



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 28, 2020 – 12:11 PM EDT

PDB ID : 6UKB
Title : Crystal structure of human GAC in complex with inhibitor UPGL00012
Authors : Huang, Q.; Cerione, R.A.
Deposited on : 2019-10-04
Resolution : 3.00 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 : 2.14.6
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) : 2.14.6

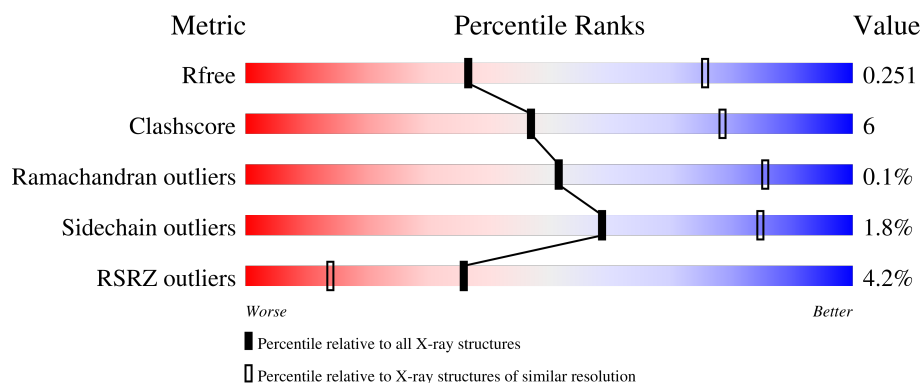
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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	527	<div> <div>4%</div> <div>65% 13% 22%</div> </div>
1	B	527	<div> <div>4%</div> <div>64% 13% 22%</div> </div>
1	C	527	<div> <div>2%</div> <div>66% 12% 22%</div> </div>
1	D	527	<div> <div>3%</div> <div>68% 9% 22%</div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12818 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.

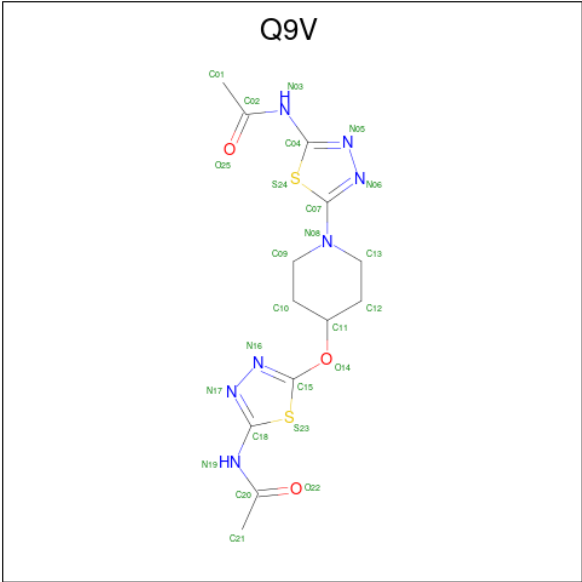
- Molecule 1 is a protein called Glutaminase kidney isoform, mitochondrial.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	1	0	0
			3190	2034	539	589	28			
1	B	409	Total	C	N	O	S	1	0	0
			3190	2034	539	589	28			
1	C	410	Total	C	N	O	S	1	0	0
			3194	2036	540	590	28			
1	D	410	Total	C	N	O	S	1	0	0
			3194	2036	540	590	28			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	268	ALA	VAL	conflict	UNP O94925
B	268	ALA	VAL	conflict	UNP O94925
C	268	ALA	VAL	conflict	UNP O94925
D	268	ALA	VAL	conflict	UNP O94925

- Molecule 2 is N-[5-(4-{[5-(acetylamino)-1,3,4-thiadiazol-2-yl]oxy}piperidin-1-yl)-1,3,4-thiadiazol-2-yl]acetamide (three-letter code: Q9V) (formula: C₁₃H₁₇N₇O₃S₂) (labeled as "Ligand of Interest" by author).

