



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 01:38 AM UTC

PDB ID : 5UKL / pdb_00005ukl
Title : Human GRK2 in complex with Gbetagamma subunits and CCG222886 (14bd)
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Deposited on : 2017-01-23
Resolution : 2.15 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

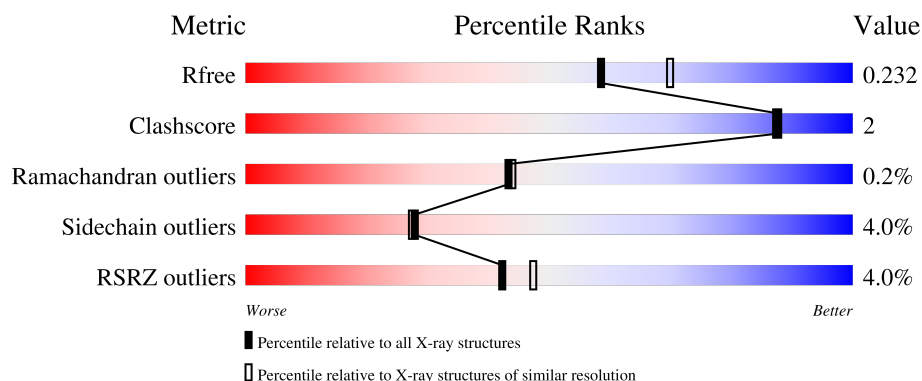
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.15 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}	180053	2057 (2.16-2.16)
Clashscore	190562	2159 (2.16-2.16)
Ramachandran outliers	187476	2134 (2.16-2.16)
Sidechain outliers	187428	2133 (2.16-2.16)
RSRZ outliers	180081	2059 (2.16-2.16)

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	642	5% 87% 10% ..
2	B	339	% 92% 7% .
3	G	62	6% 90% 8% .

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 8685 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 Beta-adrenergic receptor kinase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	630	Total	C	N	O	S	0	0	0
			5158	3286	902	935	35			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	670	ALA	SER	engineered mutation	UNP P25098

- Molecule 2 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	339	Total	C	N	O	S	0	2	0
			2619	1613	470	513	23			

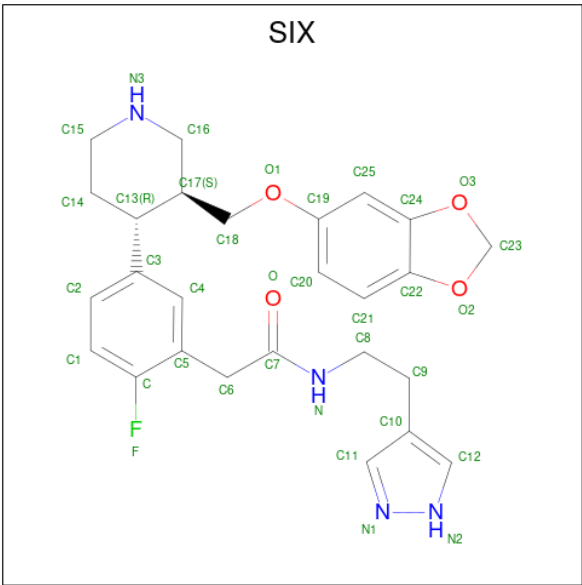
- Molecule 3 is a protein called Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	62	Total	C	N	O	S	0	0	0
			484	307	84	89	4			

- Molecule 4 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Mg	0	0
			1	1		

- Molecule 5 is 2-{5-[(3S,4R)-3-{[(2H-1,3-benzodioxol-5-yl)oxy]methyl}piperidin-4-yl]-2-fluorophenyl}-N-[2-(1H-pyrazol-4-yl)ethyl]acetamide (CCD ID: SIX) (formula: C₂₆H₂₉FN₄O₄).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	F	N	O	0	0
			35	26	1	4	4		

