Full wwPDB X-ray Structure Validation Report ⓘ

Feb 11, 2025 – 12:20 PM EST

PDB ID	:	9BRG
Title	:	Crystal Structure of Human G Protein-Coupled Receptor Kinase 5 in Complex with GRL055-22
Authors	:	Chen, Y.; Tesmer, J.J.G.
Deposited on	:	2024-05-11
Resolution	:	2.70 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:

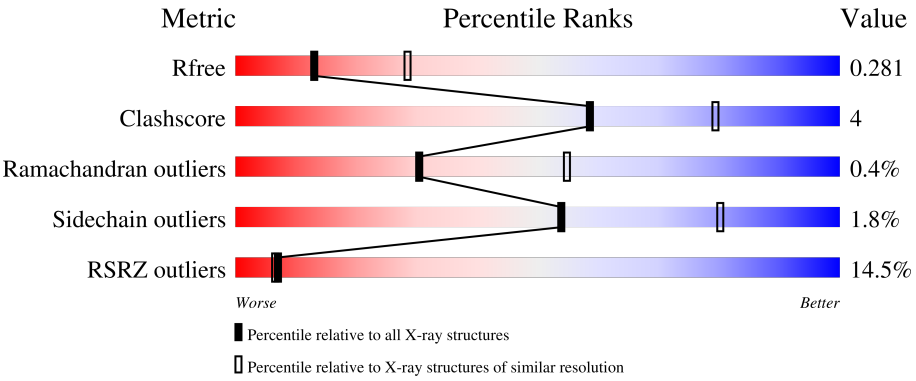
MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.21
EDS	:	3.0
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.004 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.40

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (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 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 <=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	598	12% 76% 8% • 16%

2 Entry composition (i)

There are 3 unique types of molecules in this entry. The entry contains 8242 atoms, of which 4082 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.

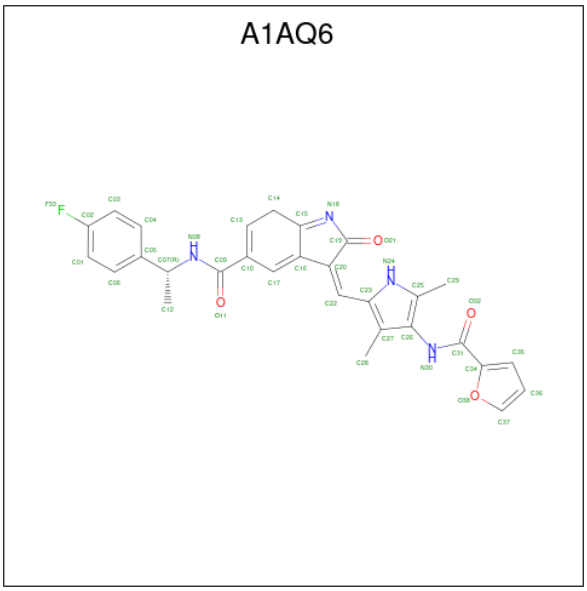
- Molecule 1 is a protein called G protein-coupled receptor kinase 5.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	503	Total	C	H	N	O	S	0	0	0
			8151	2600	4059	709	754	29			

There are 9 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	311	ASN	ASP	engineered mutation	UNP P34947
A	591	VAL	-	expression tag	UNP P34947
A	592	ASP	-	expression tag	UNP P34947
A	593	HIS	-	expression tag	UNP P34947
A	594	HIS	-	expression tag	UNP P34947
A	595	HIS	-	expression tag	UNP P34947
A	596	HIS	-	expression tag	UNP P34947
A	597	HIS	-	expression tag	UNP P34947
A	598	HIS	-	expression tag	UNP P34947

- Molecule 2 is (3Z)-N-[(1R)-1-(4-fluorophenyl)ethyl]-3-({4-[(furan-2-carbonyl)amino]-3,5-dimethyl-1H-pyrrol-2-yl}methylidene)-2-oxo-3,7-dihydro-2H-indole-5-carboxamide (three-letter code: A1AQ6) (formula: $C_{29}H_{25}FN_4O_4$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
2	A	1	Total	C	F	H	N	O	0	0
			61	29	1	23	4	4		