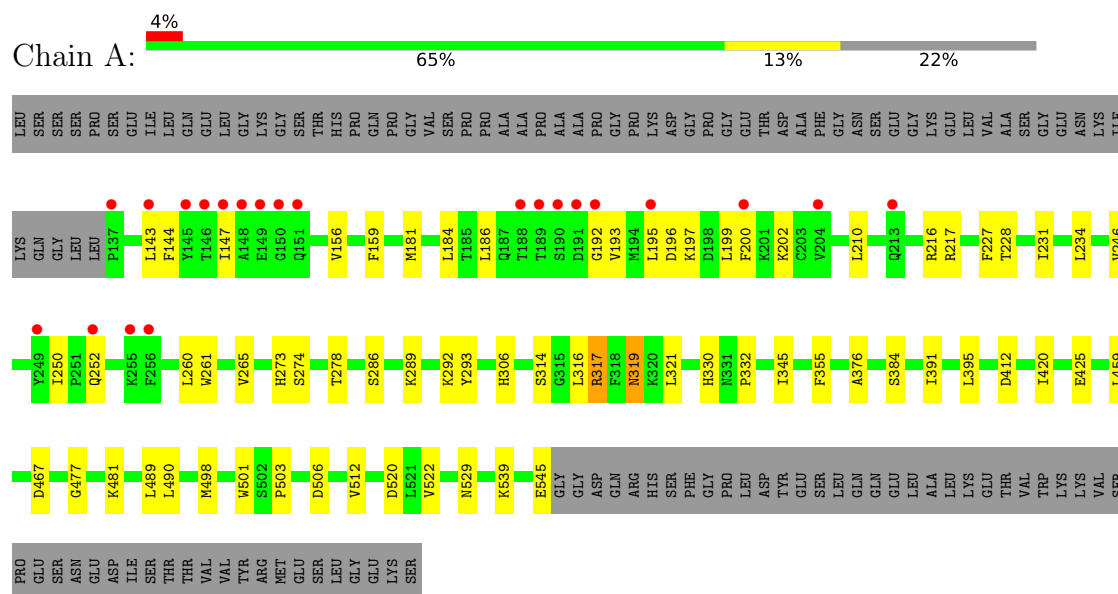


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	S	0	0
			25	13	7	3	2		
2	B	1	Total	C	N	O	S	0	0
			25	13	7	3	2		

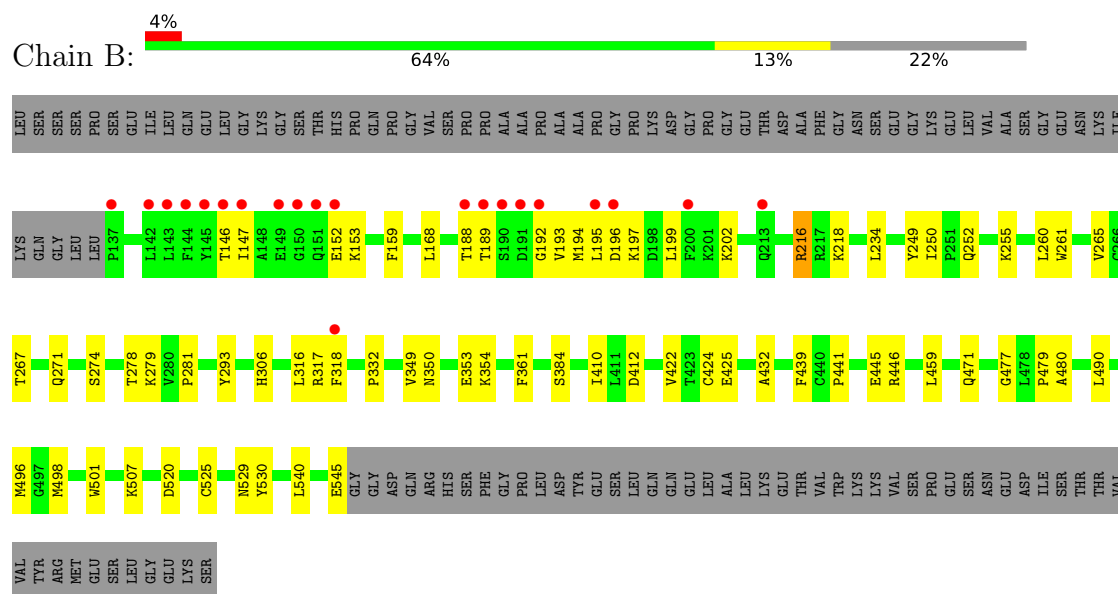
3 Residue-property plots

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.

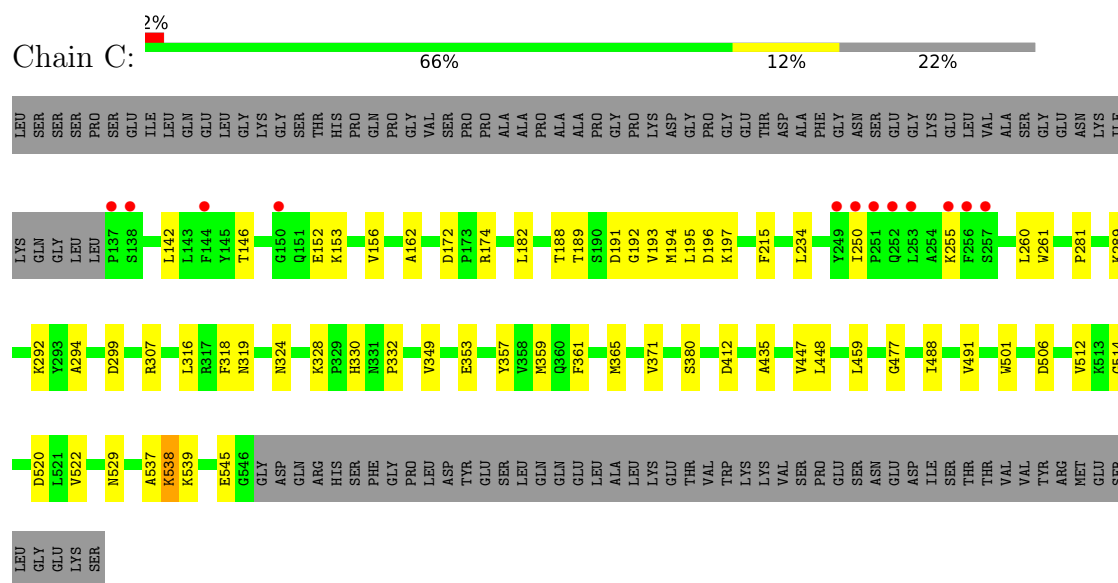
- Molecule 1: Glutaminase kidney isoform, mitochondrial



