:B:215:HOH:O	2.20	0.41
1:A:374:PHE:HD2	1:A:374:PHE:HA	1.79	0.41
1:B:379:LEU:HD23	1:B:379:LEU:C	2.45	0.41
2:A:1:PQC:N17	2:A:1:PQC:C21	2.84	0.41
1:A:562:ARG:NH1	1:A:575:PHE:CE2	2.89	0.41
1:B:403:PHE:CE2	1:B:431:ILE:HG22	2.56	0.41
1:B:586:HIS:HB3	1:B:615:ILE:CD1	2.50	0.41
1:B:527:PRO:HA	1:B:530:PHE:CD1	2.56	0.41
1:A:360:PRO:CG	1:A:362:GLU:HG3	2.51	0.41
1:A:525:ALA:O	1:A:530:PHE:CE1	2.74	0.41
1:A:616:ALA:C	1:A:618:SER:H	2.29	0.41
1:B:614:GLU:HB3	4:B:67:HOH:O	2.20	0.41
1:A:493:ASN:O	1:A:494:GLN:HB3	2.21	0.40
1:B:493:ASN:O	1:B:494:GLN:CB	2.68	0.40
1:A:369:ILE:HG12	4:A:814:HOH:O	2.21	0.40
1:B:413:LEU:HD13	1:B:473:LEU:CD2	2.50	0.40
1:B:425:CYS:HB2	1:B:432:CYS:SG	2.60	0.40
1:A:373:GLN:O	1:A:374:PHE:HB2	2.21	0.40
1:B:481:ARG:HA	4:B:830:HOH:O	2.21	0.40
1:A:373:GLN:HG3	1:A:394:LYS:HD2	2.04	0.40
1:A:378:HIS:CE1	4:A:897:HOH:O	2.72	0.40
1:A:384:ASN:ND2	4:A:930:HOH:O	2.54	0.40
1:A:492:GLU:N	1:A:493:ASN:HD22	2.20	0.40
1:B:372:GLY:H	1:B:394:LYS:HZ2	1.70	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:B:598:ARG:NH2	4:B:979:HOH:O[2_656]	1.99	0.21

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:415:HIS:O	4:A:699:HOH:O[4_555]	2.04	0.16
1:A:385:LYS:NZ	4:B:771:HOH:O[4_545]	2.10	0.10

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	241/286 (84%)	216 (90%)	14 (6%)	11 (5%)	2	0
1	B	236/286 (82%)	210 (89%)	13 (6%)	13 (6%)	1	0
All	All	477/572 (83%)	426 (89%)	27 (6%)	24 (5%)	1	0

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	361	SER
1	A	374	PHE
1	A	428	GLN
1	A	430	PRO
1	A	481	ARG
1	A	494	GLN
1	A	532	PHE
1	A	533	SER
1	B	360	PRO
1	B	395	GLU
1	B	399	SER
1	B	428	GLN
1	B	431	ILE
1	B	450	GLN
1	B	451	ARG
1	A	369	ILE
1	B	430	PRO
1	A	360	PRO

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Mol	Chain	Res	Type
1	B	398	MET
1	B	492	GLU
1	B	359	ASP
1	A	492	GLU
1	B	372	GLY
1	B	449	THR

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	216/252 (86%)	207 (96%)	9 (4%)	26	28
1	B	212/252 (84%)	199 (94%)	13 (6%)	17	15
All	All	428/504 (85%)	406 (95%)	22 (5%)	21	21

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	369	ILE
1	A	374	PHE
1	A	379	LEU
1	A	433	LEU
1	A	449	THR
1	A	486	ARG
1	A	493	ASN
1	A	585	THR
1	A	600	GLU
1	B	359	ASP
1	B	363	LEU
1	B	373	GLN
1	B	388	VAL
1	B	397	SER
1	B	398	MET
1	B	453	LEU
1	B	464	LEU

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Mol	Chain	Res	Type
1	B	479	ILE
1	B	499	SER
1	B	531	SER
1	B	561	ASN
1	B	581	ARG

