



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2020 – 10:33 AM EDT

PDB ID : 6ULJ
Title : Crystal structure of human GAC in complex with inhibitor UPGL00012
Authors : Huang, Q.; Cerione, R.A.
Deposited on : 2019-10-08
Resolution : 2.69 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

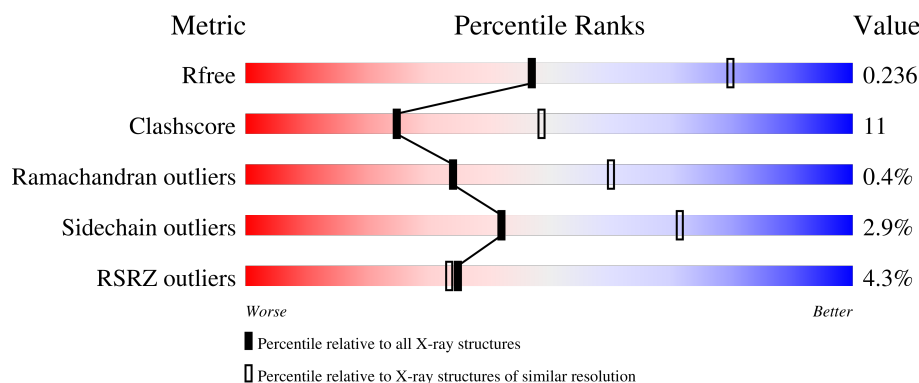
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.69 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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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>3%</div> <div>59%</div> <div>17%</div> <div>•</div> <div>22%</div> </div>
1	B	527	<div> <div>4%</div> <div>56%</div> <div>20%</div> <div>•</div> <div>22%</div> </div>
1	C	527	<div> <div>3%</div> <div>63%</div> <div>14%</div> <div>•</div> <div>22%</div> </div>
1	D	527	<div> <div>3%</div> <div>62%</div> <div>15%</div> <div>•</div> <div>22%</div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard

residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	QAA	B	601	-	-	-	X

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 13032 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.

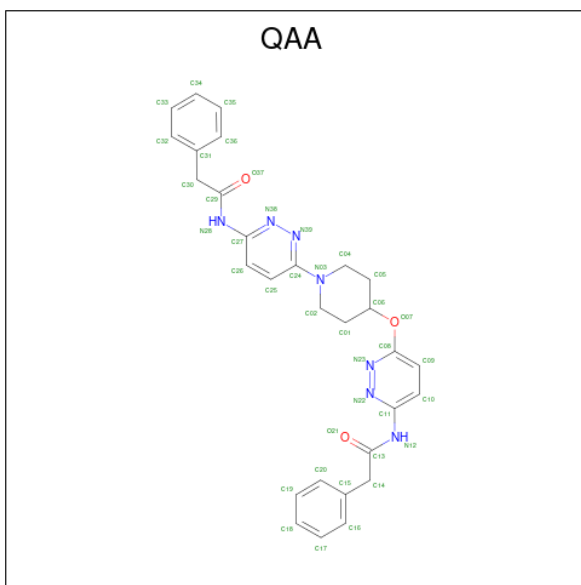
- Molecule 1 is a protein called Glutaminase kidney isoform, mitochondrial.

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	410	Total	C	N	O	S	1	0	0
			3194	2036	540	590	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 2-phenyl-N-{6-[4-({6-[(phenylacetyl)amino]pyridazin-3-yl}oxy)piperidin-1-yl]pyridazin-3-yl}acetamide (three-letter code: QAA) (formula: C₂₉H₂₉N₇O₃) (labeled as "Ligand of Interest" by author).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total 39	C 29	N 7	O 3	0	0
2	C	1	Total 39	C 29	N 7	O 3	0	0

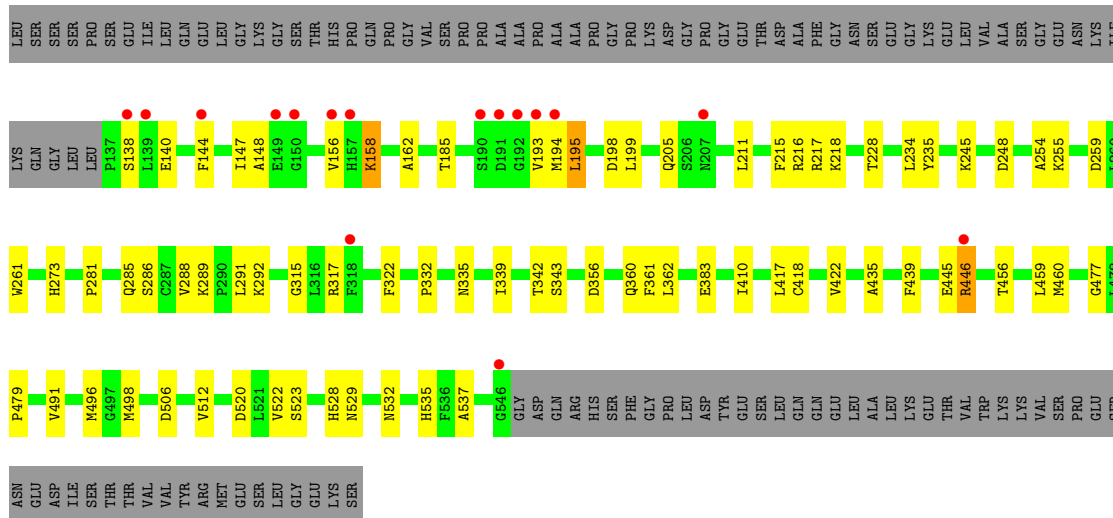
- Molecule 3 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	44	Total O 44 44	0	0
3	B	50	Total O 50 50	0	0
3	C	30	Total O 30 30	0	0
3	D	58	Total O 58 58	0	0