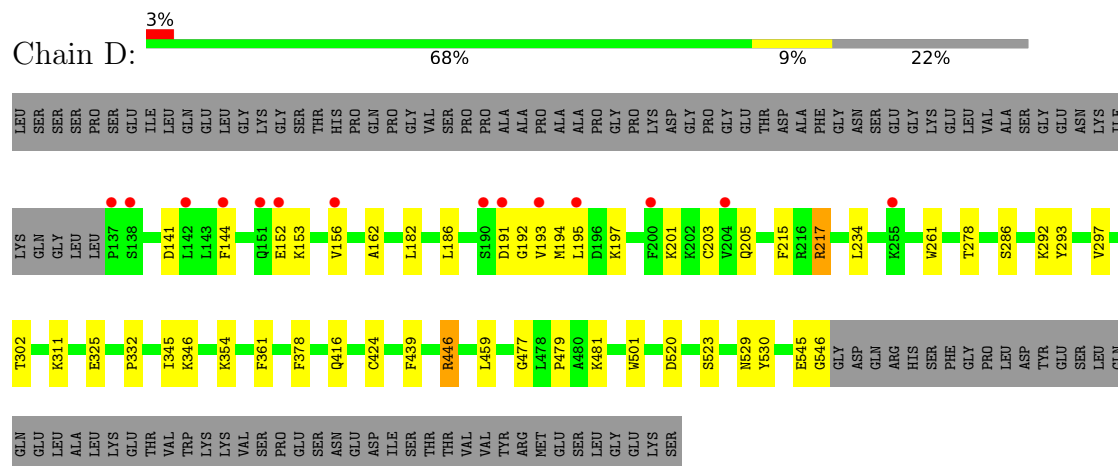
- Molecule 1: Glutaminase kidney isoform, mitochondrial



- Molecule 1: Glutaminase kidney isoform, mitochondrial



- Molecule 1: Glutaminase kidney isoform, mitochondrial



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.23Å 139.39Å 178.13Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.74 – 3.00 46.74 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.3 (46.74-3.00) 99.3 (46.74-3.00)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.17	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 3.01Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.195 , 0.250 0.195 , 0.251	Depositor DCC
R_{free} test set	1988 reflections (3.99%)	wwPDB-VP
Wilson B-factor (Å ²)	51.1	Xtriage
Anisotropy	0.664	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12818	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 57.94 % of the origin peak, indicating pseudo-translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo-translational symmetry is equal to 2.1992e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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: Q9V

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	0.51	0/3262	0.68	2/4403 (0.0%)
1	B	0.51	0/3262	0.70	2/4403 (0.0%)
1	C	0.49	0/3266	0.66	0/4408
1	D	0.52	0/3266	0.66	0/4408
All	All	0.51	0/13056	0.68	4/17622 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	489	LEU	CA-CB-CG	6.63	130.55	115.30
1	B	197	LYS	CD-CE-NZ	6.48	126.60	111.70
1	B	197	LYS	CB-CG-CD	-5.74	96.68	111.60
1	A	210	LEU	CB-CG-CD2	5.63	120.57	111.00

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	3190	0	3167	46	0
1	B	3190	0	3167	43	0
1	C	3194	0	3170	41	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	D	3194	0	3170	35	0
2	A	25	0	0	2	0
2	B	25	0	0	0	0
All	All	12818	0	12674	159	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 6.