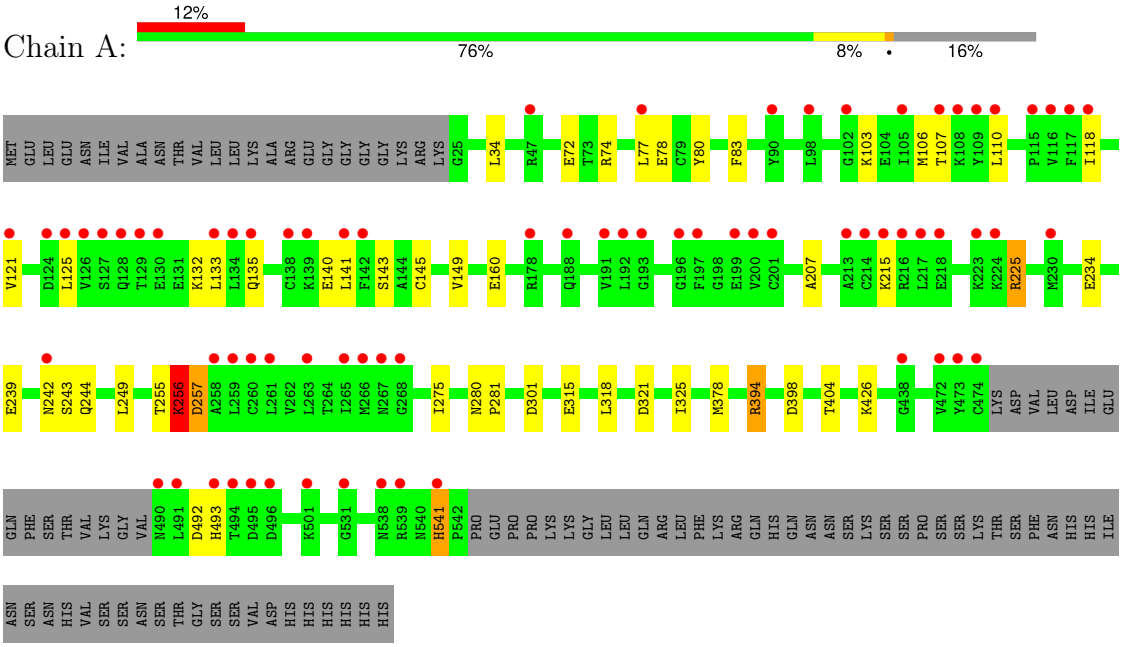
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	30	Total	O	0	0
			30	30		

3 Residue-property plots (i)

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: G protein-coupled receptor kinase 5



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α, β, γ	137.71Å 137.71Å 70.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.51 – 2.70 29.51 – 2.70	Depositor EDS
% Data completeness (in resolution range)	100.0 (29.51-2.70) 99.8 (29.51-2.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.19 (at 2.68Å)	Xtriage
Refinement program	PHENIX 1.21.1_5286	Depositor
R, R_{free}	0.238 , 0.277 0.245 , 0.281	Depositor DCC
R_{free} test set	17472 reflections (9.29%)	wwPDB-VP
Wilson B-factor (Å^2)	55.4	Xtriage
Anisotropy	0.052	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.36 , 43.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.51$, $< L^2 > = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.92	EDS
Total number of atoms	8242	wwPDB-VP
Average B, all atoms (Å^2)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.41% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: A1AQ6

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	0.26	0/4182	0.49	0/5626

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry-related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	4092	4059	4059	35	0
2	A	38	23	0	0	0
3	A	30	0	0	1	0
All	All	4160	4082	4059	35	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (35) 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:118:ILE:HG22	1:A:121:VAL:HG23	1.67	0.74