ARG
MET
GLU
SER
SER
LEU
GLY
LYS
SER

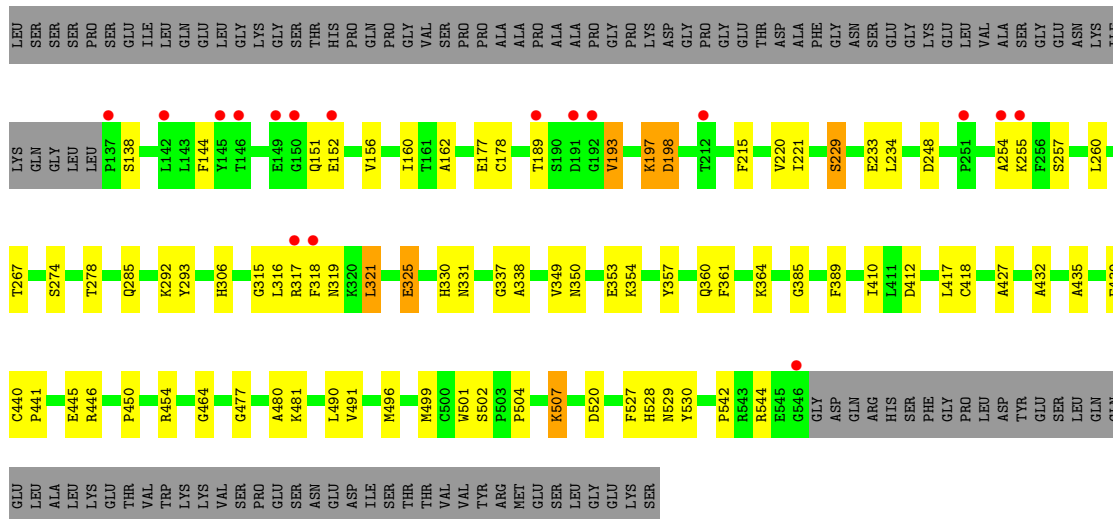
- Molecule 1: Glutaminase kidney isoform, mitochondrial

Chain C: 



- Molecule 1: Glutaminase kidney isoform, mitochondrial

Chain D: 



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	49.55Å 138.89Å 176.99Å 90.00° 93.91° 90.00°	Depositor
Resolution (Å)	36.39 – 2.69 36.39 – 2.69	Depositor EDS
% Data completeness (in resolution range)	85.5 (36.39-2.69) 85.4 (36.39-2.69)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.10	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.23 (at 2.68Å)	Xtriage
Refinement program	PHENIX 1.15.2_3472	Depositor
R, R_{free}	0.178 , 0.236 0.178 , 0.236	Depositor DCC
R_{free} test set	2010 reflections (3.55%)	wwPDB-VP
Wilson B-factor (Å ²)	40.6	Xtriage
Anisotropy	0.405	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 47.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13032	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.50% 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: QAA

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	0.48	0/3262	0.83	6/4403 (0.1%)
1	B	0.50	0/3266	0.79	8/4408 (0.2%)
1	C	0.49	1/3266 (0.0%)	0.74	4/4408 (0.1%)
1	D	0.51	1/3266 (0.0%)	0.76	10/4408 (0.2%)
All	All	0.50	2/13060 (0.0%)	0.78	28/17627 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	B	0	1
1	C	0	1
1	D	0	1
All	All	0	3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	255	LYS	CD-CE	5.94	1.66	1.51
1	D	197	LYS	CB-CG	-5.26	1.38	1.52

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	317	ARG	NE-CZ-NH1	-20.14	110.23	120.30
1	A	317	ARG	NE-CZ-NH2	17.41	129.00	120.30
1	C	217	ARG	CA-CB-CG	-10.97	89.27	113.40
1	D	544	ARG	NE-CZ-NH1	9.96	125.28	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	D	544	ARG	CB-CG-CD	-9.12	87.88	111.60
1	B	320	LYS	CD-CE-NZ	9.08	132.58	111.70
1	D	544	ARG	NE-CZ-NH2	-8.68	115.96	120.30
1	A	317	ARG	CD-NE-CZ	8.62	135.67	123.60
1	C	217	ARG	NE-CZ-NH1	-8.36	116.12	120.30
1	D	325	GLU	CA-CB-CG	-8.15	95.47	113.40
1	B	544	ARG	NE-CZ-NH1	7.58	124.09	120.30
1	D	197	LYS	CD-CE-NZ	7.46	128.86	111.70
1	A	364	LYS	CB-CG-CD	-7.44	92.25	111.60
1	B	544	ARG	NE-CZ-NH2	-7.37	116.62	120.30
1	C	195	LEU	CA-CB-CG	7.35	132.21	115.30
1	B	186	LEU	CB-CG-CD2	-6.54	99.88	111.00
1	D	197	LYS	CB-CG-CD	-6.25	95.36	111.60
1	D	255	LYS	CA-CB-CG	6.08	126.79	113.40
1	C	217	ARG	CD-NE-CZ	-5.95	115.27	123.60
1	B	186	LEU	CB-CG-CD1	5.92	121.07	111.00
1	B	507	LYS	CD-CE-NZ	5.65	124.70	111.70
1	D	544	ARG	CG-CD-NE	5.59	123.54	111.80
1	A	149	GLU	CA-CB-CG	-5.50	101.29	113.40
1	B	143	LEU	CB-CG-CD2	5.50	120.36	111.00
1	D	325	GLU	N-CA-CB	-5.47	100.74	110.60
1	B	176	LYS	CD-CE-NZ	5.20	123.66	111.70
1	D	321	LEU	CA-CB-CG	5.10	127.02	115.30
1	A	317	ARG	CG-CD-NE	-5.07	101.15	111.80

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	316	LEU	Peptide
1	C	259	ASP	Peptide
1	D	189	THR	Peptide

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	82	1
1	B	3194	0	3170	94	0
1	C	3194	0	3170	52	0
1	D	3194	0	3170	62	1
2	B	39	0	0	9	0
2	C	39	0	0	6	0
3	A	44	0	0	4	0
3	B	50	0	0	2	0
3	C	30	0	0	1	0
3	D	58	0	0	5	0
All	All	13032	0	12677	275	1