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

Mol	Chain	Res	Type
1	A	367	GLN
1	A	373	GLN
1	A	378	HIS
1	A	384	ASN
1	A	428	GLN
1	A	440	HIS
1	A	450	GLN
1	A	493	ASN
1	A	586	HIS
1	A	589	GLN
1	A	611	GLN
1	B	367	GLN
1	B	373	GLN
1	B	378	HIS
1	B	420	GLN
1	B	428	GLN
1	B	589	GLN

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 oligosaccharides 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
2	PQC	A	1	-	34,34,34	5.25	24 (70%)	49,50,50	2.97	24 (48%)
3	L7A	B	1	-	24,24,24	4.52	17 (70%)	30,32,32	2.70	12 (40%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	PQC	A	1	-	-	0/14/14/14	0/5/5/5
3	L7A	B	1	-	-	0/12/12/12	0/3/3/3

All (41) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1	PQC	S26-N29	12.51	1.84	1.60
2	A	1	PQC	C2-C1	12.46	1.63	1.36
2	A	1	PQC	C1-C3	10.24	1.56	1.39
3	B	1	L7A	C15-C16	9.68	1.54	1.39
2	A	1	PQC	C14-C13	8.96	1.54	1.42
2	A	1	PQC	C24-C25	7.88	1.51	1.38
3	B	1	L7A	C6-C1	7.68	1.51	1.39
2	A	1	PQC	C2-C14	7.22	1.57	1.42
3	B	1	L7A	C17-C16	7.02	1.50	1.39
3	B	1	L7A	C8-C9	6.55	1.47	1.36
2	A	1	PQC	O27-S26	6.21	1.54	1.43
2	A	1	PQC	C21-C20	6.19	1.49	1.39
3	B	1	L7A	C2-C1	6.07	1.48	1.39
2	A	1	PQC	C21-C25	5.68	1.49	1.39
2	A	1	PQC	C13-N17	5.59	1.48	1.37
3	B	1	L7A	C3-C2	5.30	1.48	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	1	L7A	C5-C6	5.07	1.47	1.38
3	B	1	L7A	C4-C3	4.88	1.49	1.38
3	B	1	L7A	C5-C4	4.70	1.48	1.38
2	A	1	PQC	C10-C8	4.53	1.46	1.39
2	A	1	PQC	C9-C8	4.50	1.46	1.39
2	A	1	PQC	C4-C3	4.47	1.46	1.40
3	B	1	L7A	C8-N3	4.44	1.43	1.36
3	B	1	L7A	C13-N1	4.20	1.45	1.33
3	B	1	L7A	C16-C9	3.89	1.56	1.48
2	A	1	PQC	C12-C11	3.80	1.46	1.38
3	B	1	L7A	C17-C13	3.75	1.45	1.38
2	A	1	PQC	C18-N16	3.60	1.39	1.34
3	B	1	L7A	C14-N1	3.55	1.43	1.33
2	A	1	PQC	C22-C20	3.43	1.45	1.39
3	B	1	L7A	C15-C14	3.36	1.45	1.38
2	A	1	PQC	C11-C10	3.20	1.44	1.38
2	A	1	PQC	C20-N19	3.18	1.47	1.40
2	A	1	PQC	C15-N16	2.92	1.37	1.32
2	A	1	PQC	C15-C14	-2.91	1.36	1.42
2	A	1	PQC	C30-C12	2.84	1.44	1.38
2	A	1	PQC	C23-C22	2.79	1.43	1.38
3	B	1	L7A	C12-N3	2.49	1.44	1.39
2	A	1	PQC	C18-N19	2.18	1.41	1.36
2	A	1	PQC	O28-S26	-2.15	1.40	1.43
3	B	1	L7A	C10-C9	2.13	1.48	1.42

All (36) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	1	PQC	C23-C22-C20	9.21	130.34	119.73
3	B	1	L7A	C9-C8-N3	-6.23	114.36	121.03
2	A	1	PQC	C24-C23-C22	-5.27	113.47	120.24
2	A	1	PQC	N16-C18-N17	-5.27	121.27	126.41
2	A	1	PQC	C15-N16-C18	5.17	122.78	115.81
2	A	1	PQC	O28-S26-O27	5.07	126.59	118.80
3	B	1	L7A	C11-C12-N3	4.99	120.93	116.02
3	B	1	L7A	O2-C7-N2	4.95	129.50	122.27
3	B	1	L7A	C14-N1-C13	4.79	127.83	116.86
2	A	1	PQC	C23-C24-C25	4.73	123.78	118.95
2	A	1	PQC	C4-C3-S6	-4.72	108.07	111.71
2	A	1	PQC	O28-S26-N29	-4.56	100.78	107.35
2	A	1	PQC	C13-C4-C5	-4.51	121.88	128.34