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:140:GLU:N	1:A:140:GLU:OE1	2.22	0.73
1:A:118:ILE:CG2	1:A:121:VAL:HG23	2.27	0.63
1:A:74:ARG:NH1	1:A:160:GLU:OE1	2.33	0.61
1:A:215:LYS:NZ	1:A:234:GLU:OE2	2.35	0.60
1:A:244:GLN:NE2	3:A:703:HOH:O	2.34	0.60
1:A:141:LEU:HD12	1:A:141:LEU:O	2.02	0.59
1:A:106:MET:HE3	1:A:110:LEU:HB2	1.84	0.58
1:A:80:TYR:CE1	1:A:118:ILE:HG23	2.43	0.54
1:A:492:ASP:OD1	1:A:493:HIS:N	2.41	0.54
1:A:239:GLU:HB3	1:A:249:LEU:HD23	1.91	0.53
1:A:133:LEU:HG	1:A:141:LEU:HD21	1.91	0.53
1:A:225:ARG:CZ	1:A:225:ARG:HB3	2.39	0.52
1:A:74:ARG:HG3	1:A:77:LEU:HD12	1.93	0.51
1:A:242:ASN:OD1	1:A:242:ASN:O	2.28	0.50
1:A:80:TYR:HE1	1:A:118:ILE:HG23	1.77	0.49
1:A:106:MET:CE	1:A:110:LEU:HB2	2.42	0.49
1:A:72:GLU:HA	1:A:78:GLU:OE2	2.13	0.49
1:A:541:HIS:O	1:A:541:HIS:CG	2.67	0.48
1:A:256:LYS:N	1:A:256:LYS:HD3	2.28	0.47
1:A:121:VAL:HG12	1:A:125:LEU:HB3	1.96	0.47
1:A:255:THR:O	1:A:257:ASP:N	2.48	0.47
1:A:243:SER:OG	1:A:301:ASP:OD2	2.20	0.45
1:A:103:LYS:HE2	1:A:107:THR:HG21	1.99	0.43
1:A:275:ILE:HD11	1:A:378:MET:HG2	2.00	0.42
1:A:280:ASN:N	1:A:281:PRO:CA	2.82	0.42
1:A:318:LEU:O	1:A:325:ILE:HA	2.21	0.41
1:A:404:THR:O	1:A:426:LYS:NZ	2.50	0.41
1:A:34:LEU:HD21	1:A:207:ALA:HB1	2.03	0.41
1:A:83:PHE:CG	1:A:118:ILE:HD11	2.56	0.41
1:A:106:MET:HE3	1:A:106:MET:HA	2.03	0.40
1:A:145:CYS:O	1:A:149:VAL:HG23	2.22	0.40
1:A:34:LEU:CD2	1:A:207:ALA:HB1	2.52	0.40
1:A:132:LYS:HD3	1:A:141:LEU:HD13	2.03	0.40
1:A:394:ARG:NE	1:A:398:ASP:OD2	2.54	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	499/598 (83%)	477 (96%)	20 (4%)	2 (0%)	30 55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	135	GLN
1	A	256	LYS

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	446/532 (84%)	438 (98%)	8 (2%)	54 80

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	143	SER
1	A	225	ARG
1	A	256	LYS
1	A	257	ASP
1	A	315	GLU
1	A	321	ASP
1	A	394	ARG
1	A	541	HIS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	82	GLN
1	A	244	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry (i)

1 ligand is modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	A1AQ6	A	601	-	33,42,42	2.10	10 (30%)	36,61,61	2.10	11 (30%)

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	A1AQ6	A	601	-	-	7/19/49/49	0/5/5/5

All (10) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	601	A1AQ6	C14-C13	-5.40	1.39	1.49
2	A	601	A1AQ6	C09-N08	5.30	1.45	1.34
2	A	601	A1AQ6	C16-C15	-4.26	1.36	1.42
2	A	601	A1AQ6	C31-N30	3.47	1.45	1.35
2	A	601	A1AQ6	C23-C22	2.74	1.52	1.41
2	A	601	A1AQ6	O21-C19	-2.63	1.19	1.23
2	A	601	A1AQ6	O11-C09	-2.42	1.19	1.23
2	A	601	A1AQ6	C22-C20	-2.30	1.32	1.35
2	A	601	A1AQ6	C34-C31	2.25	1.53	1.49
2	A	601	A1AQ6	C17-C10	-2.14	1.39	1.43