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 (275) 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:B:143:LEU:CD2	1:B:200:PHE:HZ	1.40	1.33
1:B:143:LEU:HD22	1:B:200:PHE:CZ	1.64	1.31
1:B:143:LEU:CD2	1:B:200:PHE:CZ	2.29	1.07
1:B:143:LEU:HD22	1:B:200:PHE:HZ	0.86	1.01
1:B:148:ALA:O	1:B:149:GLU:HB2	1.60	0.98
1:D:360:GLN:NE2	3:D:601:HOH:O	1.95	0.94
1:A:156:VAL:HG12	1:A:195:LEU:HD13	1.49	0.93
1:C:532:ASN:HD22	1:C:535:HIS:H	1.19	0.90
1:B:221:ILE:CD1	1:B:542:PRO:HB2	2.02	0.89
1:A:147:ILE:O	1:A:158:LYS:NZ	2.06	0.88
1:B:498:MET:HE1	1:B:517:PHE:HE1	1.42	0.84
1:C:234:LEU:HD22	1:C:520:ASP:HB3	1.59	0.84
1:B:145:TYR:CE1	1:B:152:GLU:OE2	2.31	0.83
1:B:320:LYS:HB3	1:B:387:ARG:HH22	1.46	0.81
1:B:145:TYR:HE1	1:B:152:GLU:OE2	1.64	0.80
1:A:289:LYS:HA	1:A:292:LYS:HZ2	1.47	0.79
1:D:151:GLN:HG2	1:D:152:GLU:H	1.48	0.78
1:B:320:LYS:HG3	2:B:601:QAA:N38	1.99	0.78
1:B:316:LEU:HD21	1:B:467:ASP:O	1.84	0.77
1:A:317:ARG:HH21	2:C:601:QAA:C16	1.98	0.77
1:D:234:LEU:HD22	1:D:520:ASP:HB3	1.67	0.76
1:A:322:PHE:H	2:B:601:QAA:C25	1.97	0.75
1:A:307:ARG:O	1:A:328:LYS:NZ	2.20	0.74
1:A:139:LEU:HD22	1:A:212:THR:HG21	1.69	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:234:LEU:HD22	1:A:520:ASP:HB3	1.71	0.73
1:B:506:ASP:OD2	3:B:701:HOH:O	2.08	0.72
1:B:320:LYS:CG	2:B:601:QAA:N38	2.55	0.70
1:C:185:THR:HG21	1:C:199:LEU:HD21	1.72	0.70
1:B:176:LYS:HE3	1:B:180:ASP:OD2	1.91	0.70
1:B:143:LEU:HD23	1:B:200:PHE:CZ	2.27	0.69
1:A:529:ASN:ND2	1:D:529:ASN:OD1	2.19	0.69
1:C:144:PHE:O	1:C:148:ALA:N	2.26	0.68
1:B:529:ASN:OD1	1:C:529:ASN:ND2	2.18	0.67
1:A:317:ARG:HB2	1:A:318:PHE:CE2	2.29	0.67
1:D:318:PHE:N	3:D:603:HOH:O	2.27	0.67
1:A:317:ARG:HD3	1:D:325:GLU:OE2	1.95	0.67
1:B:234:LEU:HD22	1:B:520:ASP:HB3	1.75	0.66
1:A:147:ILE:HG22	1:A:158:LYS:NZ	2.10	0.65
1:B:457:LEU:HD12	1:B:479:PRO:HG2	1.79	0.64
1:A:481:LYS:NZ	3:A:603:HOH:O	2.31	0.64
1:D:220:VAL:HG13	1:D:221:ILE:HG12	1.80	0.64
1:B:320:LYS:CB	1:B:387:ARG:HH22	2.10	0.63
1:D:318:PHE:CD1	1:D:321:LEU:HG	2.33	0.63
1:A:252:GLN:HA	1:A:255:LYS:HE3	1.79	0.63
1:B:156:VAL:H	1:B:193:VAL:HG22	1.63	0.61
1:B:457:LEU:HD11	1:B:491:VAL:HG11	1.82	0.61
1:D:151:GLN:HG2	1:D:152:GLU:N	2.15	0.61
1:B:289:LYS:NZ	1:B:333:MET:O	2.32	0.61
1:B:221:ILE:HD12	1:B:542:PRO:HB2	1.81	0.61
1:B:166:THR:HG21	1:B:214:ALA:HB1	1.83	0.61
1:C:156:VAL:HG12	1:C:195:LEU:HG	1.83	0.60
1:A:319:ASN:N	3:A:605:HOH:O	2.34	0.60
1:B:320:LYS:HB3	1:B:387:ARG:NH2	2.16	0.60
1:B:446:ARG:NH1	3:B:703:HOH:O	2.35	0.60
1:C:477:GLY:O	1:C:529:ASN:HB2	2.02	0.60
1:B:143:LEU:HD22	1:B:200:PHE:CE1	2.32	0.59
1:B:316:LEU:HD11	1:B:467:ASP:HA	1.84	0.59
1:D:248:ASP:OD1	3:D:602:HOH:O	2.16	0.59
1:B:454:ARG:HD3	1:C:528:HIS:CD2	2.38	0.59
1:A:320:LYS:HB3	2:B:601:QAA:N23	2.18	0.59
1:A:318:PHE:HD1	1:A:321:LEU:HD23	1.68	0.58
1:D:507:LYS:H	1:D:507:LYS:HD2	1.69	0.58
1:C:383:GLU:HG3	1:C:383:GLU:O	2.03	0.58
1:A:317:ARG:HH12	1:D:330:HIS:CE1	2.22	0.57
1:C:140:GLU:N	1:C:140:GLU:OE1	2.33	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:LEU:HD12	1:A:202:LYS:HD3	1.87	0.57
1:B:326:ASP:HB2	1:B:328:LYS:HE3	1.86	0.56
1:B:181:MET:O	1:B:185:THR:HG23	2.04	0.56
1:A:319:ASN:OD1	3:A:601:HOH:O	2.18	0.56
1:A:140:GLU:OE1	1:A:140:GLU:N	2.38	0.56
2:C:601:QAA:C09	1:D:321:LEU:HD22	2.35	0.56
1:A:316:LEU:HD12	1:A:467:ASP:OD1	2.06	0.56
1:B:144:PHE:O	1:B:148:ALA:HB2	2.06	0.56
1:B:435:ALA:HB2	1:B:491:VAL:HG13	1.87	0.56
1:D:477:GLY:O	1:D:529:ASN:HB2	2.06	0.56
1:B:316:LEU:HD21	1:B:467:ASP:CA	2.35	0.56
1:B:316:LEU:HD21	1:B:467:ASP:C	2.26	0.56
1:A:252:GLN:NE2	1:A:376:ALA:O	2.40	0.55
1:C:285:GLN:HA	1:C:418:CYS:HB3	1.88	0.55
1:A:190:SER:O	3:A:602:HOH:O	2.18	0.55
2:B:601:QAA:C15	1:C:317:ARG:HH12	2.19	0.55
1:D:292:LYS:HZ1	1:D:338:ALA:HB1	1.72	0.55
1:D:317:ARG:N	3:D:603:HOH:O	2.40	0.55
1:B:192:GLY:C	1:B:194:MET:H	2.11	0.54
1:A:144:PHE:O	1:A:148:ALA:N	2.39	0.54
1:B:292:LYS:NZ	1:B:338:ALA:HB1	2.22	0.54
1:C:162:ALA:HB1	1:C:215:PHE:HE1	1.72	0.54
1:A:217:ARG:HH11	1:A:217:ARG:HG3	1.73	0.54
1:A:488:ILE:HD12	1:A:514:GLY:HA3	1.90	0.54
1:B:248:ASP:HA	1:B:254:ALA:HB2	1.90	0.54
1:C:435:ALA:HB2	1:C:491:VAL:HG13	1.90	0.54