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	1	L7A	C15-C14-N1	-4.50	115.92	123.60
2	A	1	PQC	C22-C20-C21	-4.35	114.39	119.66
2	A	1	PQC	C3-C4-C13	4.23	123.30	119.69
3	B	1	L7A	C1-C7-N2	-3.38	111.38	116.25
2	A	1	PQC	C3-C4-C5	3.35	114.78	111.52
3	B	1	L7A	C16-C9-C8	-3.34	118.43	121.37
3	B	1	L7A	C17-C13-N1	-3.23	118.09	123.60
3	B	1	L7A	C12-C11-N2	3.19	117.68	112.47
2	A	1	PQC	C3-S6-C7	2.93	94.89	91.12
3	B	1	L7A	O1-C12-C11	-2.91	117.89	121.91
2	A	1	PQC	C11-C10-C8	-2.85	117.57	120.36
2	A	1	PQC	C2-C1-C3	-2.81	114.08	119.07
2	A	1	PQC	C4-C13-N17	2.68	122.30	119.12
2	A	1	PQC	C25-S26-N29	-2.67	104.68	108.40
2	A	1	PQC	C20-N19-C18	-2.48	122.69	129.38
3	B	1	L7A	C6-C1-C2	2.45	121.68	118.57
2	A	1	PQC	C14-C13-N17	-2.44	119.61	122.68
2	A	1	PQC	C21-C25-S26	2.40	123.67	119.34
2	A	1	PQC	C2-C14-C13	2.30	121.92	118.26
2	A	1	PQC	C1-C2-C14	-2.20	117.55	120.84
2	A	1	PQC	C8-C7-S6	2.15	122.99	119.70
3	B	1	L7A	C2-C1-C7	-2.10	113.79	120.60
2	A	1	PQC	C9-C8-C7	-2.04	117.71	121.12

There are no chirality outliers.

There are no torsion outliers.

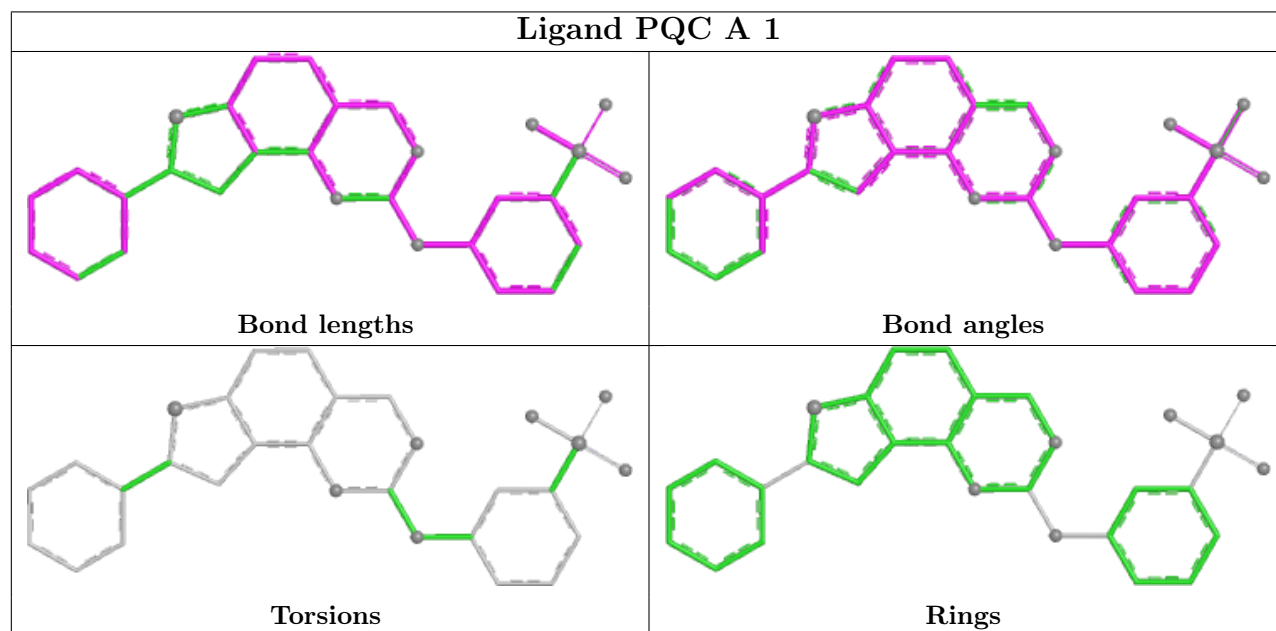
There are no ring outliers.