All (159) 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:217:ARG:HH22	1:D:545:GLU:HB3	1.31	0.94
1:A:319:ASN:ND2	1:A:467:ASP:OD1	2.01	0.92
1:B:529:ASN:ND2	1:D:529:ASN:OD1	2.10	0.84
1:A:156:VAL:HG21	1:A:186:LEU:HD21	1.67	0.76
1:B:250:ILE:HG22	1:B:252:GLN:H	1.50	0.76
1:C:234:LEU:HD22	1:C:520:ASP:HB3	1.68	0.74
1:A:274:SER:HB3	1:A:278:THR:HG21	1.73	0.69
1:D:156:VAL:HG12	1:D:195:LEU:HD11	1.75	0.68
1:A:143:LEU:HD22	1:A:200:PHE:HZ	1.60	0.67
1:A:227:PHE:CE2	1:A:231:ILE:HD11	2.29	0.67
1:D:332:PRO:HD2	1:D:459:LEU:HD13	1.76	0.67
1:D:439:PHE:CE2	1:D:446:ARG:HB2	2.30	0.66
1:B:332:PRO:HD2	1:B:459:LEU:HD13	1.76	0.66
1:B:153:LYS:HB3	1:B:194:MET:HE2	1.79	0.64
1:D:201:LYS:O	1:D:205:GLN:HG3	1.97	0.64
1:B:216:ARG:HB3	1:B:218:LYS:HE2	1.79	0.63
1:C:537:ALA:HB1	1:C:538:LYS:HD2	1.80	0.63
1:B:152:GLU:HG2	1:B:153:LYS:HB2	1.80	0.63
1:C:152:GLU:HG2	1:C:153:LYS:HG3	1.80	0.63
1:A:250:ILE:HG22	1:A:252:GLN:H	1.63	0.62
1:D:234:LEU:HD22	1:D:520:ASP:HB3	1.82	0.61
1:B:349:VAL:CG1	1:B:353:GLU:HB2	2.30	0.61
1:D:152:GLU:HG2	1:D:153:LYS:HG3	1.83	0.61
1:A:477:GLY:O	1:A:529:ASN:HB2	2.01	0.61
1:A:316:LEU:O	1:A:317:ARG:HD2	2.01	0.60
1:B:234:LEU:HD22	1:B:520:ASP:HB3	1.83	0.60
1:B:146:THR:OG1	1:B:216:ARG:NH1	2.35	0.60
1:A:156:VAL:HG11	1:A:186:LEU:HD11	1.85	0.59
1:C:359:MET:CE	1:C:371:VAL:HG12	2.34	0.58
1:D:293:TYR:O	1:D:297:VAL:HG12	2.03	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:349:VAL:O	1:B:354:LYS:HE3	2.04	0.57
1:D:144:PHE:CE2	1:D:197:LYS:HB3	2.40	0.57
1:B:530:TYR:CE1	1:D:479:PRO:HG3	2.39	0.57
1:B:471:GLN:NE2	1:D:311:LYS:HE3	2.20	0.57
1:C:188:THR:HG22	1:C:189:THR:HG23	1.87	0.56
1:D:153:LYS:HB3	1:D:194:MET:HG2	1.88	0.56
1:D:153:LYS:CB	1:D:194:MET:HG2	2.36	0.56
1:A:332:PRO:HD2	1:A:459:LEU:HD13	1.87	0.55
1:A:260:LEU:HD13	1:A:501:TRP:CH2	2.42	0.55
1:C:332:PRO:HD2	1:C:459:LEU:HD13	1.89	0.55
1:D:141:ASP:O	1:D:144:PHE:HB3	2.06	0.55
1:A:293:TYR:OH	1:A:306:HIS:NE2	2.31	0.55
1:A:355:PHE:CE1	1:A:420:ILE:HD11	2.42	0.54
1:B:525:CYS:HA	1:B:540:LEU:O	2.07	0.54
1:B:278:THR:HA	1:B:424:CYS:HB2	1.89	0.54
1:B:317:ARG:HD2	1:D:325:GLU:OE1	2.07	0.53
1:D:156:VAL:HG11	1:D:186:LEU:HD21	1.89	0.53
1:C:359:MET:HE1	1:C:371:VAL:HG12	1.91	0.53
1:A:231:ILE:HD13	1:A:265:VAL:HG21	1.91	0.53
1:D:162:ALA:HB1	1:D:215:PHE:HE1	1.73	0.53
1:B:261:TRP:HA	1:B:501:TRP:O	2.09	0.53
1:A:181:MET:HE2	1:A:184:LEU:HD12	1.91	0.52
1:B:316:LEU:O	1:B:317:ARG:HG3	2.10	0.52
1:A:321:LEU:HD23	2:A:601:Q9V:N03	2.26	0.51
1:C:349:VAL:CG1	1:C:353:GLU:HB2	2.41	0.50
1:D:477:GLY:O	1:D:529:ASN:HB2	2.12	0.50
1:A:144:PHE:CE2	1:A:197:LYS:HG2	2.47	0.50
1:B:480:ALA:HB2	1:B:490:LEU:HD12	1.93	0.49
1:B:479:PRO:HG3	1:D:530:TYR:CE1	2.47	0.49
1:D:217:ARG:NH2	1:D:545:GLU:HB3	2.14	0.49
1:B:267:THR:HA	1:B:496:MET:HA	1.95	0.49
1:C:477:GLY:O	1:C:529:ASN:HB2	2.13	0.48
1:C:435:ALA:HB2	1:C:491:VAL:HG13	1.95	0.48
1:A:490:LEU:HB3	1:A:498:MET:HB2	1.94	0.48
1:B:293:TYR:HH	1:B:306:HIS:HE2	0.57	0.48
1:D:156:VAL:HG12	1:D:195:LEU:CD1	2.43	0.48
1:A:252:GLN:HE21	1:A:376:ALA:HB1	1.79	0.48
1:A:234:LEU:HD22	1:A:520:ASP:HB3	1.95	0.48
1:C:538:LYS:H	1:C:538:LYS:HD2	1.78	0.48
1:C:545:GLU:N	1:C:545:GLU:OE1	2.47	0.47
1:A:286:SER:O	1:A:481:LYS:HE3	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:192:GLY:HA3	1:B:193:VAL:HA	1.52	0.47
1:A:252:GLN:NE2	1:A:376:ALA:HB1	2.30	0.47
1:B:188:THR:HG22	1:C:281:PRO:HD2	1.96	0.47
1:C:289:LYS:HA	1:C:292:LYS:HE2	1.97	0.47
1:D:286:SER:O	1:D:481:LYS:HE3	2.15	0.47
1:C:307:ARG:O	1:C:328:LYS:HD3	2.15	0.46
1:D:545:GLU:OE1	1:D:545:GLU:N	2.48	0.46
1:B:477:GLY:O	1:B:529:ASN:HB2	2.15	0.46
1:B:274:SER:HB3	1:B:278:THR:HG21	1.96	0.46
1:A:181:MET:CE	1:A:184:LEU:HD12	2.46	0.46
1:C:260:LEU:HD13	1:C:501:TRP:HH2	1.81	0.46