1:B:316:LEU:HD21	1:B:467:ASP:HA	1.90	0.53
1:D:315:GLY:O	1:D:317:ARG:N	2.35	0.53
1:A:147:ILE:HG22	1:A:158:LYS:HZ3	1.73	0.53
1:B:213:GLN:HB3	1:B:218:LYS:HB2	1.91	0.53
1:B:286:SER:HA	1:B:289:LYS:HD3	1.89	0.53
1:B:257:SER:OG	1:B:259:ASP:HB2	2.08	0.53
1:A:162:ALA:HB1	1:A:215:PHE:HE1	1.74	0.53
1:A:154:ILE:HG23	1:A:158:LYS:HD3	1.90	0.52
1:C:439:PHE:CZ	1:C:446:ARG:HG3	2.44	0.52
1:B:335:ASN:O	1:B:339:ILE:HG13	2.09	0.52
1:C:292:LYS:HE3	1:C:342:THR:OG1	2.10	0.52
1:D:507:LYS:H	1:D:507:LYS:CD	2.22	0.52
1:B:322:PHE:H	2:B:601:QAA:C09	2.24	0.51
1:A:317:ARG:NH2	2:C:601:QAA:C16	2.71	0.51
1:C:185:THR:CG2	1:C:199:LEU:HD21	2.40	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:506:ASP:HB3	1:C:512:VAL:HG22	1.92	0.51
1:B:189:THR:O	1:B:191:ASP:N	2.42	0.51
1:B:292:LYS:HZ1	1:B:338:ALA:HB1	1.74	0.51
1:B:498:MET:HE1	1:B:517:PHE:CE1	2.33	0.51
1:C:216:ARG:O	1:C:218:LYS:HG2	2.11	0.51
1:A:315:GLY:O	1:A:317:ARG:N	2.39	0.51
1:B:488:ILE:HD12	1:B:514:GLY:HA3	1.92	0.51
1:B:320:LYS:HG2	2:B:601:QAA:N38	2.26	0.51
1:B:450:PRO:HG2	1:C:537:ALA:HB2	1.94	0.50
1:A:324:ASN:HB3	1:A:330:HIS:CD2	2.46	0.50
1:A:317:ARG:HH12	1:D:330:HIS:HE1	1.60	0.50
1:A:454:ARG:HD2	1:D:528:HIS:CD2	2.47	0.50
1:A:153:LYS:HB2	1:A:194:MET:HE2	1.93	0.50
1:C:322:PHE:H	2:C:601:QAA:C25	2.25	0.50
1:C:477:GLY:HA3	1:C:528:HIS:CE1	2.47	0.50
1:B:289:LYS:HE2	1:B:338:ALA:HB2	1.94	0.50
1:D:435:ALA:HB2	1:D:491:VAL:HG13	1.94	0.50
1:B:182:LEU:O	1:B:186:LEU:HB2	2.12	0.50
1:A:228:THR:HB	1:A:273:HIS:CE1	2.47	0.50
1:D:274:SER:HB3	1:D:278:THR:HG21	1.92	0.50
1:A:316:LEU:C	1:A:317:ARG:HG2	2.31	0.49
1:B:526:ASN:OD1	1:B:543:ARG:NH2	2.46	0.49
1:D:144:PHE:CD2	1:D:197:LYS:HG2	2.47	0.49
1:A:537:ALA:HB2	1:D:450:PRO:HG2	1.94	0.49
1:B:184:LEU:O	1:B:187:GLN:HB2	2.12	0.49
1:C:289:LYS:HA	1:C:292:LYS:NZ	2.28	0.49
1:C:315:GLY:C	1:C:317:ARG:H	2.15	0.49
1:D:156:VAL:HG12	1:D:193:VAL:HG12	1.93	0.49
1:D:292:LYS:NZ	1:D:338:ALA:HB1	2.28	0.49
1:B:153:LYS:HB3	1:B:194:MET:HB3	1.94	0.49
1:B:332:PRO:HD2	1:B:459:LEU:HD13	1.94	0.49
1:A:147:ILE:HG22	1:A:158:LYS:HZ2	1.78	0.49
1:C:532:ASN:ND2	1:C:535:HIS:H	2.00	0.48
1:A:155:PRO:HD2	1:A:158:LYS:HD2	1.96	0.48
1:B:192:GLY:O	1:B:194:MET:N	2.43	0.48
1:C:456:THR:O	1:C:460:MET:HG2	2.13	0.48
1:A:292:LYS:HZ1	1:A:338:ALA:HB1	1.77	0.48
1:C:147:ILE:O	1:C:158:LYS:NZ	2.46	0.48
1:C:216:ARG:HD2	1:C:216:ARG:N	2.28	0.48
2:C:601:QAA:C08	1:D:321:LEU:HD22	2.44	0.48
1:C:446:ARG:NH1	3:C:702:HOH:O	2.46	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:157:HIS:O	1:A:161:THR:OG1	2.22	0.48
1:A:252:GLN:N	1:A:252:GLN:OE1	2.46	0.48
1:D:162:ALA:HB1	1:D:215:PHE:HE1	1.78	0.48
1:B:258:PRO:HB3	1:B:504:PRO:HG3	1.96	0.47
1:A:528:HIS:CD2	1:D:454:ARG:HD2	2.50	0.47
1:B:216:ARG:O	1:B:218:LYS:HG2	2.14	0.47
1:D:229:SER:O	1:D:233:GLU:HG3	2.15	0.47
1:A:156:VAL:CG1	1:A:195:LEU:HD13	2.34	0.47
1:B:281:PRO:HA	1:B:422:VAL:O	2.14	0.47
1:B:249:TYR:HE1	1:B:484:VAL:HG21	1.79	0.47
1:B:316:LEU:CD2	1:B:467:ASP:O	2.59	0.47
1:A:252:GLN:HE21	1:A:376:ALA:C	2.18	0.47
1:B:320:LYS:CG	2:B:601:QAA:N39	2.78	0.47
1:A:212:THR:O	1:A:216:ARG:HG2	2.15	0.47
1:A:261:TRP:CE3	1:A:502:SER:HB2	2.50	0.47
1:D:319:ASN:N	3:D:603:HOH:O	2.45	0.47
1:C:343:SER:HA	1:C:410:ILE:HD12	1.97	0.47
1:D:285:GLN:HA	1:D:418:CYS:HB3	1.96	0.46
1:A:252:GLN:NE2	1:A:380:SER:OG	2.48	0.46
1:B:480:ALA:HB2	1:B:490:LEU:HD12	1.98	0.46
1:D:293:TYR:OH	1:D:306:HIS:NE2	2.41	0.46
1:A:315:GLY:C	1:A:317:ARG:H	2.19	0.46
1:B:221:ILE:HD13	1:B:542:PRO:HB2	1.94	0.46
1:C:286:SER:HB3	1:C:289:LYS:HD2	1.98	0.46
1:C:289:LYS:HA	1:C:292:LYS:HZ2	1.81	0.46
1:B:163:LEU:O	1:B:166:THR:HB	2.15	0.46
1:D:349:VAL:HG23	1:D:354:LYS:HG3	1.97	0.46
1:A:192:GLY:O	1:A:193:VAL:HG23	2.16	0.45
1:B:216:ARG:HA	1:B:216:ARG:HD2	1.76	0.45
1:A:318:PHE:HZ	1:D:318:PHE:CE2	2.34	0.45
1:A:195:LEU:HD23	1:A:200:PHE:HD1	1.81	0.45
1:A:156:VAL:O	1:A:160:ILE:HG12	2.16	0.45
1:A:359:MET:HE2	1:A:420:ILE:HG12	1.97	0.45
1:D:267:THR:HA	1:D:496:MET:HA	1.98	0.45
1:A:299:ASP:OD2	1:A:357:TYR:OH	2.29	0.45
1:B:346:LYS:O	1:B:354:LYS:HE2	2.16	0.45
1:B:143:LEU:O	1:B:146:THR:OG1	2.33	0.45
1:B:308:TYR:HB3	1:B:340:VAL:HG11	1.98	0.45
