

Full wwPDB EM Validation Report (i)

Nov 21, 2022 – 03:44 pm GMT

PDB ID : 7PBS

EMDB ID : EMD-13301

Title: RuvAB branch migration motor complexed to the Holliday junction - RuvB

AAA+ state s0+A [t1 dataset]

Authors: Goessweiner-Mohr, N.; Fahrenkamp, D.; Wald, J.; Marlovits, T.C.

Deposited on : 2021-08-02

Resolution : 3.30 Å(reported)

This is a Full wwPDB EM 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/EMValidationReportHelp with specific help available everywhere you see the (i) symbol.

The following versions of software and data (see references (i)) were used in the production of this report:

EMDB validation analysis : 0.0.0.dev97

Mogul : 1.8.4, CSD as541be (2020)

MolProbity : 4.02b-467 buster-report : 1.1.7 (2018)

Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)

Ideal geometry (proteins) : Engh & Huber (2001) Ideal geometry (DNA, RNA) : Parkinson et al. (1996)

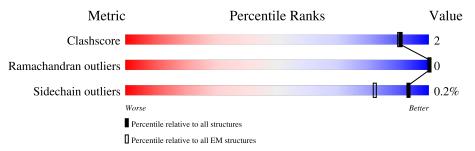
Validation Pipeline (wwPDB-VP) : 2.26

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $ELECTRON\ MICROSCOPY$

The reported resolution of this entry is 3.30 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 $(\# ext{Entries})$	${ m EM~structures} \ (\#{ m Entries})$		
Clashscore	158937	4297		
Ramachandran outliers	154571	4023		
Sidechain outliers	154315	3826		

The table below summarises the geometric issues observed across the polymeric chains and their fit to the map. The red, orange, yellow and green segments of the 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%

Mol	Chain	Length	Quality of chain	
1	A	315	96%	
1	В	315	96%	
1	С	315	94%	
1	D	315	95%	5% •
1	Е	315	93%	6% •
1	F	315	96%	
2	G	48	94%	6%
3	U	15	93%	7%
4	V	15	73%	27%



2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 31410 atoms, of which 15521 are hydrogens and 0 are deuteriums.

In the tables below, 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 Holliday junction ATP-dependent DNA helicase RuvB.

Mol	Chain	Residues			Atom	.S			AltConf	Trace
1	A	312	Total	С	Н	N	О	S	0	0
1	Λ	312	4910	1555	2455	412	472	16		
1	В	312	Total	С	Н	N	О	S	0	0
1	Б	312	4910	1555	2455	412	472	16	0	
1	С	309	Total	С	Н	N	О	S	0	0
1		309	4895	1549	2451	412	467	16	0	
1	D	313	Total	С	Н	N	О	S	0	0
1	ט	313	4934	1561	2468	416	473	16	0	
1	Е	312	Total	С	Н	N	О	S	0	0
1	<u> 1</u> 2	312	4910	1555	2455	412	472	16		
1	F	312	Total	С	Н	N	О	S	0	0
1	1'	312	4910	1555	2455	412	472	16		

• Molecule 2 is a protein called Holliday junction ATP-dependent DNA helicase RuvA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
2	G	48	Total 719	C 218	H 362	N 64	O 74	S 1	0	0

• Molecule 3 is a DNA chain called random DNA.

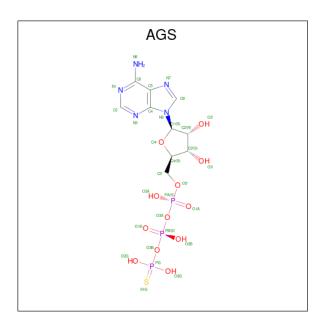
Mol	Chain	Residues	Atoms					AltConf	Trace	
3	U	15	Total 479	C 147	H 167	N 63	O 87	P 15	0	0

• Molecule 4 is a DNA chain called random DNA.

Mol	Chain	Residues	Atoms					AltConf	Trace	
4	V	15	Total 474	_	H 171	- '	O 93	P 15	0	0

• Molecule 5 is PHOSPHOTHIOPHOSPHORIC ACID-ADENYLATE ESTER (three-letter code: AGS) (formula: C₁₀H₁₆N₅O₁₂P₃S).





