



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 19, 2026 – 04:44 AM UTC

PDB ID : 6UE5 / pdb_00006ue5
Title : Crystal structure of full-length human DCAF15-DDB1-deltaPBP-DDA1-RB M39 in complex with 4-(aminomethyl)-N-(3-cyano-4-methyl-1H-indol-7-yl)benzenesulfonamide
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Deposited on : 2019-09-20
Resolution : 2.61 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

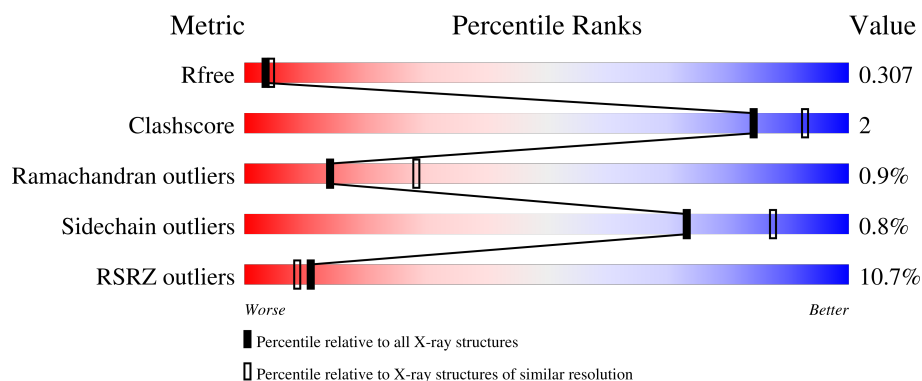
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	4951 (2.64-2.60)
Clashscore	190562	5303 (2.64-2.60)
Ramachandran outliers	187476	5217 (2.64-2.60)
Sidechain outliers	187428	5217 (2.64-2.60)
RSRZ outliers	180081	4950 (2.64-2.60)

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	601	
2	B	836	
3	C	81	
4	D	101	

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11268 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 DDB1- and CUL4-associated factor 15.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	424	Total	C	N	O	S	0	2	0
			3354	2155	563	616	20			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	GLY	-	expression tag	UNP Q66K64
A	1	PRO	-	expression tag	UNP Q66K64

- Molecule 2 is a protein called DNA damage-binding protein 1,DNA damage-binding protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	799	Total	C	N	O	S	0	1	0
			6170	3924	1032	1181	33			

There are 6 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	700	GLY	-	linker	UNP Q16531
B	701	ASN	-	linker	UNP Q16531
B	702	GLY	-	linker	UNP Q16531
B	703	ASN	-	linker	UNP Q16531
B	704	SER	-	linker	UNP Q16531
B	705	GLY	-	linker	UNP Q16531

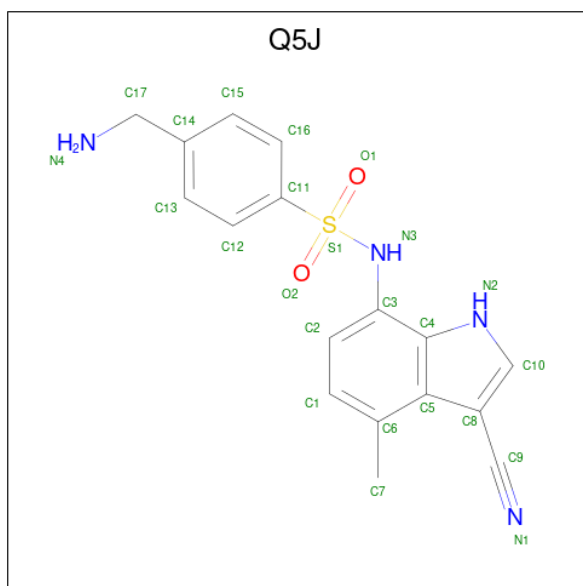
- Molecule 3 is a protein called RBM39.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	81	Total	C	N	O	S	0	0	0
			622	395	108	113	6			

- Molecule 4 is a protein called DET1- and DDB1-associated protein 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	73	Total	C	N	O	S	0	0	0
			577	367	103	106	1			

- Molecule 5 is 4-(aminomethyl)-N-(3-cyano-4-methyl-1H-indol-7-yl)benzene-1-sulfonamide (CCD ID: Q5J) (formula: C₁₇H₁₆N₄O₂S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	S	0	0
			24	17	4	2	1		