1:C:439:PHE:HA	1:C:445:GLU:O	2.16	0.45
1:D:316:LEU:HA	1:D:316:LEU:HD23	1.76	0.45
1:D:350:ASN:ND2	1:D:353:GLU:OE2	2.50	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:228:THR:HB	1:C:273:HIS:CE1	2.51	0.45
1:D:432:ALA:HB1	1:D:441:PRO:HG2	1.98	0.45
1:B:166:THR:HG22	1:B:168:LEU:HG	1.99	0.45
1:B:155:PRO:HB3	1:B:193:VAL:HG13	1.99	0.44
1:C:291:LEU:HD13	1:C:362:LEU:HD22	2.00	0.44
1:D:357:TYR:O	1:D:360:GLN:HB3	2.17	0.44
1:A:318:PHE:CZ	1:D:318:PHE:CE2	3.05	0.44
1:A:365:MET:HG3	1:A:447:VAL:HG11	1.99	0.44
1:C:335:ASN:O	1:C:339:ILE:HG13	2.17	0.44
1:D:292:LYS:HD2	1:D:417:LEU:HD13	1.98	0.44
1:B:149:GLU:C	1:B:151:GLN:H	2.21	0.44
1:B:170:THR:O	1:B:179:MET:HG3	2.18	0.44
1:B:477:GLY:O	1:B:529:ASN:HB2	2.18	0.44
1:D:427:ALA:HB3	1:D:499:MET:HG2	2.00	0.44
1:D:439:PHE:CE2	1:D:446:ARG:HB2	2.53	0.43
1:D:502:SER:OG	1:D:504:PRO:HD2	2.17	0.43
1:A:479:PRO:HG3	1:D:530:TYR:CE1	2.53	0.43
1:C:315:GLY:O	1:C:317:ARG:N	2.51	0.43
1:A:261:TRP:HE3	1:A:502:SER:HB2	1.83	0.43
1:B:156:VAL:N	1:B:193:VAL:O	2.49	0.43
1:B:298:ASN:OD1	1:B:449:SER:N	2.48	0.43
1:B:346:LYS:HB3	1:B:354:LYS:HG2	2.00	0.43
1:D:480:ALA:HB2	1:D:490:LEU:HD12	2.00	0.43
1:C:288:VAL:O	1:C:292:LYS:HG3	2.18	0.43
1:D:331:ASN:O	1:D:337:GLY:HA3	2.19	0.43
1:C:332:PRO:HD2	1:C:459:LEU:HD13	1.99	0.43
1:D:260:LEU:HD13	1:D:501:TRP:CH2	2.53	0.43
1:B:235:TYR:CE1	1:B:261:TRP:CD1	3.07	0.42
1:A:185:THR:HA	1:A:188:THR:HG1	1.83	0.42
1:A:289:LYS:HG2	1:A:292:LYS:HZ1	1.84	0.42
1:C:356:ASP:O	1:C:360:GLN:HB2	2.19	0.42
1:B:464:GLY:O	1:B:481:LYS:HD2	2.20	0.42
1:C:211:LEU:HA	1:C:211:LEU:HD23	1.84	0.42
1:C:460:MET:HG3	1:C:479:PRO:HB3	2.00	0.42
1:A:384:SER:OG	1:A:384:SER:O	2.33	0.42
1:B:407:MET:HB3	1:B:407:MET:HE3	1.92	0.42
1:B:169:ARG:HH21	1:B:272:ARG:CZ	2.32	0.42
1:B:320:LYS:HG2	2:B:601:QAA:N39	2.35	0.42
1:A:197:LYS:HB3	1:A:197:LYS:HE2	1.75	0.42
1:A:295:ILE:HG12	1:A:361:PHE:CD2	2.54	0.42
1:C:235:TYR:CE1	1:C:261:TRP:CD1	3.08	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:260:LEU:HD13	1:D:501:TRP:HH2	1.84	0.42
1:B:365:MET:HG3	1:B:447:VAL:HG11	2.02	0.42
1:B:318:PHE:CZ	1:C:317:ARG:HD2	2.55	0.42
1:C:322:PHE:H	2:C:601:QAA:C26	2.33	0.42
1:D:410:ILE:HA	1:D:410:ILE:HD13	1.82	0.42
1:A:201:LYS:O	1:A:205:GLN:HG2	2.19	0.42
1:A:277:ASP:HB3	1:A:280:VAL:HG21	2.02	0.42
1:A:316:LEU:CD1	1:A:467:ASP:HA	2.49	0.42
1:B:355:PHE:HE1	1:B:420:ILE:HD11	1.85	0.42
1:C:522:VAL:CG1	1:C:528:HIS:HB2	2.50	0.42
1:D:177:GLU:N	1:D:177:GLU:OE2	2.47	0.42
1:A:525:CYS:HA	1:A:540:LEU:O	2.20	0.41
1:B:318:PHE:CE2	1:C:317:ARG:HB2	2.55	0.41
1:D:248:ASP:HA	1:D:254:ALA:HB2	2.00	0.41
1:A:435:ALA:HB2	1:A:491:VAL:HG13	2.00	0.41
1:D:364:LYS:HD3	1:D:445:GLU:OE1	2.19	0.41
1:B:274:SER:HB3	1:B:278:THR:HG21	2.02	0.41
1:C:281:PRO:HA	1:C:422:VAL:O	2.21	0.41
1:C:292:LYS:HD2	1:C:417:LEU:HD13	2.02	0.41
1:A:292:LYS:NZ	1:A:338:ALA:HB1	2.35	0.41
1:A:361:PHE:HE1	1:A:447:VAL:HG12	1.85	0.41
1:C:245:LYS:HD3	1:C:245:LYS:HA	1.89	0.41
1:B:221:ILE:HD12	1:B:542:PRO:CB	2.50	0.41
1:A:354:LYS:HB3	1:A:413:PHE:CZ	2.56	0.41
1:A:162:ALA:CB	1:A:215:PHE:HE1	2.33	0.41
1:A:270:GLY:O	1:A:272:ARG:HG2	2.21	0.41
1:B:186:LEU:N	1:B:186:LEU:CD2	2.83	0.41
1:B:290:PRO:CD	1:B:481:LYS:HG2	2.51	0.41
1:D:464:GLY:O	1:D:481:LYS:HD2	2.21	0.41
1:A:156:VAL:HG13	1:A:193:VAL:O	2.21	0.41
1:B:183:ARG:O	1:B:187:GLN:HG2	2.21	0.41
1:C:498:MET:HE2	1:C:498:MET:HB2	1.99	0.40
1:D:156:VAL:CG1	1:D:193:VAL:HG12	2.50	0.40
1:D:440:CYS:HA	1:D:441:PRO:HD3	1.97	0.40
1:A:144:PHE:CE1	1:A:197:LYS:HA	2.57	0.40
1:C:248:ASP:HA	1:C:254:ALA:HB2	2.03	0.40
1:A:538:LYS:HG2	1:A:538:LYS:O	2.20	0.40
1:A:407:MET:HE3	1:A:408:VAL:HG23	2.04	0.40
1:D:318:PHE:HB3	1:D:321:LEU:HB2	2.02	0.40
1:D:527:PHE:CZ	1:D:542:PRO:HG2	2.56	0.40
1:A:142:LEU:HD13	1:A:142:LEU:HA	1.80	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:316:LEU:HD11	1:A:467:ASP:HA	2.04	0.40
1:B:434:LEU:HB3	1:B:457:LEU:HD21	2.03	0.40
1:D:151:GLN:HE21	1:D:151:GLN:HB3	1.77	0.40
1:D:156:VAL:O	1:D:160:ILE:HG12	2.22	0.40
1:D:385:GLY:O	1:D:389:PHE:HD1	2.04	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:375:ASN:ND2	1:D:198:ASP:OD2[2_556]	2.14	0.06