1:C:261:TRP:HA	1:C:501:TRP:O	2.16	0.46
1:A:143:LEU:HD22	1:A:200:PHE:CZ	2.45	0.46
1:A:319:ASN:OD1	1:A:319:ASN:N	2.48	0.46
1:C:506:ASP:HB3	1:C:512:VAL:HG22	1.97	0.46
1:B:147:ILE:HD11	1:B:159:PHE:HA	1.98	0.45
1:C:488:ILE:HD12	1:C:514:GLY:HA3	1.97	0.45
1:C:153:LYS:HB2	1:C:194:MET:HE3	1.98	0.45
1:B:153:LYS:HB3	1:B:194:MET:CE	2.46	0.45
1:B:195:LEU:HD23	1:B:199:LEU:HG	1.97	0.45
1:C:260:LEU:HD13	1:C:501:TRP:CH2	2.51	0.45
1:A:506:ASP:HB3	1:A:512:VAL:HG22	2.00	0.44
1:D:378:PHE:CE1	1:D:416:GLN:HG3	2.52	0.44
1:A:192:GLY:HA3	1:A:193:VAL:HA	1.53	0.44
1:A:199:LEU:O	1:A:202:LYS:HB3	2.18	0.44
1:A:321:LEU:HD23	2:A:601:Q9V:C04	2.46	0.44
1:C:349:VAL:HG12	1:C:353:GLU:HB2	1.98	0.44
1:A:195:LEU:HD23	1:A:199:LEU:HG	1.98	0.44
1:A:545:GLU:OE1	1:A:545:GLU:N	2.51	0.44
1:B:271:GLN:H	1:B:271:GLN:HG3	1.63	0.44
1:D:292:LYS:HB2	1:D:345:ILE:HD11	1.99	0.44
1:A:147:ILE:HD11	1:A:159:PHE:HA	1.98	0.44
1:B:265:VAL:HG22	1:B:498:MET:HE2	2.00	0.44
1:B:459:LEU:HD23	1:B:459:LEU:HA	1.86	0.43
1:C:522:VAL:O	1:C:539:LYS:HE2	2.18	0.43
1:D:191:ASP:OD1	1:D:191:ASP:N	2.50	0.43
1:C:197:LYS:H	1:C:197:LYS:HG3	1.50	0.43
1:C:162:ALA:HB1	1:C:215:PHE:HE1	1.84	0.43
1:A:260:LEU:HD13	1:A:501:TRP:HH2	1.82	0.43
1:C:294:ALA:HB1	1:C:448:LEU:HD13	2.00	0.43
1:C:459:LEU:HD23	1:C:459:LEU:HA	1.78	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:250:ILE:HB	1:C:380:SER:OG	2.19	0.43
1:C:299:ASP:OD2	1:C:357:TYR:OH	2.30	0.43
1:A:286:SER:HA	1:A:289:LYS:HZ3	1.84	0.43
1:B:279:LYS:HE2	1:B:425:GLU:OE1	2.19	0.43
1:A:228:THR:HA	1:A:231:ILE:HD12	2.01	0.42
1:B:188:THR:OG1	1:B:189:THR:HG23	2.19	0.42
1:B:199:LEU:O	1:B:202:LYS:HB3	2.18	0.42
1:C:153:LYS:HB2	1:C:194:MET:CE	2.49	0.42
1:B:168:LEU:HA	1:B:168:LEU:HD23	1.85	0.42
1:C:324:ASN:HB3	1:C:330:HIS:CD2	2.55	0.42
1:C:359:MET:HE3	1:C:371:VAL:HG12	1.99	0.42
1:B:439:PHE:CE2	1:B:446:ARG:HB2	2.54	0.42
1:A:316:LEU:HD23	1:A:316:LEU:HA	1.83	0.42
1:A:391:ILE:HG22	1:A:395:LEU:HD11	2.02	0.42
1:C:316:LEU:HD23	1:C:316:LEU:HA	1.81	0.42
1:D:278:THR:HA	1:D:424:CYS:HB2	2.02	0.42
1:A:314:SER:HB3	1:A:330:HIS:CG	2.55	0.42
1:C:172:ASP:OD1	1:C:174:ARG:HD3	2.19	0.42
1:A:246:VAL:HG22	1:A:503:PRO:HB2	2.02	0.41
1:D:182:LEU:HD23	1:D:203:CYS:SG	2.60	0.41
1:B:350:ASN:ND2	1:B:353:GLU:OE2	2.54	0.41
1:A:292:LYS:HB2	1:A:345:ILE:HD11	2.03	0.41
1:A:216:ARG:HE	1:A:216:ARG:HA	1.85	0.41
1:A:278:THR:O	1:A:425:GLU:HG3	2.20	0.41
1:C:182:LEU:HA	1:C:182:LEU:HD23	1.86	0.41
1:D:261:TRP:HA	1:D:501:TRP:O	2.20	0.41
1:D:545:GLU:HG2	1:D:546:GLY:H	1.86	0.41
1:B:545:GLU:N	1:B:545:GLU:OE1	2.53	0.41
1:B:260:LEU:HD13	1:B:501:TRP:CH2	2.56	0.41
1:B:432:ALA:HB1	1:B:441:PRO:HG3	2.01	0.41
1:C:156:VAL:HG12	1:C:195:LEU:HD11	2.02	0.41
1:C:538:LYS:N	1:C:538:LYS:HD2	2.36	0.41
1:A:228:THR:HB	1:A:273:HIS:CE1	2.56	0.41
1:D:346:LYS:HB3	1:D:354:LYS:HG2	2.03	0.41
1:A:261:TRP:HA	1:A:501:TRP:O	2.21	0.41
1:B:281:PRO:HA	1:B:422:VAL:O	2.20	0.41
1:C:365:MET:HG2	1:C:447:VAL:HG11	2.02	0.41
1:D:302:THR:HG23	1:D:302:THR:H	1.68	0.41
1:C:318:PHE:HA	1:C:318:PHE:HD1	1.75	0.41
1:A:143:LEU:O	1:A:147:ILE:HG22	2.20	0.41
1:B:410:ILE:HA	1:B:410:ILE:HD13	1.83	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:278:THR:CA	1:B:424:CYS:HB2	2.51	0.41
1:C:192:GLY:HA3	1:C:193:VAL:HA	1.55	0.41
1:C:142:LEU:O	1:C:146:THR:HG23	2.21	0.40
1:D:192:GLY:HA3	1:D:193:VAL:HA	1.68	0.40
1:D:156:VAL:HG13	1:D:193:VAL:O	2.21	0.40
1:A:522:VAL:O	1:A:539:LYS:HE2	2.22	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	407/527 (77%)	394 (97%)	13 (3%)	0	100	100
1	B	407/527 (77%)	392 (96%)	15 (4%)	0	100	100
1	C	408/527 (77%)	395 (97%)	12 (3%)	1 (0%)	47	82
1	D	408/527 (77%)	391 (96%)	17 (4%)	0	100	100
All	All	1630/2108 (77%)	1572 (96%)	57 (4%)	1 (0%)	51	85