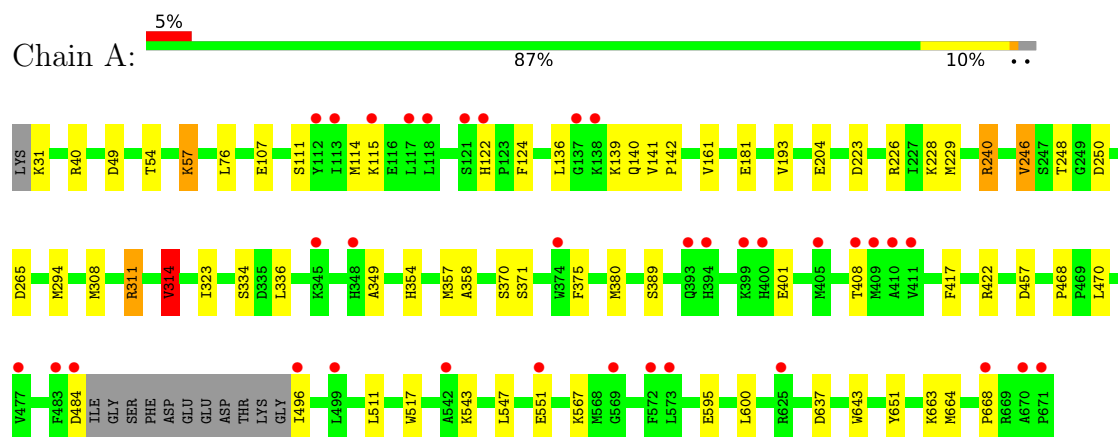
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	213	Total	O	0	0
			213	213		
6	B	156	Total	O	0	0
			156	156		
6	G	19	Total	O	0	0
			19	19		

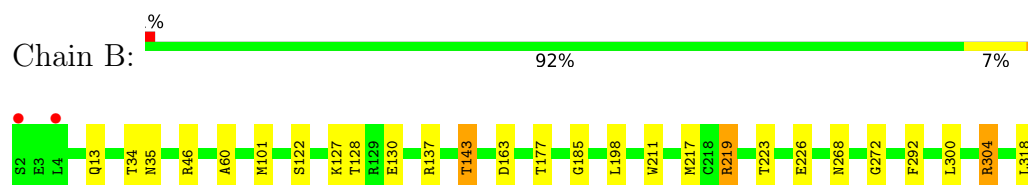
3 Residue-property plots [i](#)

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.

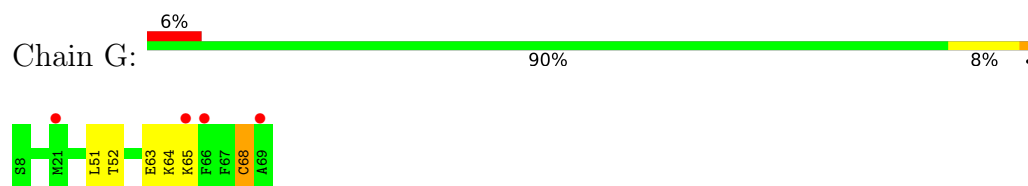
- Molecule 1: Beta-adrenergic receptor kinase 1



- Molecule 2: Guanine nucleotide-binding protein G(I)/G(S)/G(T) subunit beta-1



- Molecule 3: Guanine nucleotide-binding protein G(I)/G(S)/G(O) subunit gamma-2



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	194.25Å 71.43Å 111.26Å 90.00° 110.51° 90.00°	Depositor
Resolution (Å)	30.00 – 2.15 30.00 – 2.15	Depositor EDS
% Data completeness (in resolution range)	99.0 (30.00-2.15) 99.1 (30.00-2.15)	Depositor EDS
R_{merge}	0.16	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.11 (at 2.16Å)	Xtriage
Refinement program	REFMAC 5.8.0151	Depositor
R, R_{free}	0.182 , 0.228 0.188 , 0.232	Depositor DCC
R_{free} test set	3884 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	40.9	Xtriage
Anisotropy	0.139	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 33.6	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	0.96	EDS
Total number of atoms	8685	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.04% 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: MG, SIX

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	1.17	12/5276 (0.2%)	1.14	7/7094 (0.1%)
2	B	1.27	7/2666 (0.3%)	1.14	3/3613 (0.1%)
3	G	1.28	1/492 (0.2%)	1.21	1/661 (0.2%)
All	All	1.21	20/8434 (0.2%)	1.15	11/11368 (0.1%)