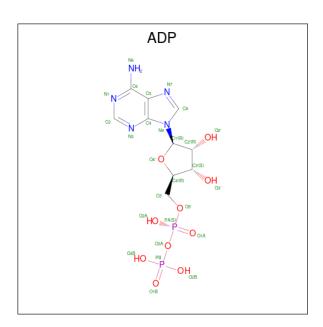
Mol	Chain	Residues			Ato	ms				AltConf
5	Λ	1	Total	С	Н	N	О	Р	S	0
9	A	1	45	10	14	5	12	3	1	0
5	В	1	Total	С	Н	N	О	Р	S	0
9	Ъ	1	45	10	14	5	12	3	1	0
5	С	1	Total	С	Н	N	О	Р	S	0
9	C	1	45	10	14	5	12	3	1	0
5	D	1	Total	С	Н	N	О	Р	S	0
9	ע	1	45	10	14	5	12	3	1	0
5	F	1	Total	С	Н	N	О	Р	S	0
	I.	1	45	10	14	5	12	3	1	

• Molecule 6 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	AltConf
6	A	1	Total Mg 1 1	0
6	В	1	Total Mg 1 1	0
6	С	1	Total Mg 1 1	0
6	D	1	Total Mg 1 1	0
6	F	1	Total Mg 1 1	0

 \bullet Molecule 7 is ADENOSINE-5'-DIPHOSPHATE (three-letter code: ADP) (formula: $C_{10}H_{15}N_5O_{10}P_2).$





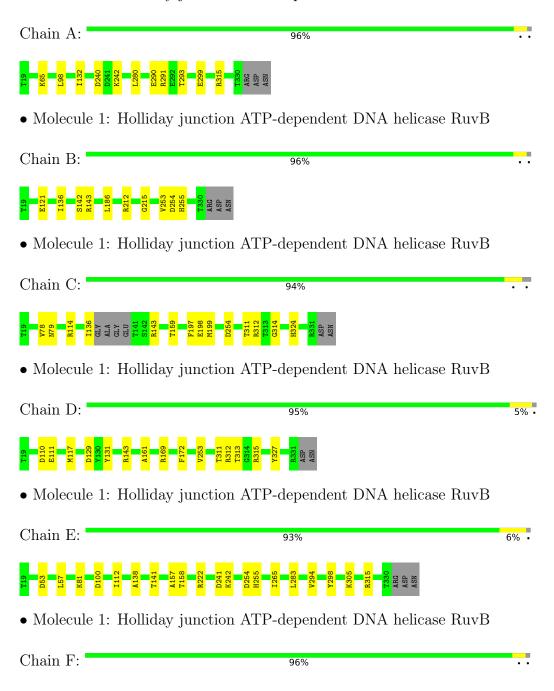
Mol	Chain	Residues		Atoms				AltConf	
7	Ŀ	1	Total	С	Н	N	О	Р	0
'	E	1	39	10	12	5	10	2	U



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. 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. 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: Holliday junction ATP-dependent DNA helicase RuvB







• Molecule 2: Holliday junction ATP-dependent DNA helicase RuvA

Chain G: 94% 6%



• Molecule 3: random DNA

Chain U: 93% 7%



• Molecule 4: random DNA

Chain V: 73% 27%





4 Experimental information (i)

Property	Value	Source
EM reconstruction method	SINGLE PARTICLE	Depositor
Imposed symmetry	POINT, Not provided	
Number of particles used	45834	Depositor
Resolution determination method	FSC 0.143 CUT-OFF	Depositor
CTF correction method	PHASE FLIPPING AND AMPLITUDE	Depositor
	CORRECTION	
Microscope	FEI TITAN KRIOS	Depositor
Voltage (kV)	300	Depositor
Electron dose $(e^-/\text{Å}^2)$	53.3	Depositor
Minimum defocus (nm)	500	Depositor
Maximum defocus (nm)	4000	Depositor
Magnification	Not provided	
Image detector	GATAN K3 BIOQUANTUM (6k x 4k)	Depositor