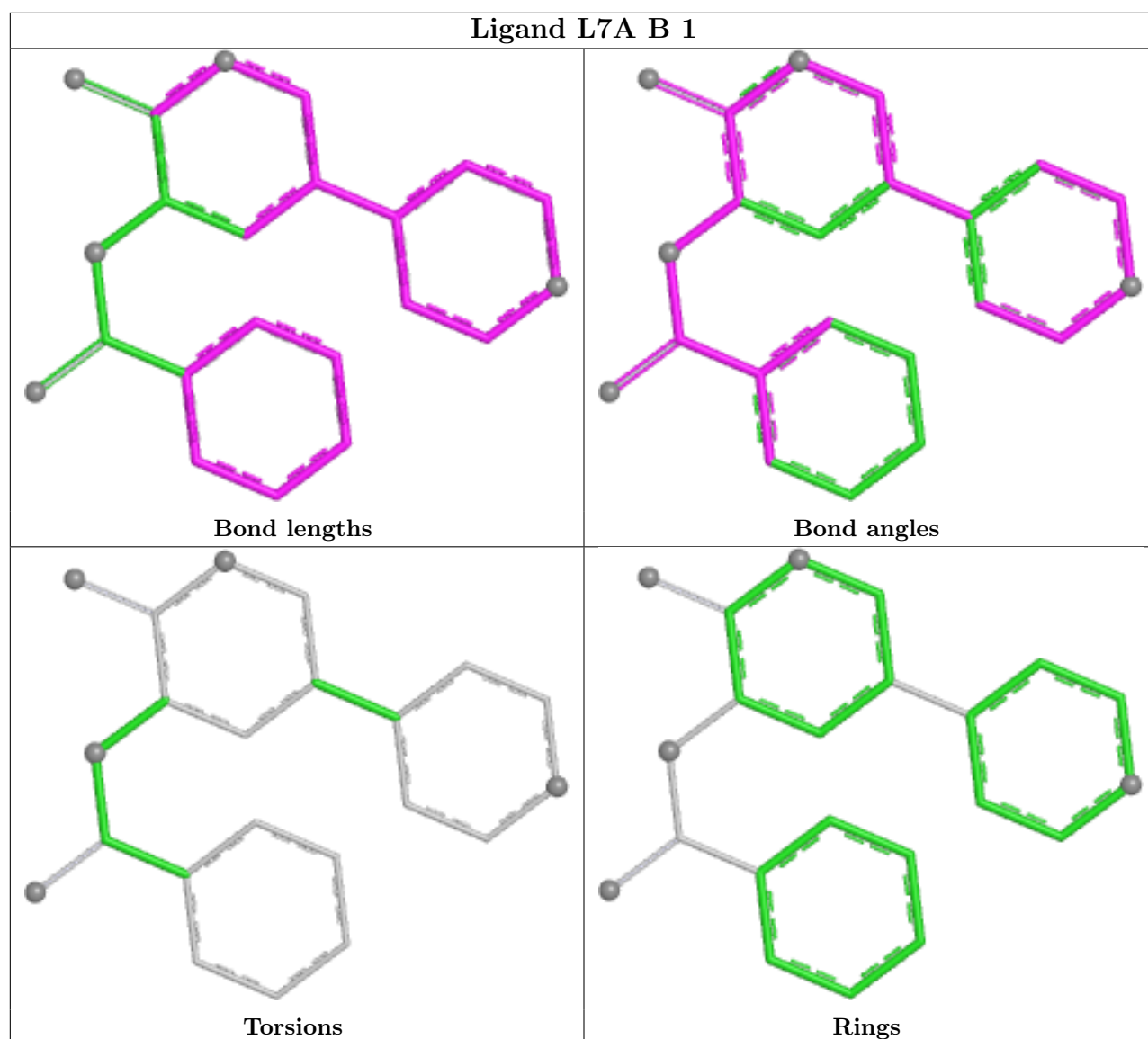
2 monomers are involved in 6 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1	PQC	4	0
3	B	1	L7A	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	244/286 (85%)	1.58	63 (25%)	1 2	20, 26, 45, 52	1 (0%)
1	B	240/286 (83%)	1.82	83 (34%)	1 1	23, 26, 42, 46	0
All	All	484/572 (84%)	1.70	146 (30%)	1 1	20, 26, 43, 52	1 (0%)