All (20) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	468	PRO	CA-C	10.13	1.58	1.52
1	A	57	LYS	C-O	-6.69	1.16	1.24
3	G	52	THR	C-N	6.33	1.41	1.33
1	A	76	LEU	C-O	6.28	1.29	1.23
1	A	142	PRO	CA-C	6.19	1.57	1.52
1	A	122	HIS	CA-C	6.16	1.59	1.53
2	B	60	ALA	CA-C	-6.12	1.45	1.52
1	A	49	ASP	C-O	-6.07	1.16	1.24
2	B	185	GLY	N-CA	5.91	1.50	1.45
1	A	250	ASP	CA-C	5.71	1.60	1.53
1	A	668	PRO	CA-C	5.58	1.59	1.52
2	B	335	PHE	N-CA	5.20	1.52	1.45
1	A	161	VAL	CA-C	5.17	1.59	1.52
1	A	40	ARG	C-O	5.15	1.30	1.24
2	B	223	THR	C-O	-5.10	1.17	1.23
1	A	637	ASP	C-O	-5.08	1.19	1.24
1	A	643	TRP	N-CA	5.07	1.52	1.46
2	B	122	SER	C-O	5.07	1.30	1.23
2	B	304	ARG	C-O	-5.04	1.18	1.24
2	B	226	GLU	C-O	-5.01	1.17	1.23

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	314	VAL	CB-CA-C	-8.41	100.48	110.91
1	A	314	VAL	N-CA-CB	7.76	119.18	110.72
1	A	246	VAL	N-CA-CB	-6.96	104.05	112.33
2	B	268	ASN	N-CA-C	6.66	121.12	113.19
2	B	272	GLY	N-CA-C	6.35	119.46	112.15
1	A	468	PRO	CA-C-N	6.05	125.60	119.19
1	A	468	PRO	C-N-CA	6.05	125.60	119.19
1	A	349	ALA	N-CA-C	5.67	117.85	110.43
2	B	35	ASN	N-CA-C	5.49	118.78	111.75
3	G	51	LEU	N-CA-C	-5.33	104.44	111.96
1	A	240	ARG	N-CA-C	5.16	116.90	111.28

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	5158	0	5134	24	0
2	B	2619	0	2518	9	0
3	G	484	0	496	1	0
4	A	1	0	0	0	0
5	A	35	0	0	0	0
6	A	213	0	0	1	1
6	B	156	0	0	1	0
6	G	19	0	0	0	0
All	All	8685	0	8148	33	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 2.

All (33) 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:323:ILE:HG13	1:A:380:MET:HE1	1.73	0.71

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:248:THR:OG1	1:A:311:ARG:NH2	2.27	0.67
1:A:308:MET:HE2	1:A:336:LEU:HD21	1.80	0.62
1:A:240:ARG:NH1	1:A:511:LEU:HD22	2.20	0.57
1:A:223:ASP:HB3	1:A:226:ARG:HD3	1.86	0.56
1:A:314:VAL:HG13	1:A:370:SER:HA	1.89	0.53
1:A:323:ILE:CG1	1:A:380:MET:HE1	2.38	0.52
1:A:141:VAL:O	1:A:141:VAL:HG23	2.08	0.52
1:A:354:HIS:HA	1:A:357:MET:HE2	1.93	0.50
1:A:600:LEU:C	1:A:600:LEU:HD12	2.38	0.49
1:A:54:THR:OG1	1:A:57:LYS:HG2	2.11	0.49
2:B:217:MET:HE2	2:B:219:ARG:HE	1.78	0.49
1:A:664:MET:HE3	2:B:101:MET:HG3	1.93	0.49
1:A:107:GLU:O	1:A:111:SER:HB3	2.13	0.48
1:A:417:PHE:O	1:A:422:ARG:NH2	2.48	0.47
1:A:663:LYS:HD3	6:A:895:HOH:O	2.16	0.46
2:B:217:MET:HE2	2:B:219:ARG:HD2	1.98	0.45
1:A:595:GLU:O	1:A:595:GLU:HG3	2.16	0.45
1:A:181:GLU:HB2	1:A:517:TRP:CZ3	2.52	0.45
1:A:354:HIS:HA	1:A:357:MET:CE	2.47	0.44
2:B:46:ARG:NH1	6:B:402:HOH:O	2.49	0.44
1:A:358:ALA:HA	1:A:375:PHE:CD1	2.53	0.44
2:B:318:LEU:C	2:B:318:LEU:HD12	2.43	0.43
3:G:63:GLU:O	3:G:63:GLU:HG3	2.17	0.43
1:A:114:MET:HE1	1:A:124:PHE:CD2	2.54	0.43
2:B:217:MET:HE2	2:B:219:ARG:NE	2.35	0.41
1:A:370:SER:O	1:A:371:SER:C	2.62	0.41
1:A:229:MET:HE2	1:A:496:ILE:HD12	2.01	0.41
2:B:34:THR:HG21	2:B:300:LEU:HB3	2.01	0.41
1:A:314:VAL:CG1	1:A:370:SER:HA	2.52	0.40
1:A:457:ASP:C	1:A:457:ASP:OD1	2.64	0.40
2:B:143:THR:HG22	2:B:163:ASP:HB2	2.03	0.40
2:B:198:LEU:HA	2:B:211:TRP:O	2.21	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)
6:A:926:HOH:O	6:A:926:HOH:O[2_556]	2.03	0.17