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: AGS, ADP, MG

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		
IVIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.32	0/2498	0.54	0/3377	
1	В	0.33	0/2498	0.55	0/3377	
1	С	0.33	0/2486	0.55	0/3359	
1	D	0.30	0/2509	0.55	0/3391	
1	Е	0.28	0/2498	0.53	0/3377	
1	F	0.29	0/2498	0.55	0/3377	
2	G	0.24	0/359	0.48	0/483	
3	U	0.69	0/351	0.92	0/540	
4	V	0.67	0/337	1.17	$2/517 \ (0.4\%)$	
All	All	0.33	0/16034	0.58	2/21798 (0.0%)	

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	F	0	2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
4	V	4	DT	OP1-P-OP2	-6.92	109.22	119.60
4	V	3	DT	OP1-P-O3'	5.87	118.12	105.20

There are no chirality outliers.

All (2) planarity outliers are listed below:



Mol	Chain	Res	Type	Group
1	F	218	ARG	Sidechain
1	F	228	ARG	Sidechain

5.2 Too-close contacts (i)

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	2455	2455	2453	6	0
1	В	2455	2455	2453	6	0
1	С	2444	2451	2448	8	0
1	D	2466	2468	2467	9	0
1	Е	2455	2455	2454	12	0
1	F	2455	2455	2453	6	0
2	G	357	362	361	2	0
3	U	312	167	168	1	0
4	V	303	171	171	2	0
5	A	31	14	12	1	0
5	В	31	14	12	0	0
5	С	31	14	12	0	0
5	D	31	14	12	0	0
5	F	31	14	12	2	0
6	A	1	0	0	0	0
6	В	1	0	0	0	0
6	С	1	0	0	0	0
6	D	1	0	0	0	0
6	F	1	0	0	0	0
7	Ε	27	12	12	0	0
All	All	15889	15521	15500	48	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 (48) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	Clash overlap (Å)
1:B:254:ASP:OD1	1:B:255:HIS:N	2.24	0.71
1:F:81:LYS:NZ	1:F:100:ASP:O	2.23	0.70

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Continued from previous		Interatomic	Clash
Atom-1	Atom-2	${\rm distance}({\rm \AA})$	$\text{overlap } (\mathring{\mathbf{A}})$
5:F:401:AGS:O2B	5:F:401:AGS:O2A	2.11	0.62
1:F:81:LYS:NZ	1:F:100:ASP:OD2	2.33	0.60
1:A:65:LYS:NZ	5:A:401:AGS:S1G	2.70	0.60
1:A:240:ASP:OD1	1:A:242:LYS:N	2.37	0.58
1:E:254:ASP:OD1	1:E:255:HIS:N	2.37	0.58
1:E:81:LYS:NZ	1:E:100:ASP:O	2.30	0.55
1:A:299:GLU:OE1	1:A:315:ARG:NH1	2.36	0.53
1:E:138:ALA:N	1:E:141:THR:OG1	2.42	0.53
1:B:212:ARG:NH1	1:B:253:VAL:O	2.43	0.52
1:D:143:ARG:NH1	2:G:162:GLU:OE2	2.42	0.50
1:F:299:GLU:OE2	1:F:315:ARG:NH1	2.39	0.50
1:D:315:ARG:NH1	3:U:10:DA:OP1	2.46	0.48
1:C:159:THR:HG22	1:C:159:THR:O	2.13	0.48
1:F:66:THR:OG1	5:F:401:AGS:O2B	2.33	0.46
1:F:241:ASP:OD1	1:F:242:LYS:N	2.48	0.46
1:A:98:LEU:HD13	1:A:132:ILE:HD11	1.97	0.45
1:E:57:LEU:O	1:E:157:ALA:HA	2.17	0.45
1:B:186:LEU:HD11	1:B:215:GLY:HA2	1.97	0.45
1:D:253:VAL:HG13	1:D:253:VAL:O	2.16	0.44
1:C:136:ILE:O	1:C:143:ARG:N	2.42	0.44
2:G:189:ALA:HB1	2:G:193:THR:OG1	2.18	0.44
1:C:311:THR:HG22	1:C:312:ARG:N	2.33	0.44
1:D:161:ALA:O	1:D:169:ARG:NH2	2.51	0.44
1:E:53:ASP:OD2	1:F:226:ARG:NH2	2.45	0.44
1:A:280:LEU:HD23	1:A:291:ARG:HE	1.82	0.43
1:B:121:GLU:OE1	1:C:114:ARG:HG3	2.17	0.43
1:B:136:ILE:O	1:B:142:SER:HA	2.17	0.43
1:A:290:GLU:OE1	1:A:293:THR:N	2.46	0.43
1:D:313:THR:HG22	1:D:313:THR:O	2.18	0.43
1:E:265:ILE:HG23	1:E:283:LEU:HD21	1.99	0.43
1:B:136:ILE:O	1:B:143:ARG:N	2.42	0.42
4:V:6:DC:H2"	4:V:7:DT:C5	2.55	0.42
1:D:129:ASP:HB3	1:D:131:TYR:CE2	2.54	0.42
1:D:172:PHE:O	1:E:222:ARG:NH2	2.47	0.42
1:E:241:ASP:OD1	1:E:242:LYS:N	2.51	0.42
1:E:305:LYS:HA	1:E:305:LYS:HE2	2.01	0.42
1:E:112:ILE:HG22	1:E:158:THR:CG2	2.50	0.42
1:C:254:ASP:OD2	1:C:324:HIS:NE2	2.50	0.42
1:D:110:ASP:OD1	1:D:111:GLU:N	2.52	0.41
1:C:78:VAL:HG12	1:C:79:ASN:N	2.35	0.41
1:D:311:THR:HG22	1:D:312:ARG:N	2.35	0.41

