



# Full wwPDB X-ray Structure Validation Report ⓘ

May 19, 2020 – 02:11 pm BST

PDB ID : 5R67  
Title : PanDDA analysis group deposition – Crystal Structure of HUMAN CLEAVAGE FACTOR IM in complex with FMOPL000589a  
Authors : Talon, R.; Krojer, T.; Diaz-Saez, L.; Bradley, A.R.; Aimon, A.; Fairhead, M.; Arrowsmith, C.H.; Bountra, C.; Edwards, A.M.; Huber, K.V.M.; von Delft, F.  
Deposited on : 2020-02-28  
Resolution : 1.52 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](mailto: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.

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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 : 2.11  
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) : 2.11

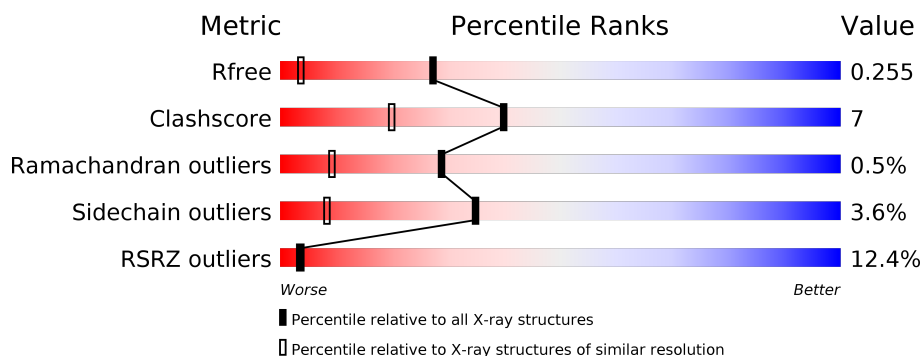
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 1.52 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	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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  $\geq 3$ , 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.

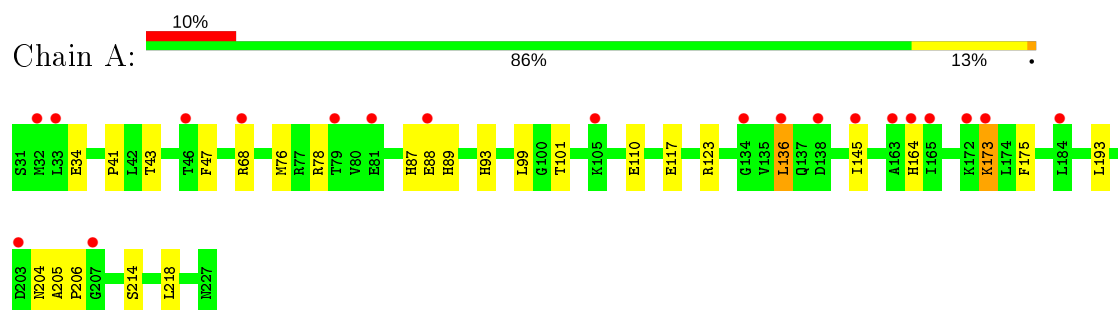
Mol	Chain	Length	Quality of chain
1	A	197	<div> <div>10%</div> <div>86%</div> <div>13%</div> <div>.</div> </div>
1	B	197	<div> <div>15%</div> <div>82%</div> <div>14%</div> <div>..</div> </div>

ENTRY-COMPOSITION INFOmissingINFO

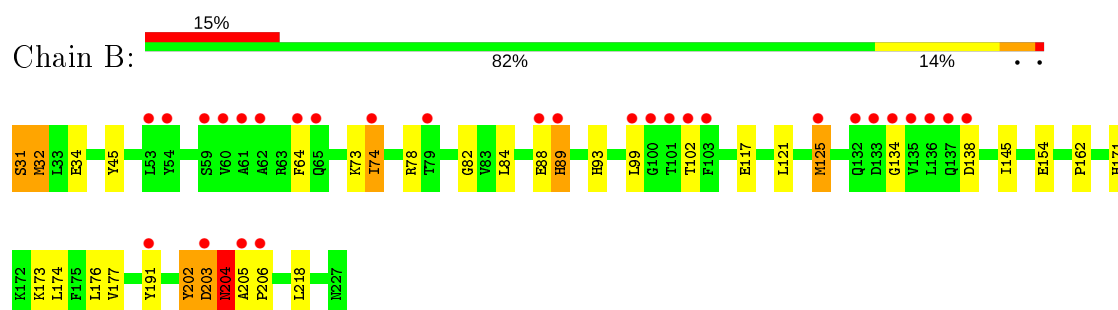
## 2 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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: Cleavage and polyadenylation specificity factor subunit 5