5.3 Torsion angles

5.3.1 Protein backbone

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	626/642 (98%)	602 (96%)	24 (4%)	0	100	100
2	B	339/339 (100%)	325 (96%)	14 (4%)	0	100	100
3	G	60/62 (97%)	55 (92%)	3 (5%)	2 (3%)	3	0
All	All	1025/1043 (98%)	982 (96%)	41 (4%)	2 (0%)	43	44

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	G	68	CYS
3	G	64	LYS

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	562/572 (98%)	538 (96%)	24 (4%)	26	24
2	B	284/282 (101%)	274 (96%)	10 (4%)	32	32
3	G	51/51 (100%)	49 (96%)	2 (4%)	28	28
All	All	897/905 (99%)	861 (96%)	36 (4%)	28	27

All (36) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	31	LYS

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Mol	Chain	Res	Type
1	A	115	LYS
1	A	136	LEU
1	A	139	LYS
1	A	140	GLN
1	A	193	VAL
1	A	204	GLU
1	A	228	LYS
1	A	246	VAL
1	A	265	ASP
1	A	294	MET
1	A	311	ARG
1	A	314	VAL
1	A	334	SER
1	A	389	SER
1	A	401	GLU
1	A	408	THR
1	A	470	LEU
1	A	484	ASP
1	A	543	LYS
1	A	547	LEU
1	A	551	GLU
1	A	567	LYS
1	A	651	TYR
2	B	13	GLN
2	B	127	LYS
2	B	128	THR
2	B	130	GLU
2	B	137	ARG
2	B	143	THR
2	B	177	THR
2	B	219	ARG
2	B	292	PHE
2	B	304	ARG
3	G	65	LYS
3	G	68	CYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (11) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	140	GLN
1	A	570	ASN
1	A	607	GLN

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Mol	Chain	Res	Type
2	B	44	GLN
2	B	88	ASN
2	B	132	ASN
2	B	175	GLN
2	B	220	GLN
2	B	230	ASN
3	G	24	ASN
3	G	44	HIS

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](#)

Of 2 ligands modelled in this entry, 1 is monoatomic - leaving 1 for Mogul analysis.

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	$\# Z > 2$
5	SIX	A	702	-	39,39,39	1.01	2 (5%)	48,53,53	1.22	4 (8%)

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
5	SIX	A	702	-	-	0/19/36/36	0/5/5/5

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	702	SIX	N2-N1	2.49	1.41	1.35
5	A	702	SIX	C3-C13	-2.37	1.48	1.51

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	702	SIX	C12-C10-C11	3.95	108.18	104.17
5	A	702	SIX	C10-C11-N1	-3.23	108.09	111.37
5	A	702	SIX	O1-C18-C17	2.24	111.23	107.44
5	A	702	SIX	C21-C20-C19	2.08	122.11	119.73