All (146) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	396	GLY	7.6
1	B	501	PHE	5.9
1	B	409	VAL	5.1
1	A	360	PRO	5.1
1	A	370	GLY	4.9
1	B	373	GLN	4.7
1	A	371	SER	4.5
1	A	532	PHE	4.5
1	B	428	GLN	4.5
1	B	521	PRO	4.4
1	A	430	PRO	4.4
1	B	358	ILE	4.3
1	A	382	TRP	4.2
1	B	430	PRO	4.1
1	A	374	PHE	4.1
1	A	565	SER	4.0
1	A	429	ALA	3.9
1	B	397	SER	3.9
1	A	431	ILE	3.9
1	B	561	ASN	3.9
1	B	399	SER	3.8
1	B	530	PHE	3.8
1	B	383	LEU	3.8
1	B	492	GLU	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	369	ILE	3.6
1	B	403	PHE	3.5
1	B	449	THR	3.5
1	A	521	PRO	3.5
1	A	380	GLY	3.5
1	B	382	TRP	3.4
1	B	398	MET	3.4
1	B	371	SER	3.4
1	B	429	ALA	3.4
1	A	381	TYR	3.3
1	B	404	ILE	3.3
1	B	402	ASP	3.3
1	A	366	VAL	3.3
1	A	501	PHE	3.2
1	A	520	PHE	3.2
1	A	384	ASN	3.2
1	A	383	LEU	3.1
1	A	361	SER	3.1
1	A	359	ASP	3.1
1	B	452	GLY	3.1
1	A	530	PHE	3.1
1	B	599	PRO	3.1
1	B	475	GLU	3.0
1	B	401	ASP	3.0
1	B	431	ILE	3.0
1	A	385	LYS	3.0
1	B	451	ARG	3.0
1	B	450	GLN	2.9
1	B	473	LEU	2.9
1	B	598	ARG	2.9
1	B	542	TRP	2.9
1	A	376	LEU	2.8
1	B	484	ALA	2.8
1	A	364	THR	2.8
1	B	616	ALA	2.8
1	B	567	VAL	2.8
1	A	492	GLU	2.8
1	B	427	GLU	2.8
1	A	502	GLY	2.7
1	A	358	ILE	2.7
1	A	377	VAL	2.6
1	A	379	LEU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	618	SER	2.6
1	B	522	VAL	2.6
1	A	372	GLY	2.6
1	A	375	GLY	2.6
1	A	449	THR	2.6
1	B	472	TYR	2.6
1	B	479	ILE	2.6
1	A	427	GLU	2.6
1	B	379	LEU	2.6
1	A	373	GLN	2.5
1	A	452	GLY	2.5
1	B	469	GLY	2.5
1	A	533	SER	2.5
1	A	428	GLN	2.5
1	A	457	GLU	2.5
1	B	541	VAL	2.5
1	B	493	ASN	2.5
1	B	595	TRP	2.5
1	A	396	GLY	2.5
1	A	522	VAL	2.5
1	B	442	CYS	2.5
1	B	489	LEU	2.5
1	B	555	GLY	2.5
1	B	615	ILE	2.5
1	B	395	GLU	2.4
1	A	575	PHE	2.4
1	A	386	ASP	2.4
1	B	425	CYS	2.4
1	B	535	TYR	2.4
1	B	570	ASP	2.4
1	B	360	PRO	2.4
1	B	432	CYS	2.4
1	A	588	TYR	2.3
1	B	547	LEU	2.3
1	A	445	ASP	2.3
1	A	395	GLU	2.3
1	B	533	SER	2.3
1	B	407	ALA	2.3
1	A	562	ARG	2.3
1	B	426	LEU	2.3
1	B	495	VAL	2.3
1	A	500	ASP	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	559	TYR	2.3
1	B	536	SER	2.2
1	A	388	VAL	2.2
1	B	529	VAL	2.2
1	B	500	ASP	2.2
1	A	613	ALA	2.2
1	B	381	TYR	2.2
1	B	490	VAL	2.2
1	B	455	ALA	2.2
1	A	443	LEU	2.2
1	B	593	HIS	2.2
1	B	549	TRP	2.2
1	B	544	PHE	2.2
1	A	561	ASN	2.2
1	B	411	MET	2.2
1	A	403	PHE	2.1
1	B	444	SER	2.1
1	B	526	SER	2.1
1	B	364	THR	2.1
1	A	426	LEU	2.1
1	A	563	SER	2.1
1	A	617	GLU	2.1
1	B	562	ARG	2.1
1	A	434	VAL	2.1
1	A	541	VAL	2.1
1	A	546	VAL	2.1
1	B	377	VAL	2.1
1	B	604	ALA	2.1
1	B	380	GLY	2.1
1	B	545	GLY	2.1
1	B	412	LYS	2.1
1	A	442[A]	CYS	2.0
1	B	601	ASP	2.0
1	B	390	ILE	2.0
1	B	591	MET	2.0
1	A	425	CYS	2.0
1	A	467	CYS	2.0
1	B	538	LYS	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](#)