- Molecule 6 is GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	B	1	Total	C	O	0	0
			6	3	3		

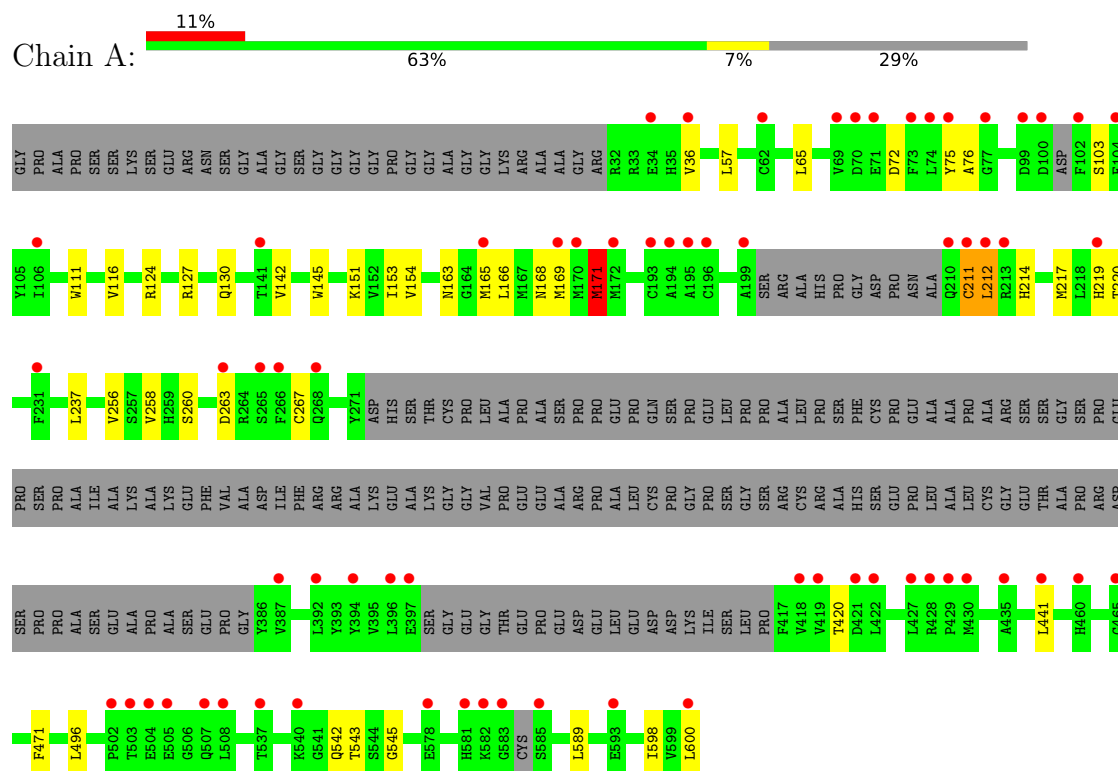
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	146	Total	O	0	0
			146	146		
7	B	307	Total	O	0	0
			307	307		
7	C	28	Total	O	0	0
			28	28		
7	D	34	Total	O	0	0
			34	34		

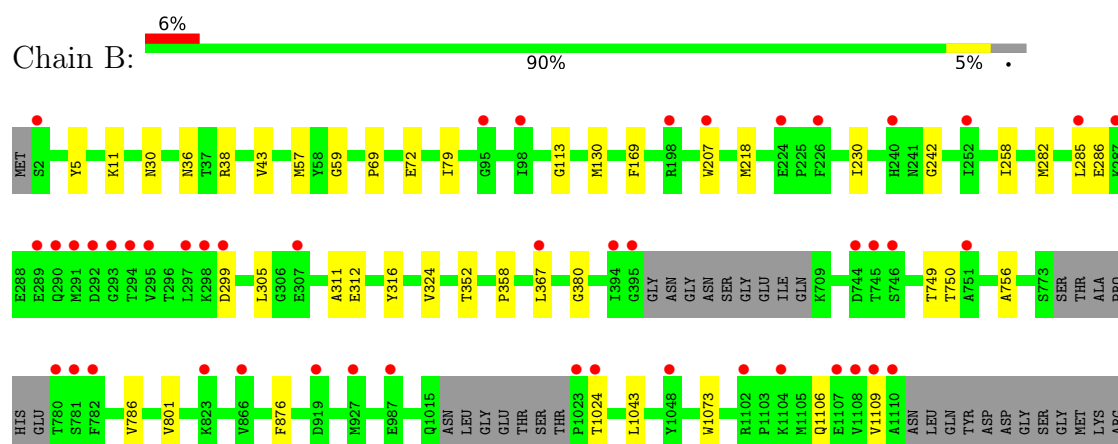
3 Residue-property plots

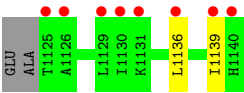
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: DDB1- and CUL4-associated factor 15