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%)	390 (96%)	16 (4%)	1 (0%)	47	73
1	B	408/527 (77%)	389 (95%)	16 (4%)	3 (1%)	22	46
1	C	408/527 (77%)	392 (96%)	15 (4%)	1 (0%)	47	73
1	D	408/527 (77%)	393 (96%)	14 (3%)	1 (0%)	47	73
All	All	1631/2108 (77%)	1564 (96%)	61 (4%)	6 (0%)	34	60

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	188	THR
1	B	190	SER
1	B	193	VAL
1	C	193	VAL
1	A	193	VAL

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Mol	Chain	Res	Type
1	D	193	VAL

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	353/451 (78%)	341 (97%)	12 (3%)	37	66
1	B	353/451 (78%)	341 (97%)	12 (3%)	37	66
1	C	353/451 (78%)	344 (98%)	9 (2%)	47	76
1	D	353/451 (78%)	345 (98%)	8 (2%)	50	78
All	All	1412/1804 (78%)	1371 (97%)	41 (3%)	42	71

All (41) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	138	SER
1	A	191	ASP
1	A	229	SER
1	A	245	LYS
1	A	255	LYS
1	A	319	ASN
1	A	328	LYS
1	A	361	PHE
1	A	384	SER
1	A	496	MET
1	A	507	LYS
1	A	523	SER
1	B	141	ASP
1	B	186	LEU
1	B	237	SER
1	B	286	SER
1	B	317	ARG
1	B	320	LYS
1	B	361	PHE
1	B	384	SER

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Mol	Chain	Res	Type
1	B	387	ARG
1	B	426	SER
1	B	507	LYS
1	B	544	ARG
1	C	138	SER
1	C	158	LYS
1	C	194	MET
1	C	198	ASP
1	C	205	GLN
1	C	361	PHE
1	C	446	ARG
1	C	496	MET
1	C	523	SER
1	D	138	SER
1	D	178	CYS
1	D	198	ASP
1	D	229	SER
1	D	257	SER
1	D	361	PHE
1	D	412	ASP
1	D	507	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	532	ASN
1	D	151	GLN
1	D	205	GLN
1	D	330	HIS

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 [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	QAA	C	601	-	43,43,43	1.29	4 (9%)	54,57,57	2.55	10 (18%)
2	QAA	B	601	-	43,43,43	1.46	5 (11%)	54,57,57	2.79	19 (35%)

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	QAA	C	601	-	-	12/24/34/34	0/5/5/5
2	QAA	B	601	-	-	12/24/34/34	0/5/5/5

All (9) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	601	QAA	C13-N12	4.41	1.45	1.35
2	B	601	QAA	C24-N03	4.11	1.45	1.37
2	C	601	QAA	C13-N12	3.79	1.44	1.35
2	C	601	QAA	C24-N03	3.72	1.45	1.37
2	B	601	QAA	C29-N28	3.67	1.43	1.35
2	C	601	QAA	C29-N28	3.40	1.43	1.35
2	B	601	QAA	C11-N12	3.23	1.47	1.40
2	C	601	QAA	C11-N12	2.65	1.46	1.40
2	B	601	QAA	O07-C08	2.61	1.41	1.36