- Molecule 1: Cleavage and polyadenylation specificity factor subunit 5



### 3 Data and refinement statistics

Property	Value	Source
Space group	P 32 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	59.77Å 59.77Å 214.23Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	46.65 – 1.52 46.61 – 1.52	Depositor EDS
% Data completeness (in resolution range)	99.9 (46.65-1.52) 99.9 (46.61-1.52)	Depositor EDS
$R_{merge}$	0.06	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.49 (at 1.52Å)	Xtriage
Refinement program	REFMAC 5.8.0238	Depositor
R, $R_{free}$	0.209 , 0.245 0.220 , 0.255	Depositor DCC
$R_{free}$ test set	3481 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	26.2	Xtriage
Anisotropy	0.012	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 40.5	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.027 for -h,-k,l	Xtriage
$F_o, F_c$ correlation	0.96	EDS
Total number of atoms	3523	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.02% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical 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.

## 4 Model quality

### 4.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: S6V, ZN, ACT

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	1.01	4/1677 (0.2%)	1.10	2/2279 (0.1%)
1	B	0.97	1/1646 (0.1%)	1.08	6/2242 (0.3%)
All	All	0.99	5/3323 (0.2%)	1.09	8/4521 (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	3

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	154	GLU	CD-OE2	6.30	1.32	1.25
1	A	110	GLU	CD-OE2	-5.35	1.19	1.25
1	A	214	SER	CB-OG	-5.31	1.35	1.42
1	A	110	GLU	C-O	5.17	1.33	1.23
1	A	34	GLU	CD-OE1	5.01	1.31	1.25

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	78	ARG	NE-CZ-NH1	7.59	124.10	120.30
1	B	45	TYR	CB-CG-CD2	6.08	124.65	121.00
1	B	125[A]	MET	CG-SD-CE	-5.88	90.78	100.20
1	B	125[B]	MET	CG-SD-CE	-5.88	90.78	100.20
1	A	123	ARG	NE-CZ-NH1	5.72	123.16	120.30
1	B	78	ARG	NE-CZ-NH1	5.68	123.14	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	64	PHE	CB-CA-C	5.04	120.48	110.40
1	B	204	ASN	CB-CA-C	5.01	120.42	110.40

There are no chirality outliers.

All (3) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	202	TYR	Mainchain,Peptide
1	B	31	SER	Peptide

## 4.2 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	1632	0	1606	21	1
1	B	1599	0	1542	26	1
2	A	2	0	0	0	0
2	B	4	0	0	0	1
3	A	8	0	6	1	0
3	B	4	0	3	1	0
4	A	18	0	0	0	0
5	A	133	0	0	9	4
5	B	123	0	0	1	4
All	All	3523	0	3157	47	7

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 7.

All (47) 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:76:MET:SD	5:A:524:HOH:O	2.12	1.08
1:B:88[A]:GLU:C	1:B:89[A]:HIS:HD2	1.67	0.98
1:B:88[A]:GLU:C	1:B:89[A]:HIS:CD2	2.39	0.95
1:A:93:HIS:NE2	5:A:404:HOH:O	2.05	0.89