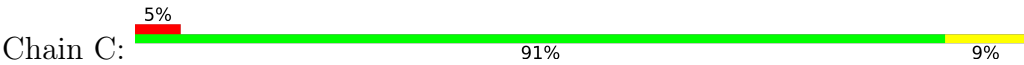


- Molecule 2: DNA damage-binding protein 1, DNA damage-binding protein 1

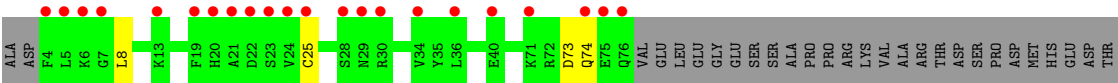




• Molecule 3: RBM39



• Molecule 4: DET1- and DDB1-associated protein 1



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	81.69Å 94.24Å 267.58Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	78.13 – 2.61 78.13 – 2.61	Depositor EDS
% Data completeness (in resolution range)	99.6 (78.13-2.61) 99.6 (78.13-2.61)	Depositor EDS
R_{merge}	0.49	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.20 (at 2.62Å)	Xtriage
Refinement program	BUSTER 2.11.7	Depositor
R, R_{free}	0.239 , 0.266 0.279 , 0.307	Depositor DCC
R_{free} test set	3191 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	41.9	Xtriage
Anisotropy	0.502	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 75.8	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	0.89	EDS
Total number of atoms	11268	wwPDB-VP
Average B, all atoms (Å ²)	75.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.75% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: GOL, Q5J

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	0.65	1/3437 (0.0%)	1.10	5/4674 (0.1%)
2	B	0.60	0/6285	1.00	1/8517 (0.0%)
3	C	0.67	0/634	1.23	0/848
4	D	0.64	0/591	1.12	2/803 (0.2%)
All	All	0.63	1/10947 (0.0%)	1.05	8/14842 (0.1%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	171	MET	SD-CE	-6.14	1.64	1.79

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	74	GLN	N-CA-C	-6.94	103.80	111.36
1	A	212	LEU	CA-C-N	6.29	128.95	120.65
1	A	212	LEU	C-N-CA	6.29	128.95	120.65
1	A	212	LEU	N-CA-C	6.04	116.25	108.34
4	D	73	ASP	CA-CB-CG	5.86	118.46	112.60
2	B	312	GLU	N-CA-C	-5.72	105.97	113.12
1	A	260	SER	CA-C-N	5.46	127.53	120.44
1	A	260	SER	C-N-CA	5.46	127.53	120.44

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	3354	0	3229	21	0
2	B	6170	0	6058	25	0
3	C	622	0	611	4	0
4	D	577	0	545	3	0
5	A	24	0	0	0	0
6	B	6	0	8	1	0
7	A	146	0	0	0	0
7	B	307	0	0	1	0
7	C	28	0	0	0	0
7	D	34	0	0	0	0
All	All	11268	0	10451	49	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 2.