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	601	QAA	C08-O07-C06	-15.12	102.22	117.75
2	B	601	QAA	C08-O07-C06	-11.87	105.56	117.75
2	B	601	QAA	O21-C13-N12	-5.75	113.14	123.63
2	B	601	QAA	C14-C13-N12	5.57	126.28	114.77
2	B	601	QAA	C04-C05-C06	5.10	115.92	110.32
2	B	601	QAA	C27-N38-N39	4.85	122.81	119.37
2	B	601	QAA	C11-N12-C13	4.72	136.69	128.25
2	C	601	QAA	O21-C13-N12	-4.19	115.99	123.63
2	B	601	QAA	C25-C24-N39	-3.99	117.91	123.86
2	C	601	QAA	O07-C08-C09	3.98	120.83	115.89
2	B	601	QAA	C27-N28-C29	-3.27	122.40	128.25
2	C	601	QAA	C11-N12-C13	-3.18	122.55	128.25
2	B	601	QAA	O07-C08-C09	3.15	119.80	115.89
2	C	601	QAA	C25-C24-N03	-3.03	116.25	121.70
2	C	601	QAA	C25-C24-N39	-2.85	119.60	123.86
2	B	601	QAA	C05-C04-N03	2.82	116.91	111.10
2	C	601	QAA	C14-C13-N12	2.77	120.50	114.77
2	B	601	QAA	C01-C02-N03	2.71	116.69	111.10
2	B	601	QAA	C02-C01-C06	2.69	113.28	110.32
2	B	601	QAA	C26-C25-C24	2.66	121.20	117.53
2	B	601	QAA	C04-N03-C02	2.63	117.32	111.52
2	B	601	QAA	O07-C06-C01	2.56	113.96	108.31
2	C	601	QAA	C26-C27-N28	-2.50	115.59	123.06
2	B	601	QAA	C25-C24-N03	-2.39	117.41	121.70
2	C	601	QAA	C24-N39-N38	2.39	121.42	118.97
2	B	601	QAA	C26-C27-N38	-2.29	118.17	122.56
2	C	601	QAA	C36-C31-C32	2.12	121.50	118.17
2	B	601	QAA	C30-C29-N28	2.10	119.11	114.77
2	B	601	QAA	C30-C31-C32	-2.05	117.96	120.89

There are no chirality outliers.

All (24) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	601	QAA	C10-C11-N12-C13
2	C	601	QAA	N22-C11-N12-C13
2	C	601	QAA	C09-C08-O07-C06
2	C	601	QAA	N23-C08-O07-C06
2	B	601	QAA	C09-C08-O07-C06
2	B	601	QAA	N23-C08-O07-C06
2	B	601	QAA	N38-C27-N28-C29
2	B	601	QAA	C26-C27-N28-C29
2	B	601	QAA	N22-C11-N12-C13

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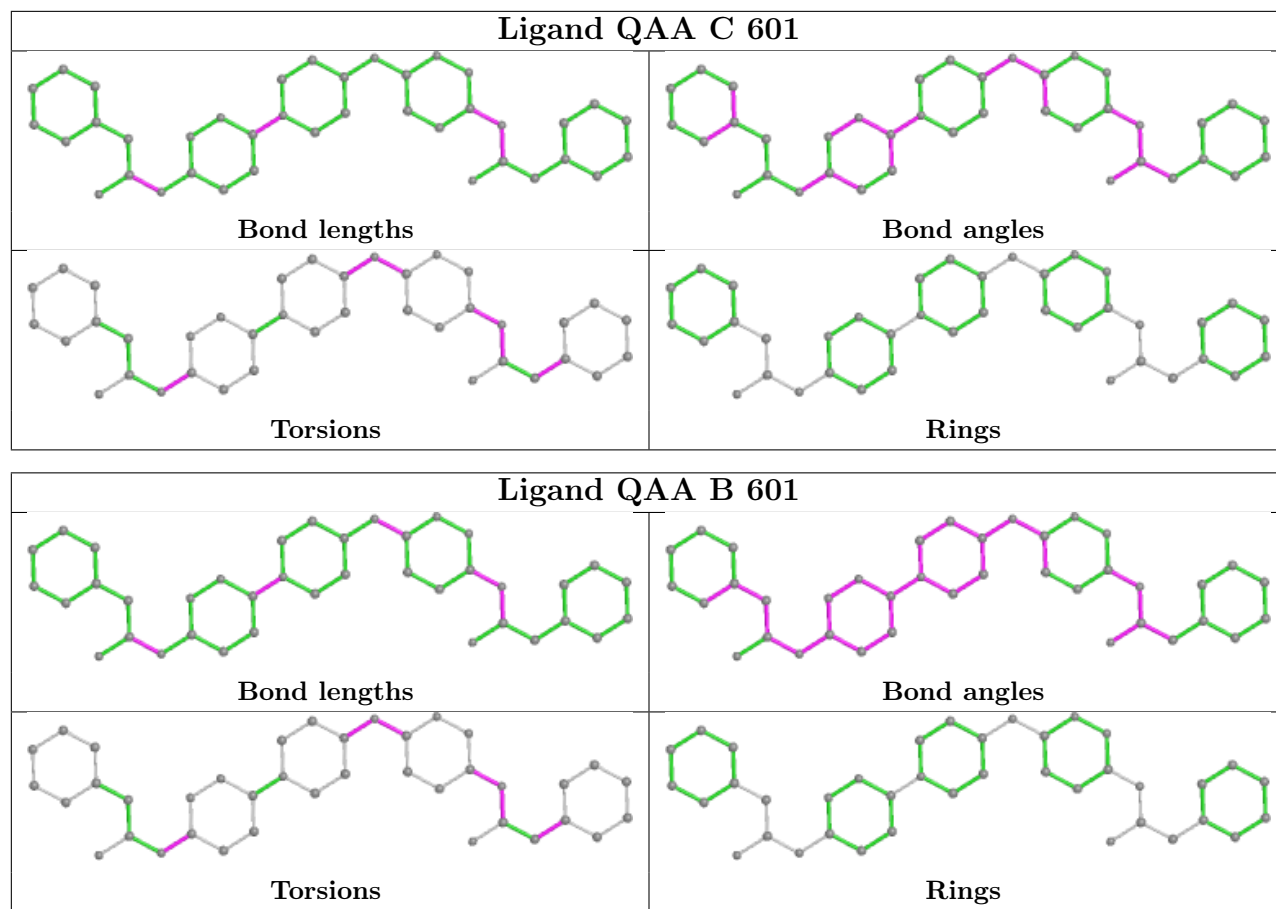
Mol	Chain	Res	Type	Atoms
2	B	601	QAA	C10-C11-N12-C13
2	C	601	QAA	N38-C27-N28-C29
2	C	601	QAA	C26-C27-N28-C29
2	B	601	QAA	C13-C14-C15-C16
2	B	601	QAA	C13-C14-C15-C20
2	B	601	QAA	C05-C06-O07-C08
2	C	601	QAA	C13-C14-C15-C20
2	C	601	QAA	C01-C06-O07-C08
2	C	601	QAA	C05-C06-O07-C08
2	B	601	QAA	C01-C06-O07-C08
2	C	601	QAA	C13-C14-C15-C16
2	C	601	QAA	C14-C13-N12-C11
2	B	601	QAA	C14-C13-N12-C11
2	C	601	QAA	O21-C13-N12-C11
2	B	601	QAA	O21-C13-N12-C11