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:88[B]:GLU:OE2	5:A:402:HOH:O	1.94	0.85
1:B:32:MET:HE2	1:B:34:GLU:H	1.45	0.82
1:A:136:LEU:HD22	1:A:136:LEU:N	1.99	0.77
1:A:136:LEU:HD22	1:A:136:LEU:H	1.51	0.76
1:A:43:THR:OG1	5:A:403:HOH:O	2.04	0.74
1:B:82:GLY:HA3	1:B:125[A]:MET:HE1	1.69	0.73
1:B:88[A]:GLU:O	1:B:89[A]:HIS:CD2	2.44	0.70
1:B:117:GLU:OE2	1:B:173:LYS:HE3	1.91	0.70
1:A:47:PHE:CD1	1:A:193:LEU:HD23	2.27	0.69
1:B:89[A]:HIS:CD2	1:B:89[A]:HIS:N	2.63	0.67
1:A:173[A]:LYS:HD3	1:A:175:PHE:CZ	2.30	0.67
1:A:93:HIS:CE1	5:A:404:HOH:O	2.46	0.64
1:B:121:LEU:O	1:B:125[B]:MET:HG3	2.02	0.59
1:B:31:SER:O	1:B:31:SER:OG	2.19	0.59
1:B:205:ALA:N	1:B:206:PRO:CD	2.67	0.57
1:B:82:GLY:HA3	1:B:125[A]:MET:CE	2.36	0.56
1:A:47:PHE:CE1	1:A:193:LEU:HD23	2.41	0.56
1:A:164:HIS:CE1	5:A:407:HOH:O	2.60	0.55
1:B:84:LEU:HD11	1:B:125[B]:MET:HE1	1.87	0.55
1:A:204:ASN:HB2	3:A:304:ACT:O	2.07	0.54
1:B:73:LYS:CB	1:B:74:ILE:HD13	2.37	0.53
1:B:125[A]:MET:HE3	1:B:177:VAL:HG21	1.90	0.53
1:B:88[A]:GLU:HG2	1:B:93:HIS:CE1	2.44	0.53
1:B:171:HIS:CE1	1:B:173:LYS:HE2	2.46	0.51
1:A:117:GLU:OE2	1:A:173[B]:LYS:HE3	2.11	0.50
1:A:145[B]:ILE:CD1	1:A:218:LEU:HD13	2.42	0.49
1:A:136:LEU:CD2	1:A:136:LEU:H	2.23	0.49
1:A:41:PRO:HA	1:A:87:HIS:O	2.13	0.48
1:B:32:MET:CE	1:B:34:GLU:H	2.23	0.48
1:A:68[B]:ARG:NH1	5:A:411:HOH:O	2.47	0.47
1:B:145:ILE:HG22	1:B:218:LEU:HD13	1.96	0.47
1:A:136:LEU:CD2	1:A:136:LEU:N	2.72	0.46
1:B:202:TYR:HD2	3:B:305:ACT:H1	1.80	0.46
1:A:173[A]:LYS:HE3	5:A:471:HOH:O	2.15	0.46
1:B:99:LEU:HG	1:B:191:TYR:CE1	2.50	0.45
1:B:145:ILE:HG23	1:B:218:LEU:HB3	2.00	0.44
1:B:31:SER:OG	5:B:403:HOH:O	2.21	0.44
1:A:205:ALA:N	1:A:206:PRO:CD	2.81	0.43
1:B:125[A]:MET:CE	1:B:177:VAL:HG21	2.48	0.42
1:B:176:LEU:HD23	1:B:176:LEU:C	2.40	0.42
1:B:204:ASN:HA	1:B:206:PRO:HD2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:74:ILE:HD13	1:B:74:ILE:N	2.36	0.41
1:A:173[A]:LYS:CE	5:A:471:HOH:O	2.69	0.40

All (7) 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)
5:A:523:HOH:O	5:A:523:HOH:O[4_555]	0.69	1.51
5:B:505:HOH:O	5:B:505:HOH:O[6_554]	1.28	0.92
2:B:302:ZN:ZN	5:A:404:HOH:O[4_545]	1.32	0.88
1:A:89:HIS:NE2	5:B:401:HOH:O[3_655]	1.87	0.33
5:A:404:HOH:O	5:B:497:HOH:O[4_655]	1.96	0.24
5:B:479:HOH:O	5:B:499:HOH:O[6_554]	2.08	0.12
1:B:162:PRO:CB	5:A:407:HOH:O[1_545]	2.10	0.10

## 4.3 Torsion angles

### 4.3.1 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	199/197 (101%)	196 (98%)	3 (2%)	0	100	100
1	B	199/197 (101%)	191 (96%)	6 (3%)	2 (1%)	15	3
All	All	398/394 (101%)	387 (97%)	9 (2%)	2 (0%)	29	9

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	203	ASP
1	B	134	GLY



### 4.3.2 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	175/176 (99%)	170 (97%)	5 (3%)	42	13
1	B	167/176 (95%)	158 (95%)	9 (5%)	22	3
All	All	342/352 (97%)	328 (96%)	14 (4%)	35	6

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	99	LEU
1	A	101	THR
1	A	136	LEU
1	A	173[A]	LYS
1	A	173[B]	LYS
1	B	32	MET
1	B	74	ILE
1	B	89[A]	HIS
1	B	89[B]	HIS
1	B	102	THR
1	B	138	ASP
1	B	174	LEU
1	B	203	ASP
1	B	204	ASN

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

Mol	Chain	Res	Type
1	B	204	ASN

### 4.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

## 4.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 4.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 1 could not be matched to an existing wwPDB Chemical Component Dictionary definition at this stage and 6 are monoatomic - leaving 3 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
3	ACT	A	303	-	1,3,3	5.92	1 (100%)	0,3,3	0.00	-
3	ACT	B	305	-	1,3,3	1.28	0	0,3,3	0.00	-
3	ACT	A	304	-	1,3,3	4.12	1 (100%)	0,3,3	0.00	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	303	ACT	CH3-C	5.92	1.56	1.48
3	A	304	ACT	CH3-C	4.12	1.54	1.48

There are no bond angle outliers.

There are no chirality outliers.