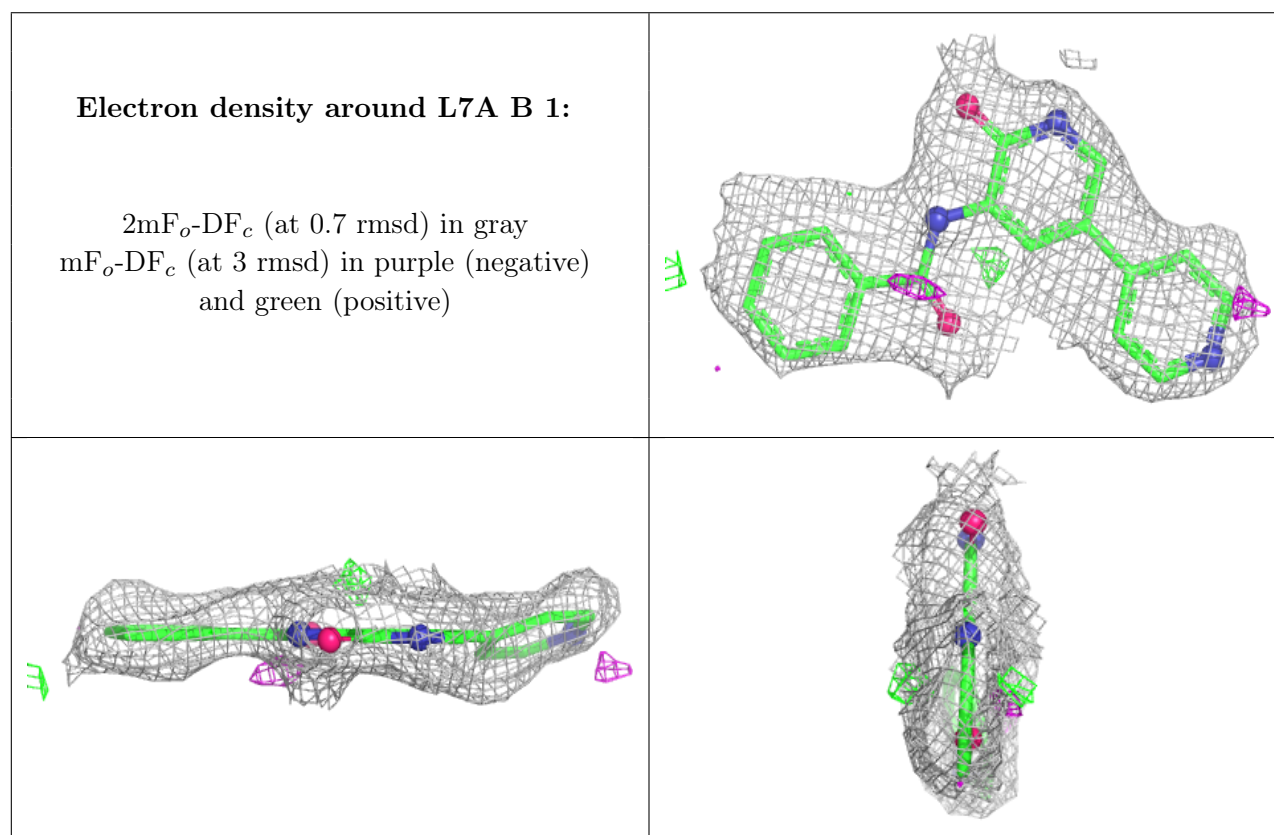
There are no oligosaccharides in this entry.