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	601	A1AQ6	C14-C15-N18	6.20	131.16	125.35
2	A	601	A1AQ6	C14-C13-C10	-5.10	119.92	125.09
2	A	601	A1AQ6	C20-C19-N18	-4.54	107.98	113.23
2	A	601	A1AQ6	C13-C14-C15	3.13	119.41	112.22
2	A	601	A1AQ6	C34-C31-N30	2.58	117.92	114.00
2	A	601	A1AQ6	C10-C09-N08	2.51	119.25	116.69
2	A	601	A1AQ6	C35-C36-C37	-2.37	104.49	112.92
2	A	601	A1AQ6	C22-C20-C19	2.23	129.07	119.73
2	A	601	A1AQ6	C05-C07-N08	-2.12	106.34	111.38
2	A	601	A1AQ6	C03-C02-C01	-2.12	120.02	122.80
2	A	601	A1AQ6	C14-C15-C16	-2.03	120.12	123.10

There are no chirality outliers.

All (7) torsion outliers are listed below:

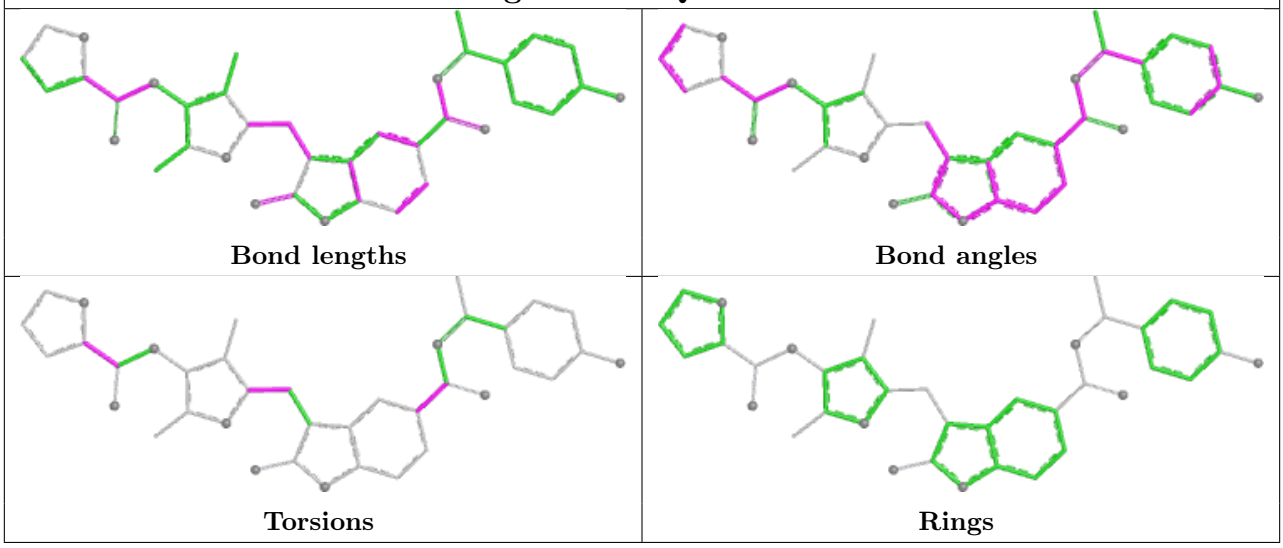
Mol	Chain	Res	Type	Atoms
2	A	601	A1AQ6	C20-C22-C23-C27
2	A	601	A1AQ6	C20-C22-C23-N24
2	A	601	A1AQ6	O32-C31-C34-C35
2	A	601	A1AQ6	O11-C09-C10-C13
2	A	601	A1AQ6	N08-C09-C10-C17
2	A	601	A1AQ6	O11-C09-C10-C17
2	A	601	A1AQ6	N08-C09-C10-C13

There are no ring outliers.

No monomer is involved in short contacts.

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 then 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.