All (49) 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:165:MET:O	1:A:171:MET:HE2	1.46	1.13
1:A:165:MET:O	1:A:171:MET:CE	2.08	1.01
2:B:69:PRO:HD2	2:B:72:GLU:HG3	1.66	0.78
3:C:273:PHE:HD1	3:C:306:LYS:HE3	1.49	0.76
1:A:211:CYS:O	1:A:212:LEU:HD12	1.96	0.65
2:B:230:ILE:HD11	2:B:285:LEU:HD21	1.83	0.61
2:B:358:PRO:HD2	2:B:380:GLY:HA2	1.83	0.60
1:A:65:LEU:HD22	1:A:600:LEU:HD23	1.84	0.58
2:B:130:MET:HE2	2:B:169:PHE:HZ	1.68	0.58
2:B:750:THR:HG23	7:B:1301:HOH:O	2.04	0.57
2:B:316:TYR:HE1	4:D:8:LEU:HD23	1.70	0.57
1:A:165:MET:O	1:A:171:MET:HE1	2.00	0.56
2:B:352:THR:HB	4:D:25:CYS:HA	1.89	0.55
1:A:589:LEU:HB2	1:A:598:ILE:HB	1.89	0.55
1:A:543:THR:HG21	3:C:306:LYS:HD2	1.89	0.54
1:A:127:ARG:NH1	1:A:130:GLN:HA	2.23	0.53
1:A:211:CYS:C	1:A:212:LEU:HD12	2.33	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:220:THR:HB	1:A:420:THR:HG22	1.91	0.52
2:B:876:PHE:HA	6:B:1201:GOL:H12	1.90	0.52
1:A:214:HIS:CE1	1:A:258:VAL:HG21	2.46	0.51
2:B:57:MET:HE2	2:B:79:ILE:HG21	1.92	0.51
1:A:471:PHE:HA	1:A:496:LEU:HA	1.92	0.50
2:B:286:GLU:HB2	2:B:299:ASP:H	1.75	0.50
1:A:153:ILE:HG21	1:A:237:LEU:HD21	1.94	0.49
2:B:5:TYR:HB2	2:B:1043:LEU:HD11	1.94	0.49
2:B:130:MET:HE2	2:B:169:PHE:CZ	2.46	0.49
2:B:1136:LEU:O	2:B:1139:ILE:HG22	2.13	0.49
2:B:316:TYR:CE1	4:D:8:LEU:HD23	2.48	0.49
2:B:1024:THR:HG21	2:B:1043:LEU:HD23	1.95	0.49
2:B:218:MET:HE1	2:B:258:ILE:HG22	1.94	0.48
2:B:59:GLY:HA2	2:B:1073:TRP:CZ3	2.49	0.48
3:C:287:THR:HB	3:C:289:ARG:HG2	1.97	0.46
1:A:256:VAL:HG13	1:A:441:LEU:HD21	1.98	0.46
2:B:749:THR:HG21	2:B:786:VAL:HG21	1.97	0.45
2:B:282:MET:HE2	2:B:305:LEU:HD11	1.99	0.45
1:A:142:VAL:HG22	1:A:154:VAL:HG22	1.98	0.45
1:A:543:THR:C	1:A:545:GLY:H	2.24	0.45
3:C:267:ARG:O	3:C:271:GLU:HB2	2.18	0.44
1:A:145:TRP:CZ3	1:A:151:LYS:HG3	2.53	0.43
2:B:11:LYS:HD3	2:B:38:ARG:HE	1.83	0.43
1:A:36:VAL:HG22	1:A:57:LEU:HD11	2.01	0.42
2:B:207:TRP:HB3	2:B:242:GLY:HA2	2.00	0.42
2:B:358:PRO:HD2	2:B:380:GLY:CA	2.49	0.42
1:A:127:ARG:HH11	1:A:130:GLN:HA	1.84	0.42
2:B:756:ALA:HB1	2:B:801:VAL:HG21	2.02	0.42
2:B:30:ASN:ND2	2:B:43:VAL:HG22	2.36	0.41
2:B:311:ALA:HB2	2:B:324:VAL:HG13	2.03	0.41
1:A:111:TRP:HB2	1:A:124:ARG:HB3	2.04	0.40
1:A:217:MET:HE2	1:A:217:MET:HB3	1.95	0.40

There are no symmetry-related clashes.

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	414/601 (69%)	371 (90%)	35 (8%)	8 (2%)	6	12
2	B	790/836 (94%)	742 (94%)	44 (6%)	4 (0%)	24	44
3	C	79/81 (98%)	78 (99%)	1 (1%)	0	100	100
4	D	71/101 (70%)	66 (93%)	5 (7%)	0	100	100
All	All	1354/1619 (84%)	1257 (93%)	85 (6%)	12 (1%)	14	28

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	72	ASP
1	A	75	TYR
1	A	168	ASN
1	A	267	CYS
1	A	103	SER
1	A	116	VAL
1	A	163	ASN
2	B	36	ASN
2	B	367	LEU
2	B	1106	GLN
1	A	76	ALA
2	B	113	GLY