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.

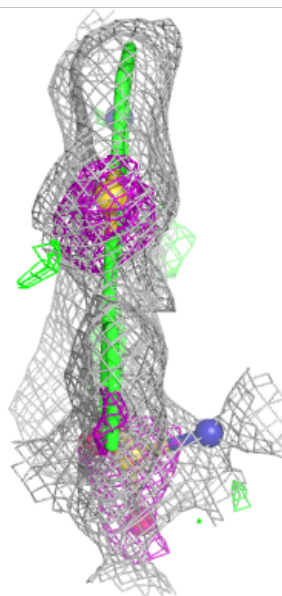
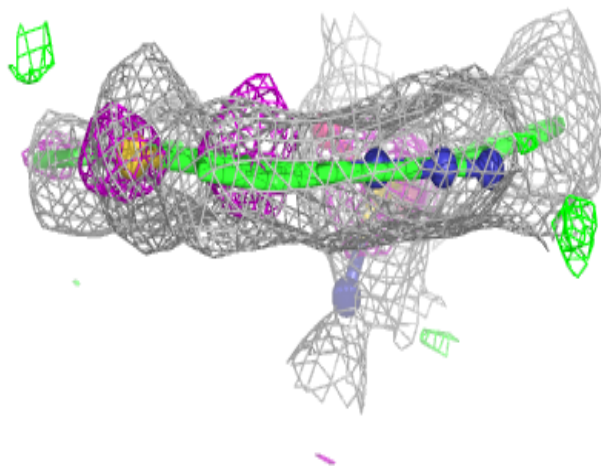
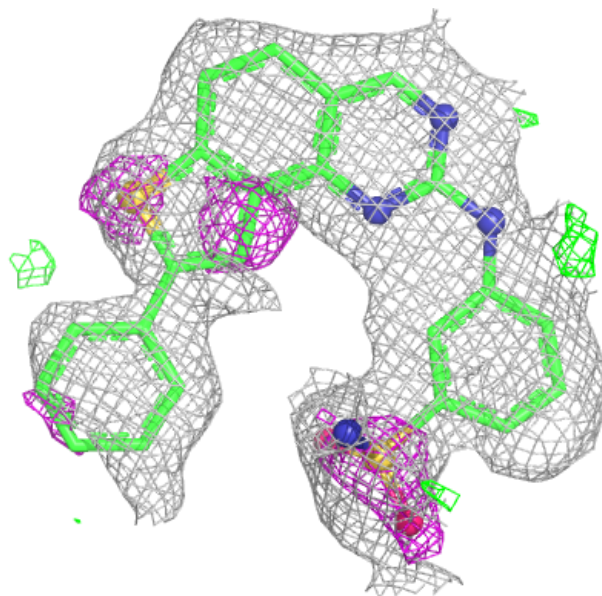
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	L7A	B	1	22/22	0.74	0.16	42,42,42,42	0
2	PQC	A	1	30/30	0.82	0.13	11,19,28,30	0

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 PQC A 1:

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



6.5 Other polymers ⓘ

There are no such residues in this entry.