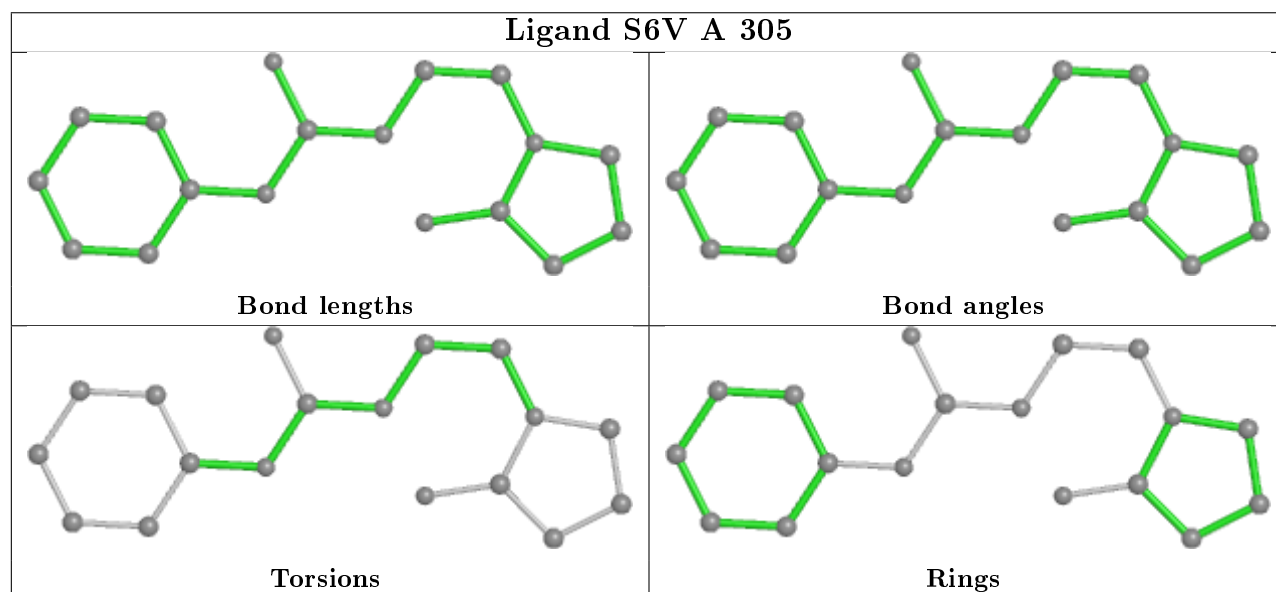
There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	B	305	ACT	1	0
3	A	304	ACT	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.



## 4.7 Other polymers [i](#)

There are no such residues in this entry.

## 4.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

## 5 Fit of model and data

### 5.1 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	197/197 (100%)	0.48	20 (10%) <b>6</b> <b>6</b>	18, 29, 48, 73	8 (4%)
1	B	197/197 (100%)	0.77	29 (14%) <b>2</b> <b>2</b>	19, 31, 68, 117	4 (2%)
All	All	394/394 (100%)	0.62	49 (12%) <b>4</b> <b>3</b>	18, 30, 60, 117	12 (3%)

All (49) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	89[A]	HIS	12.8
1	B	134	GLY	10.8
1	A	68[A]	ARG	8.0
1	B	79[A]	THR	7.7
1	B	88[A]	GLU	7.0
1	B	136	LEU	7.0
1	A	145[A]	ILE	6.7
1	A	88[A]	GLU	6.5
1	B	125[A]	MET	6.4
1	A	79	THR	6.3
1	B	135	VAL	5.1
1	B	54	TYR	5.1
1	B	132	GLN	4.7
1	B	60	VAL	4.7
1	A	173[A]	LYS	4.5
1	B	103	PHE	4.3
1	A	138	ASP	4.0
1	B	62	ALA	4.0
1	B	133	ASP	3.4
1	A	81	GLU	3.4
1	A	172	LYS	3.3
1	A	32	MET	3.3
1	A	105	LYS	3.2
1	B	64	PHE	3.2

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Mol	Chain	Res	Type	RSRZ
1	B	191	TYR	3.2
1	A	163	ALA	3.1
1	B	100	GLY	3.0
1	B	61	ALA	3.0
1	B	53	LEU	3.0
1	B	74	ILE	2.9
1	A	164	HIS	2.9
1	A	165	ILE	2.8
1	B	65	GLN	2.7
1	A	184	LEU	2.7
1	B	205	ALA	2.6
1	A	207	GLY	2.6
1	A	136	LEU	2.6
1	B	102	THR	2.5
1	B	59	SER	2.5
1	A	33	LEU	2.4
1	A	46	THR	2.4
1	A	134	GLY	2.3
1	B	99	LEU	2.2
1	A	203	ASP	2.2
1	B	138	ASP	2.2
1	B	137	GLN	2.1
1	B	206	PRO	2.1
1	B	101	THR	2.1
1	B	203	ASP	2.1

## 5.2 Non-standard residues in protein, DNA, RNA chains ⓘ

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

## 5.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

## 5.4 Ligands ⓘ

LIGAND-RSR INFOmissingINFO

## 5.5 Other polymers [i](#)

There are no such residues in this entry.