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	601	QAA	6	0
2	B	601	QAA	9	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%)	-0.22	17 (4%) 36 35	21, 39, 90, 189	0
1	B	410/527 (77%)	-0.14	21 (5%) 28 26	23, 40, 96, 162	0
1	C	410/527 (77%)	-0.18	16 (3%) 39 38	24, 40, 86, 179	0
1	D	410/527 (77%)	-0.23	17 (4%) 37 36	20, 39, 84, 171	0
All	All	1639/2108 (77%)	-0.19	71 (4%) 35 33	20, 40, 89, 189	0

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	192	GLY	8.3
1	D	546	GLY	7.4
1	B	191	ASP	6.7
1	D	192	GLY	6.4
1	D	191	ASP	6.2
1	C	191	ASP	5.7
1	A	318	PHE	5.4
1	D	318	PHE	5.4
1	D	137	PRO	4.5
1	C	192	GLY	4.4
1	B	251	PRO	4.1
1	B	316	LEU	4.1
1	D	317	ARG	4.1
1	A	317	ARG	4.1
1	B	149	GLU	4.1
1	B	318	PHE	4.0
1	B	150	GLY	3.9
1	A	191	ASP	3.9
1	B	546	GLY	3.9
1	B	213	GLN	3.8
1	C	150	GLY	3.7

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Mol	Chain	Res	Type	RSRZ
1	D	150	GLY	3.6
1	C	318	PHE	3.6
1	B	319	ASN	3.6
1	B	193	VAL	3.4
1	D	145	TYR	3.2
1	D	142	LEU	3.2
1	C	193	VAL	3.2
1	D	255	LYS	3.1
1	B	320	LYS	3.1
1	B	317	ARG	3.1
1	B	142	LEU	3.1
1	A	316	LEU	3.0
1	B	137	PRO	3.0
1	D	149	GLU	2.8
1	C	157	HIS	2.8
1	A	137	PRO	2.8
1	B	152	GLU	2.8
1	C	138	SER	2.7
1	A	144	PHE	2.7
1	D	212	THR	2.7
1	D	189	THR	2.7
1	D	152	GLU	2.6
1	C	194	MET	2.6
1	A	150	GLY	2.6
1	A	143	LEU	2.5
1	B	143	LEU	2.5
1	B	188	THR	2.5
1	B	145	TYR	2.4
1	B	160	ILE	2.4
1	C	207	ASN	2.4
1	A	138	SER	2.3
1	A	193	VAL	2.3
1	C	144	PHE	2.3
1	C	139	LEU	2.3
1	D	251	PRO	2.3
1	C	149	GLU	2.3
1	C	190	SER	2.2
1	A	192	GLY	2.2
1	A	142	LEU	2.2
1	A	139	LEU	2.2
1	D	254	ALA	2.2
1	B	148	ALA	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	204	VAL	2.1
1	C	446	ARG	2.1
1	A	319	ASN	2.1
1	C	156	VAL	2.1
1	C	546	GLY	2.1
1	D	146	THR	2.0
1	A	544	ARG	2.0
1	A	148	ALA	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](#)

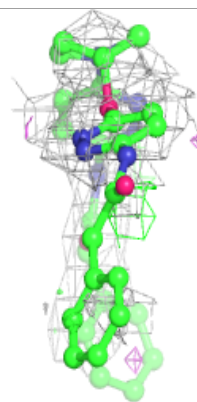
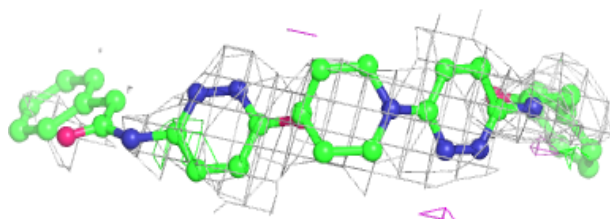
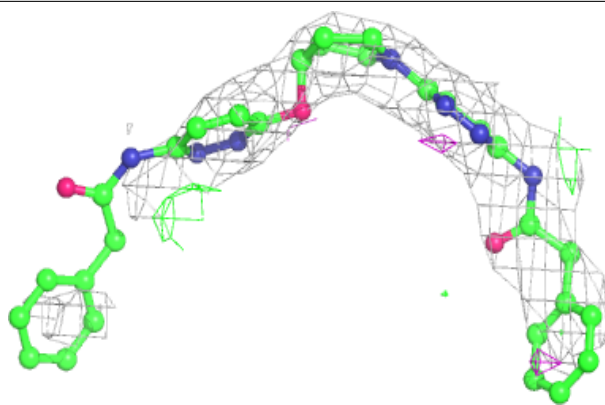
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	QAA	B	601	39/39	0.79	0.41	98,111,133,135	0
2	QAA	C	601	39/39	0.84	0.28	77,86,105,110	0

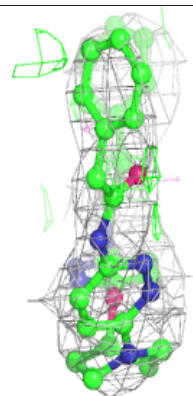
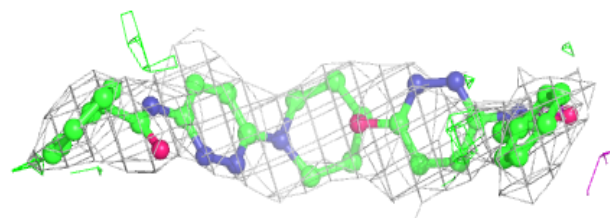
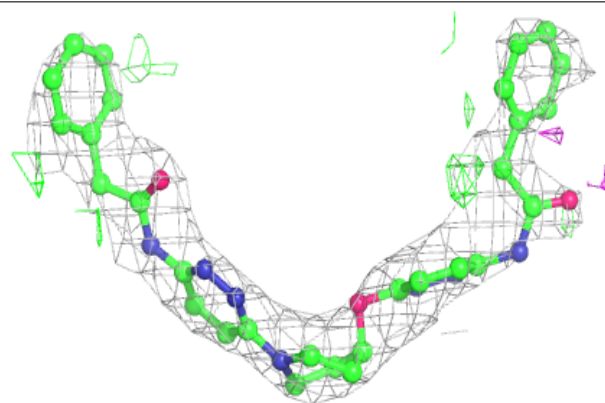
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around QAA 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 QAA C 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.