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	191	ASP

5.3.2 Protein sidechains [i](#)

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

The Analysed column shows the number of residues for which the sidechain conformation was

analysed, and the total number of residues.

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	A	353/451 (78%)	347 (98%)	6 (2%)	60	85
1	B	353/451 (78%)	343 (97%)	10 (3%)	43	77
1	C	353/451 (78%)	347 (98%)	6 (2%)	60	85
1	D	353/451 (78%)	349 (99%)	4 (1%)	73	90
All	All	1412/1804 (78%)	1386 (98%)	26 (2%)	59	85

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	196	ASP
1	A	217	ARG
1	A	317	ARG
1	A	319	ASN
1	A	384	SER
1	A	412	ASP
1	B	196	ASP
1	B	216	ARG
1	B	249	TYR
1	B	255	LYS
1	B	318	PHE
1	B	361	PHE
1	B	384	SER
1	B	412	ASP
1	B	445	GLU
1	B	507	LYS
1	C	196	ASP
1	C	255	LYS
1	C	319	ASN
1	C	361	PHE
1	C	412	ASP
1	C	538	LYS
1	D	217	ARG
1	D	361	PHE
1	D	446	ARG
1	D	523	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	455	ASN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no monosaccharides in this entry.

5.6 Ligand geometry [i](#)

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	Q9V	B	601	-	19,27,27	2.72	6 (31%)	14,37,37	2.99	6 (42%)
2	Q9V	A	601	-	19,27,27	2.82	7 (36%)	14,37,37	3.51	7 (50%)

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	Q9V	B	601	-	-	5/8/26/26	0/3/3/3
2	Q9V	A	601	-	-	4/8/26/26	0/3/3/3

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	Q9V	C07-N08	6.75	1.42	1.32
2	A	601	Q9V	C07-N08	6.46	1.42	1.32
2	A	601	Q9V	O14-C15	5.09	1.42	1.36
2	B	601	Q9V	O14-C15	4.96	1.42	1.36
2	A	601	Q9V	C04-N03	4.42	1.44	1.36
2	A	601	Q9V	C20-N19	4.32	1.44	1.36
2	B	601	Q9V	C04-N03	4.18	1.44	1.36
2	A	601	Q9V	C02-N03	4.16	1.43	1.36
2	B	601	Q9V	C02-N03	3.90	1.43	1.36
2	B	601	Q9V	C20-N19	3.68	1.42	1.36
2	A	601	Q9V	C18-N19	3.55	1.43	1.36
2	B	601	Q9V	C18-N19	3.37	1.42	1.36
2	A	601	Q9V	N17-N16	-2.05	1.33	1.37

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	601	Q9V	C09-C10-C11	-8.01	101.51	110.32
2	A	601	Q9V	C09-C10-C11	-7.87	101.66	110.32
2	A	601	Q9V	C21-C20-N19	7.27	125.65	114.98
2	A	601	Q9V	O22-C20-N19	-4.51	117.11	123.04
2	B	601	Q9V	C12-C11-C10	-3.87	104.28	111.74
2	B	601	Q9V	C21-C20-N19	3.60	120.27	114.98
2	A	601	Q9V	C01-C02-N03	3.34	119.89	114.98
2	B	601	Q9V	O22-C20-N19	-2.89	119.24	123.04
2	B	601	Q9V	O14-C11-C10	2.77	114.43	108.31
2	A	601	Q9V	O22-C20-C21	-2.60	117.23	122.06
2	A	601	Q9V	C12-C11-C10	-2.52	106.87	111.74
2	A	601	Q9V	C13-C12-C11	-2.22	107.88	110.32
2	B	601	Q9V	C01-C02-N03	2.09	118.06	114.98

There are no chirality outliers.