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	365/514 (71%)	357 (98%)	8 (2%)	45	70
2	B	671/727 (92%)	670 (100%)	1 (0%)	88	96
3	C	65/68 (96%)	64 (98%)	1 (2%)	57	79
4	D	60/92 (65%)	60 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles
All	All	1161/1401 (83%)	1151 (99%)	10 (1%)	73 86

All (10) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	166	LEU
1	A	169	MET
1	A	171	MET
1	A	211	CYS
1	A	219[A]	HIS
1	A	219[B]	HIS
1	A	263	ASP
1	A	542	GLN
2	B	1109	VAL
3	C	282	MET

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (15) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	223	GLN
1	A	241	GLN
1	A	455	ASN
1	A	486	ASN
1	A	581	HIS
2	B	731	GLN
2	B	759	GLN
2	B	796	GLN
2	B	877	ASN
2	B	970	ASN
2	B	978	GLN
2	B	1059	ASN
4	D	29	ASN
4	D	53	ASN
4	D	61	GLN

5.3.3 RNA ⓘ

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](#)

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	$\# Z > 2$
6	GOL	B	1201	-	5,5,5	0.07	0	5,5,5	0.29	0
5	Q5J	A	701	-	25,26,26	2.02	7 (28%)	35,38,38	1.42	7 (20%)

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
6	GOL	B	1201	-	-	0/4/4/4	-
5	Q5J	A	701	-	-	0/13/15/15	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	701	Q5J	S1-N3	5.20	1.71	1.63
5	A	701	Q5J	O1-S1	3.50	1.47	1.43
5	A	701	Q5J	C5-C6	3.15	1.44	1.40
5	A	701	Q5J	O2-S1	3.13	1.47	1.43
5	A	701	Q5J	C5-C4	2.22	1.44	1.41
5	A	701	Q5J	C12-C11	2.07	1.42	1.38

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	701	Q5J	C13-C12	2.03	1.42	1.38

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	701	Q5J	C4-C5-C8	-3.08	105.33	106.80
5	A	701	Q5J	C1-C6-C5	2.70	121.31	117.95
5	A	701	Q5J	C3-N3-S1	2.65	131.83	123.34
5	A	701	Q5J	C6-C5-C8	2.52	138.63	133.75
5	A	701	Q5J	C4-N2-C10	2.43	111.03	108.93
5	A	701	Q5J	C7-C6-C1	-2.37	115.71	120.28
5	A	701	Q5J	C11-S1-N3	-2.34	103.97	106.88

There are no chirality outliers.

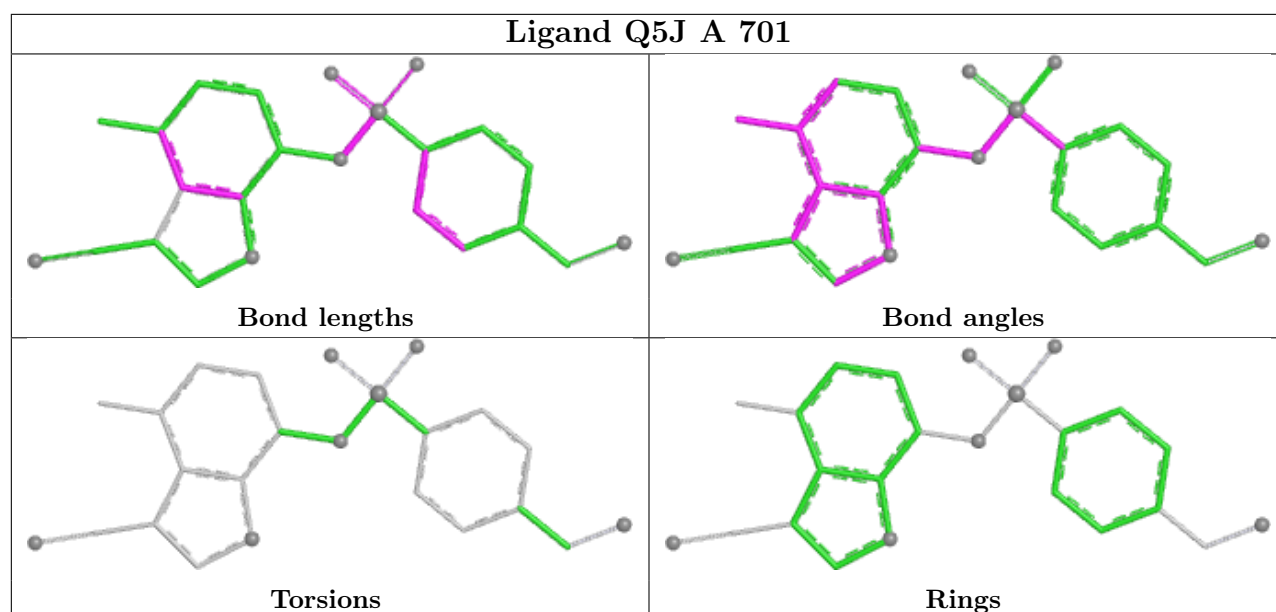
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	1201	GOL	1	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	424/601 (70%)	1.02	67 (15%) 5 4	27, 72, 128, 225	2 (0%)
2	B	799/836 (95%)	0.62	54 (6%) 23 19	37, 72, 117, 188	1 (0%)
3	C	81/81 (100%)	0.46	4 (4%) 35 29	43, 60, 89, 110	0
4	D	73/101 (72%)	1.48	22 (30%) 1 1	62, 94, 210, 256	0
All	All	1377/1619 (85%)	0.78	147 (10%) 11 9	27, 72, 126, 256	3 (0%)