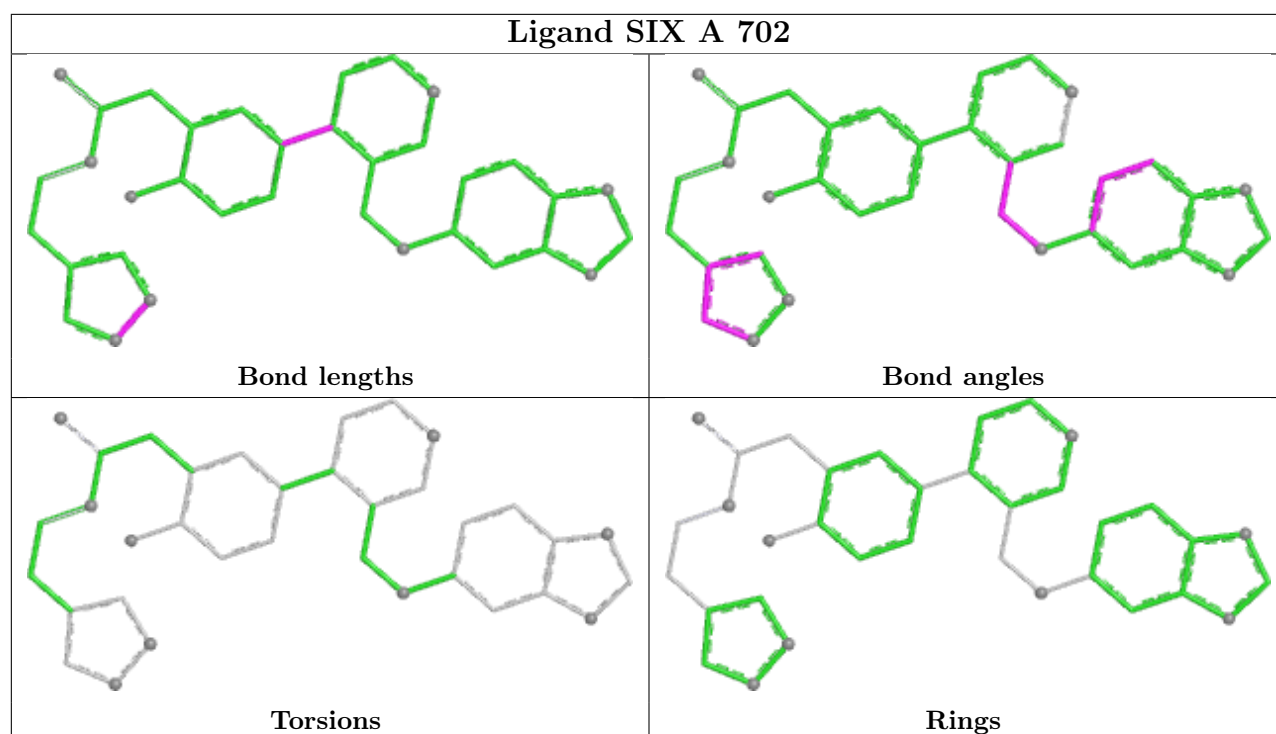
There are no chirality outliers.

There are no torsion outliers.

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 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	630/642 (98%)	0.28	35 (5%) 30 34	28, 58, 109, 156	0
2	B	339/339 (100%)	-0.40	2 (0%) 85 87	16, 36, 75, 120	2 (0%)
3	G	62/62 (100%)	0.30	4 (6%) 25 28	35, 52, 93, 125	0
All	All	1031/1043 (98%)	0.06	41 (3%) 42 47	16, 47, 103, 156	2 (0%)

All (41) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	483	PHE	6.4
3	G	66	PHE	6.1
3	G	69	ALA	5.0
1	A	671	PRO	4.8
1	A	112	TYR	4.2
1	A	670	ALA	3.9
1	A	118	LEU	3.9
1	A	668	PRO	3.6
1	A	122	HIS	3.6
1	A	477	VAL	3.5
1	A	408	THR	3.5
1	A	409	MET	3.4
3	G	65	LYS	3.4
1	A	573	LEU	3.2
1	A	410	ALA	2.9
1	A	138	LYS	2.8
1	A	121	SER	2.7
1	A	400	HIS	2.7
1	A	572	PHE	2.7
1	A	496	ILE	2.7
1	A	394	HIS	2.5
1	A	569	GLY	2.5
1	A	115	LYS	2.3

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Mol	Chain	Res	Type	RSRZ
1	A	499	LEU	2.3
3	G	21	MET	2.3
1	A	117	LEU	2.3
2	B	4	LEU	2.2
1	A	348	HIS	2.2
1	A	411	VAL	2.2
1	A	542	ALA	2.2
1	A	393	GLN	2.2
1	A	399	LYS	2.2
1	A	625	ARG	2.1
1	A	551	GLU	2.1
1	A	374	TRP	2.1
1	A	137	GLY	2.1
1	A	345	LYS	2.1
2	B	2	SER	2.1
1	A	113	ILE	2.1
1	A	405	MET	2.0
1	A	484	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 oligosaccharides in this entry.