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Atom-1	Atom-2	$\begin{array}{c} {\rm Interatomic} \\ {\rm distance} \ ({\rm \AA}) \end{array}$	$egin{aligned} \operatorname{Clash} \ \operatorname{overlap}\ (\begin{subarray}{c} \begin{subarray}{c} \begi$
1:C:197:PHE:O	1:C:198:GLU:HG2	2.20	0.41
1:E:294:VAL:HA	1:E:298:TYR:HD2	1.86	0.41
1:C:311:THR:N	1:C:314:GLY:O	2.52	0.40
4:V:6:DC:H2"	4:V:7:DT:C7	2.52	0.40
1:E:315:ARG:N	1:E:315:ARG:CD	2.85	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 PDB entries followed by that with respect to all EM entries.

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	310/315 (98%)	308 (99%)	2 (1%)	0	100 100
1	В	310/315 (98%)	308 (99%)	2 (1%)	0	100 100
1	С	305/315 (97%)	304 (100%)	1 (0%)	0	100 100
1	D	311/315 (99%)	309 (99%)	2 (1%)	0	100 100
1	E	310/315 (98%)	306 (99%)	4 (1%)	0	100 100
1	F	310/315 (98%)	308 (99%)	2 (1%)	0	100 100
2	G	46/48 (96%)	45 (98%)	1 (2%)	0	100 100
All	All	1902/1938 (98%)	1888 (99%)	14 (1%)	0	100 100

There are no Ramachandran outliers to report.

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 PDB entries followed by that with respect to all EM entries.

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	Perce	ntiles
1	A	$261/264\ (99\%)$	261 (100%)	0	100	100
1	В	$261/264\ (99\%)$	261 (100%)	0	100	100
1	C	$261/264\ (99\%)$	260 (100%)	1 (0%)	91	95
1	D	$262/264\ (99\%)$	260 (99%)	2 (1%)	81	89
1	E	$261/264\ (99\%)$	261 (100%)	0	100	100
1	F	$261/264\ (99\%)$	261 (100%)	0	100	100
2	G	$36/36 \; (100\%)$	36 (100%)	0	100	100
All	All	1603/1620 (99%)	1600 (100%)	3 (0%)	93	97

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	С	199	MET
1	D	117	MET
1	D	327	TYR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 5 are monoatomic - leaving 6 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 I		Link	Bond lengths			Bond angles		
WIOI	туре	Chain	nes	Lilik	Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	AGS	D	401	6	26,33,33	0.72	0	26,52,52	1.21	2 (7%)
5	AGS	В	401	6	26,33,33	0.75	0	26,52,52	1.03	2 (7%)
5	AGS	F	401	6	26,33,33	0.75	0	26,52,52	1.22	2 (7%)
7	ADP	E	600	-	24,29,29	0.98	2 (8%)	29,45,45	1.48	3 (10%)
5	AGS	С	401	6	26,33,33	0.76	0	26,52,52	1.09	3 (11%)
5	AGS	A	401	6	26,33,33	0.76	0	26,52,52	0.98	2 (7%)