All (147) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	B	1110	ALA	5.6
1	A	194	ALA	5.1
4	D	76	GLN	5.0
4	D	25	CYS	4.9
3	C	328	GLU	4.7
2	B	291	MET	4.7
2	B	1140	HIS	4.3
4	D	21	ALA	4.3
1	A	583	GLY	4.3
2	B	1130	ILE	4.3
1	A	212	LEU	4.1
2	B	1129	LEU	4.1
1	A	213	ARG	4.0
2	B	1107	GLU	4.0
4	D	75	GLU	4.0
1	A	397	GLU	3.9
1	A	102	PHE	3.9
1	A	75	TYR	3.8
2	B	745	THR	3.8
2	B	780	THR	3.7
1	A	73	PHE	3.7

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Mol	Chain	Res	Type	RSRZ
1	A	503	THR	3.7
2	B	207	TRP	3.7
2	B	1125	THR	3.6
1	A	199	ALA	3.6
2	B	395	GLY	3.6
2	B	1109	VAL	3.5
2	B	1139	ILE	3.3
2	B	299	ASP	3.3
2	B	293	GLY	3.3
4	D	24	VAL	3.2
2	B	1024	THR	3.2
2	B	292	ASP	3.1
2	B	285	LEU	3.1
2	B	224	GLU	3.1
1	A	387	VAL	3.1
1	A	585	SER	3.1
4	D	23	SER	3.1
1	A	394	TYR	3.1
2	B	297	LEU	3.1
1	A	430	MET	3.1
1	A	266	PHE	3.0
1	A	427	LEU	3.0
2	B	746	SER	3.0
2	B	240	HIS	3.0
1	A	170	MET	3.0
3	C	248	GLY	3.0
1	A	104	PHE	3.0
4	D	5	LEU	2.9
1	A	263	ASP	2.9
2	B	782	PHE	2.9
2	B	287	LYS	2.9
1	A	268	GLN	2.9
2	B	1108	VAL	2.9
4	D	4	PHE	2.9
4	D	28	SER	2.8
2	B	294	THR	2.8
2	B	98	ILE	2.7
4	D	74	GLN	2.7
2	B	307	GLU	2.7
4	D	36	LEU	2.7
1	A	537	THR	2.7
2	B	744	ASP	2.7