Ligand A1AQ6 A 601



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, 95^{th} 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	503/598 (84%)	0.62	73 (14%)	7 6	35, 67, 165, 216	0

All (73) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	217	LEU	7.3
1	A	267	ASN	7.0
1	A	129	THR	4.9
1	A	118	ILE	4.9
1	A	259	LEU	4.8
1	A	110	LEU	4.7
1	A	490	ASN	4.7
1	A	197	PHE	4.6
1	A	109	TYR	4.6
1	A	191	VAL	4.4
1	A	473	TYR	4.2
1	A	474	CYS	4.1
1	A	192	LEU	4.0
1	A	126	VAL	3.7
1	A	125	LEU	3.4
1	A	491	LEU	3.4
1	A	493	HIS	3.3
1	A	216	ARG	3.2
1	A	215	LYS	3.1
1	A	265	ILE	3.1
1	A	139	LYS	3.1
1	A	218	GLU	3.0
1	A	223	LYS	2.9
1	A	196	GLY	2.9
1	A	200	VAL	2.8
1	A	213	ALA	2.8
1	A	214	CYS	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	116	VAL	2.7
1	A	108	LYS	2.7
1	A	531	GLY	2.7
1	A	268	GLY	2.7
1	A	472	VAL	2.6
1	A	201	CYS	2.6
1	A	494	THR	2.6
1	A	199	GLU	2.5
1	A	141	LEU	2.5
1	A	263	LEU	2.5
1	A	133	LEU	2.5
1	A	117	PHE	2.5
1	A	124	ASP	2.5
1	A	115	PRO	2.5
1	A	260	CYS	2.5
1	A	90	TYR	2.4
1	A	242	ASN	2.4
1	A	130	GLU	2.4
1	A	178	ARG	2.4
1	A	142	PHE	2.3
1	A	127	SER	2.3
1	A	47	ARG	2.3
1	A	121	VAL	2.3
1	A	134	LEU	2.3
1	A	501	LYS	2.2
1	A	128	GLN	2.2
1	A	105	ILE	2.2
1	A	261	LEU	2.2
1	A	188	GLN	2.2
1	A	230	MET	2.2
1	A	266	MET	2.2
1	A	98	LEU	2.2
1	A	539	ARG	2.2
1	A	107	THR	2.1
1	A	102	GLY	2.1
1	A	438	GLY	2.1
1	A	541	HIS	2.1
1	A	135	GLN	2.1
1	A	193	GLY	2.1
1	A	224	LYS	2.1
1	A	538	ASN	2.1
1	A	138	CYS	2.0

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Mol	Chain	Res	Type	RSRZ
1	A	495	ASP	2.0
1	A	77	LEU	2.0
1	A	258	ALA	2.0
1	A	496	ASP	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)

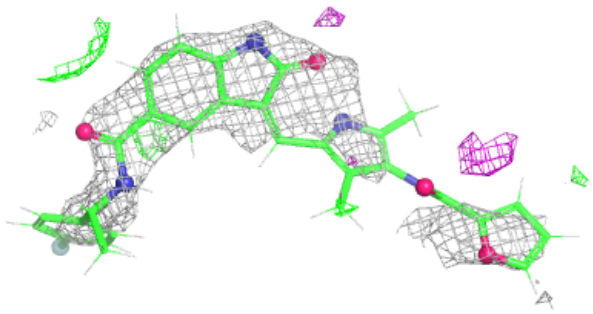
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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

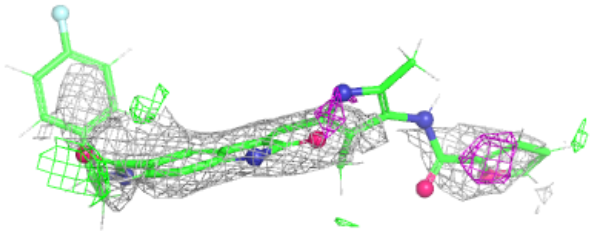
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
2	A1AQ6	A	601	38/38	0.62	0.21	80,127,164,175	0

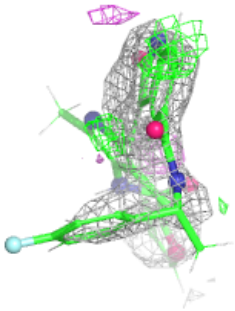
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around A1AQ6 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

There are no such residues in this entry.