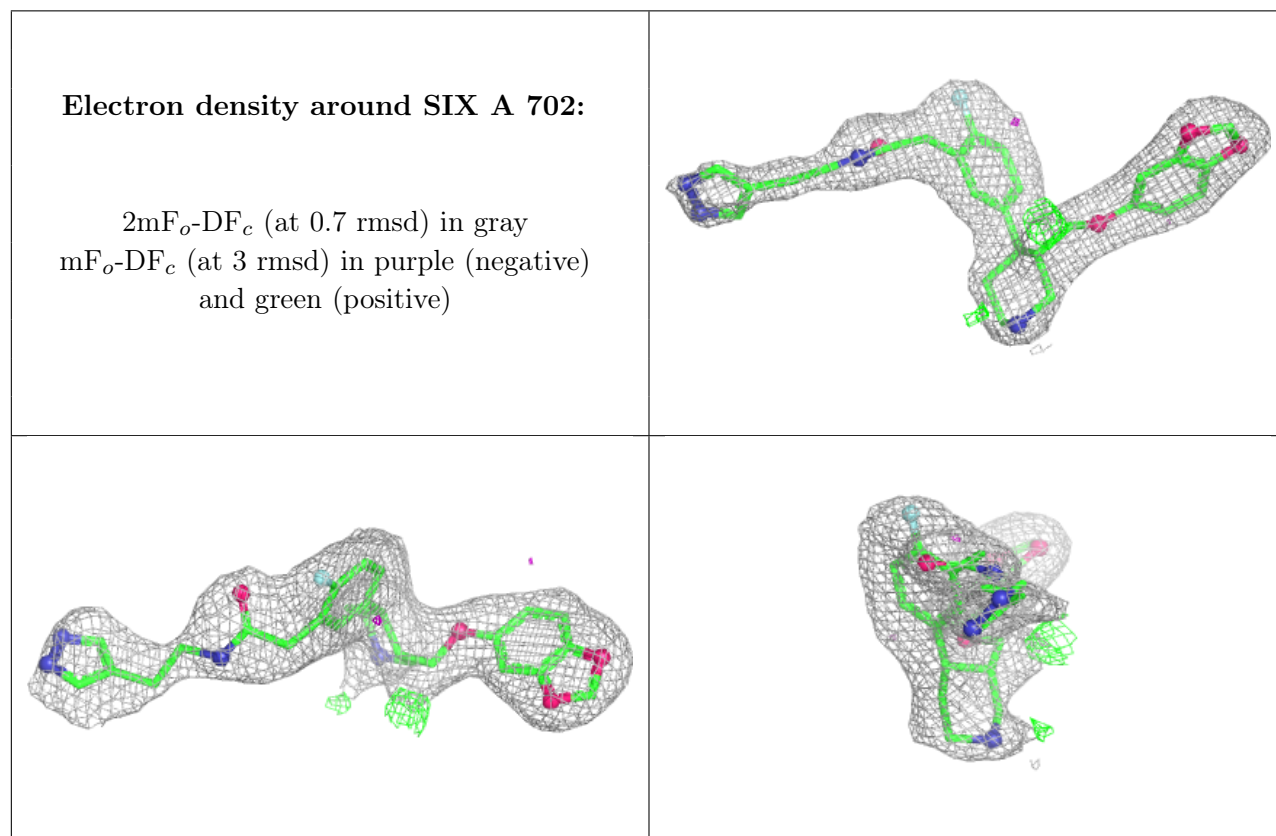
6.4 Ligands [i](#)

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
4	MG	A	701	1/1	0.89	0.11	77,77,77,77	0
5	SIX	A	702	35/35	0.93	0.10	53,65,92,95	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.