All (9) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	601	Q9V	S24-C07-N08-C09
2	B	601	Q9V	C10-C11-O14-C15
2	A	601	Q9V	S24-C07-N08-C09
2	A	601	Q9V	C21-C20-N19-C18
2	A	601	Q9V	C10-C11-O14-C15
2	B	601	Q9V	C21-C20-N19-C18

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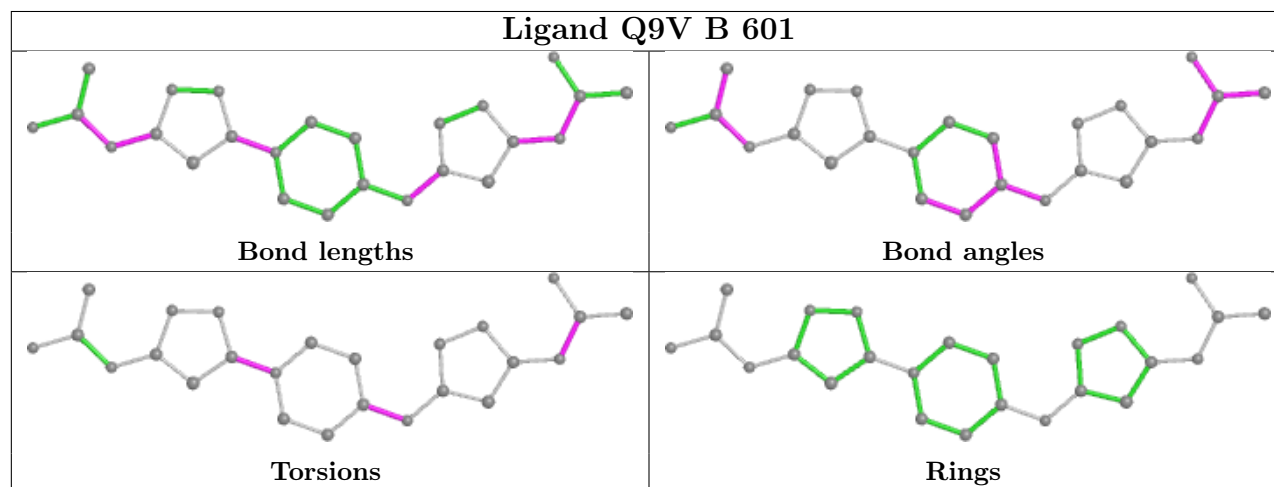
Mol	Chain	Res	Type	Atoms
2	B	601	Q9V	O22-C20-N19-C18
2	A	601	Q9V	O22-C20-N19-C18
2	B	601	Q9V	C12-C11-O14-C15

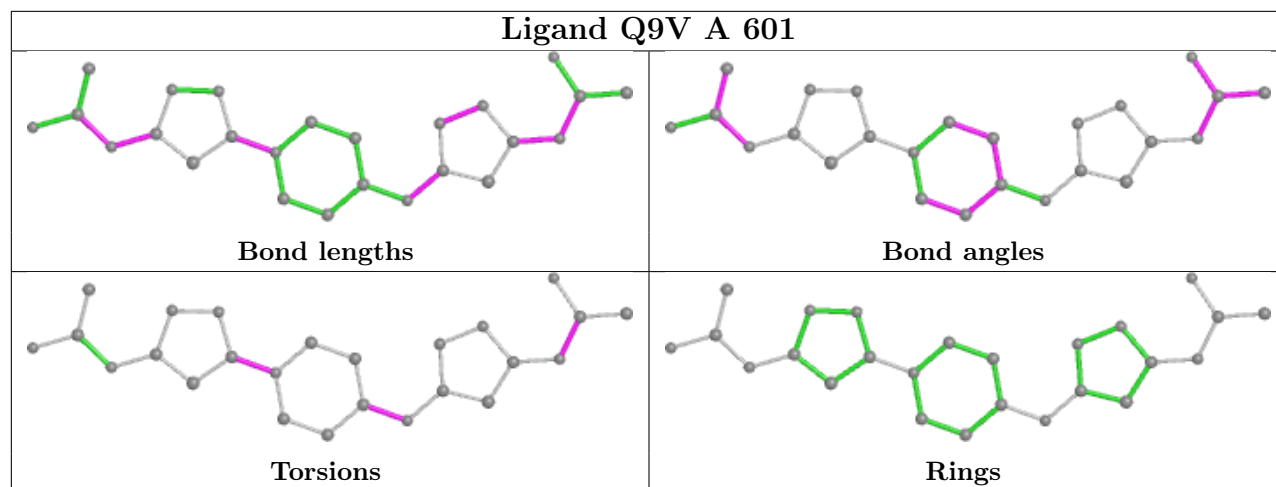
There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	601	Q9V	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	409/527 (77%)	0.03	22 (5%) 25 9	29, 49, 103, 226	0
1	B	409/527 (77%)	-0.04	21 (5%) 28 10	25, 49, 99, 196	0
1	C	410/527 (77%)	-0.10	12 (2%) 51 23	27, 48, 101, 144	0
1	D	410/527 (77%)	-0.12	14 (3%) 45 19	28, 47, 99, 147	0
All	All	1638/2108 (77%)	-0.06	69 (4%) 36 14	25, 48, 101, 226	0

All (69) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	191	ASP	11.5
1	B	191	ASP	9.4
1	A	189	THR	8.2
1	B	189	THR	7.2
1	B	192	GLY	5.8
1	C	252	GLN	4.8
1	A	252	GLN	4.7
1	A	192	GLY	4.4
1	D	137	PRO	4.1
1	B	195	LEU	4.1
1	A	146	THR	4.0
1	D	191	ASP	4.0
1	A	188	THR	3.9
1	B	145	TYR	3.8
1	B	143	LEU	3.7
1	A	149	GLU	3.7
1	B	188	THR	3.6
1	B	150	GLY	3.6
1	D	195	LEU	3.4
1	A	150	GLY	3.3
1	D	152	GLU	3.2