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Mol	Chain	Res	Type	RSRZ
2	B	295	VAL	2.6
1	A	265	SER	2.6
2	B	1023	PRO	2.6
1	A	100	ASP	2.6
4	D	20	HIS	2.6
2	B	823	LYS	2.6
1	A	396	LEU	2.6
1	A	172	MET	2.5
1	A	70	ASP	2.5
1	A	441	LEU	2.5
2	B	1104	LYS	2.5
1	A	578	GLU	2.5
1	A	507	GLN	2.5
2	B	290	GLN	2.5
1	A	219[A]	HIS	2.5
1	A	422	LEU	2.4
1	A	69	VAL	2.4
3	C	327	THR	2.4
1	A	34	GLU	2.4
1	A	465	GLY	2.4
1	A	581	HIS	2.4
2	B	1131	LYS	2.4
1	A	62	CYS	2.4
4	D	7	GLY	2.4
1	A	418	VAL	2.4
4	D	30	ARG	2.4
4	D	6	LYS	2.3
1	A	600	LEU	2.3
2	B	394	ILE	2.3
1	A	582	LYS	2.3
1	A	429	PRO	2.3
2	B	198	ARG	2.3
1	A	193	CYS	2.3
1	A	74	LEU	2.3
1	A	435	ALA	2.3
1	A	36	VAL	2.3
1	A	196	CYS	2.3
1	A	165	MET	2.3
3	C	249	PRO	2.3
1	A	231[A]	PHE	2.3
1	A	141	THR	2.2
1	A	77	GLY	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	419	VAL	2.2
1	A	460	HIS	2.2
1	A	540	LYS	2.2
4	D	19	PHE	2.2
1	A	211	CYS	2.2
4	D	40	GLU	2.2
1	A	428	ARG	2.2
2	B	298	LYS	2.2
2	B	252	ILE	2.2
2	B	1126	ALA	2.2
1	A	504	GLU	2.2
1	A	392	LEU	2.2
2	B	367	LEU	2.2
4	D	22	ASP	2.2
1	A	502	PRO	2.2
4	D	71	LYS	2.2
1	A	99	ASP	2.2
2	B	919	ASP	2.2
2	B	927	MET	2.2
1	A	169	MET	2.1
2	B	226	PHE	2.1
1	A	195	ALA	2.1
4	D	13	LYS	2.1
2	B	2	SER	2.1
2	B	751	ALA	2.1
2	B	289	GLU	2.1
2	B	1102	ARG	2.1
1	A	106	ILE	2.1
1	A	505	GLU	2.1
1	A	593	GLU	2.1
2	B	1136	LEU	2.1
2	B	987	GLU	2.0
1	A	210	GLN	2.0
4	D	29	ASN	2.0
2	B	95	GLY	2.0
1	A	71	GLU	2.0
1	A	421	ASP	2.0
2	B	781	SER	2.0
1	A	508	LEU	2.0
2	B	866	VAL	2.0
4	D	34	VAL	2.0
2	B	1048	TYR	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](#)

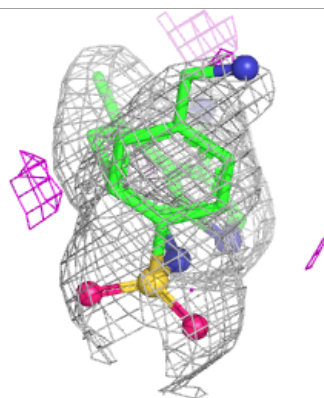
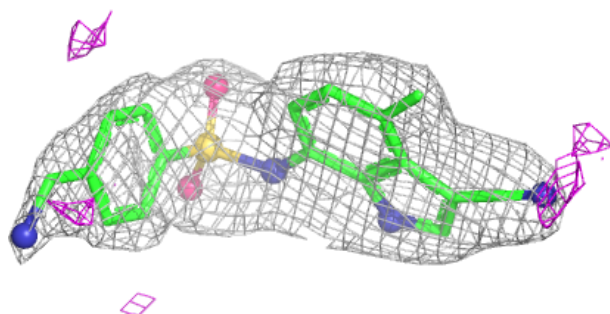
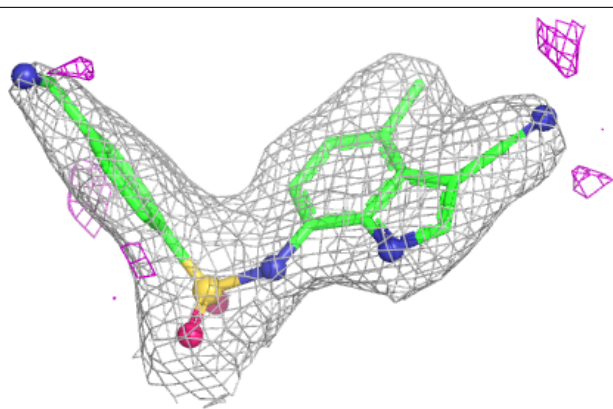
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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
6	GOL	B	1201	6/6	0.90	0.09	51,52,52,53	0
5	Q5J	A	701	24/24	0.95	0.09	32,39,50,53	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 Q5J A 701:

$2mF_o - DF_c$ (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.