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Mol	Chain	Res	Type	RSRZ
1	D	138	SER	3.2
1	A	249	TYR	3.1
1	A	151	GLN	3.1
1	A	190	SER	3.1
1	B	146	THR	3.0
1	C	150	GLY	3.0
1	B	149	GLU	2.9
1	A	213	GLN	2.9
1	C	249	TYR	2.8
1	B	196	ASP	2.8
1	A	137	PRO	2.7
1	B	142	LEU	2.7
1	A	256	PHE	2.7
1	D	200	PHE	2.7
1	D	144	PHE	2.6
1	B	137	PRO	2.6
1	C	251	PRO	2.6
1	A	200	PHE	2.6
1	A	145	TYR	2.6
1	D	151	GLN	2.5
1	D	142	LEU	2.5
1	C	250	ILE	2.4
1	B	190	SER	2.4
1	A	195	LEU	2.4
1	C	137	PRO	2.4
1	B	213	GLN	2.4
1	C	255	LYS	2.4
1	A	255	LYS	2.3
1	C	257	SER	2.3
1	A	147	ILE	2.3
1	B	147	ILE	2.3
1	B	144	PHE	2.3
1	B	200	PHE	2.3
1	B	318	PHE	2.3
1	B	151	GLN	2.3
1	A	204	VAL	2.3
1	D	190	SER	2.3
1	C	256	PHE	2.2
1	C	144	PHE	2.2
1	A	143	LEU	2.2
1	D	193	VAL	2.2
1	C	253	LEU	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	148	ALA	2.1
1	D	255	LYS	2.1
1	C	138	SER	2.1
1	B	152	GLU	2.1
1	D	204	VAL	2.0
1	D	156	VAL	2.0

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

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

6.3 Carbohydrates [i](#)

There are no monosaccharides in this entry.

6.4 Ligands [i](#)

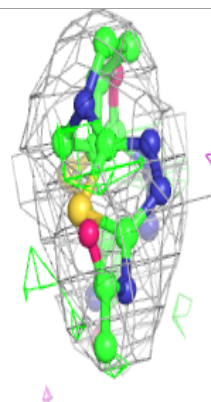
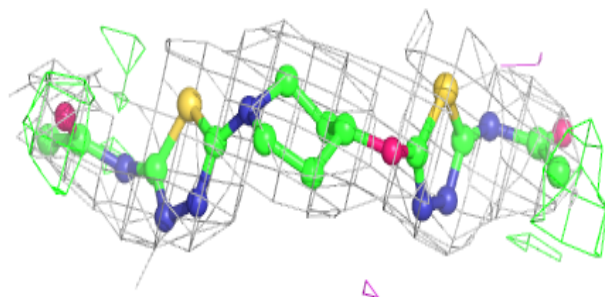
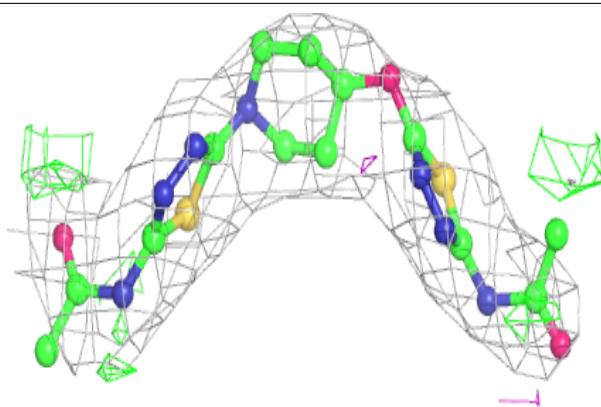
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	Q9V	B	601	25/25	0.93	0.20	51,67,88,98	0
2	Q9V	A	601	25/25	0.93	0.20	47,68,81,86	0

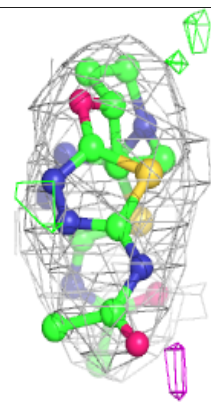
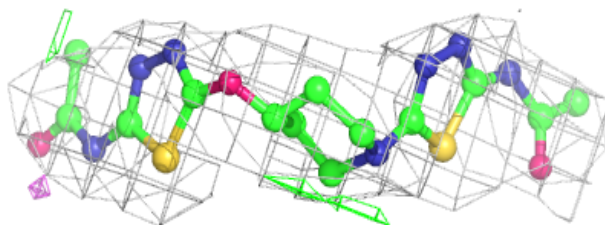
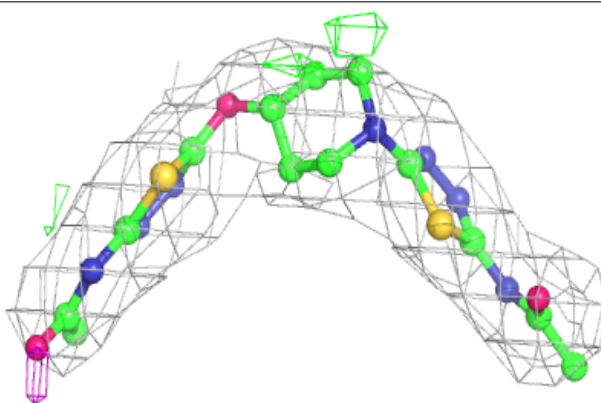
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around Q9V B 601:

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

**Electron density around Q9V 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.