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	AGS	D	401	6	-	2/17/38/38	0/3/3/3
5	AGS	В	401	6	-	1/17/38/38	0/3/3/3
5	AGS	F	401	6	-	2/17/38/38	0/3/3/3
7	ADP	Е	600	-	-	1/12/32/32	0/3/3/3
5	AGS	С	401	6	-	4/17/38/38	0/3/3/3
5	AGS	A	401	6	-	0/17/38/38	0/3/3/3

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(A)	$\operatorname{Ideal}(ext{\AA})$
7	Ε	600	ADP	C5-C4	2.17	1.46	1.40
7	Е	600	ADP	O4'-C1'	2.12	1.44	1.41

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(^o)$	$\operatorname{Ideal}({}^{o})$
5	F	401	AGS	PA-O3A-PB	-5.00	115.67	132.83
5	D	401	AGS	PA-O3A-PB	-4.56	117.16	132.83
7	Е	600	ADP	PA-O3A-PB	-3.83	119.69	132.83
5	В	401	AGS	PA-O3A-PB	-3.74	119.98	132.83
5	С	401	AGS	PA-O3A-PB	-3.71	120.10	132.83
5	A	401	AGS	PA-O3A-PB	-3.49	120.84	132.83

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COHABABACA		DIEUIUU	DUIUE
0 0 1000100000			

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^{o})$
7	Е	600	ADP	N3-C2-N1	-3.47	123.25	128.68
7	Е	600	ADP	C4-C5-N7	-2.95	106.33	109.40
5	F	401	AGS	C5-C6-N6	2.27	123.81	120.35
5	A	401	AGS	C5-C6-N6	2.25	123.78	120.35
5	D	401	AGS	C5-C6-N6	2.24	123.76	120.35
5	В	401	AGS	C5-C6-N6	2.22	123.72	120.35
5	С	401	AGS	C3'-C2'-C1'	2.21	104.31	100.98
5	С	401	AGS	C5-C6-N6	2.21	123.71	120.35

There are no chirality outliers.

All (10) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	С	401	AGS	PB-O3B-PG-O2G
5	С	401	AGS	PB-O3B-PG-O3G
5	В	401	AGS	PA-O3A-PB-O2B
5	D	401	AGS	PA-O3A-PB-O1B
5	С	401	AGS	PA-O3A-PB-O2B
5	F	401	AGS	PA-O3A-PB-O1B
7	Е	600	ADP	O4'-C4'-C5'-O5'
5	D	401	AGS	PA-O3A-PB-O2B
5	F	401	AGS	PB-O3A-PA-O2A
5	С	401	AGS	C5'-O5'-PA-O1A

There are no ring outliers.

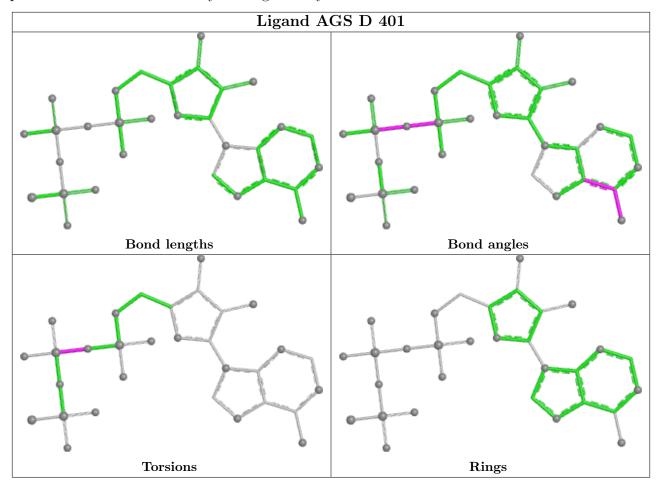
2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	F	401	AGS	2	0
5	A	401	AGS	1	0

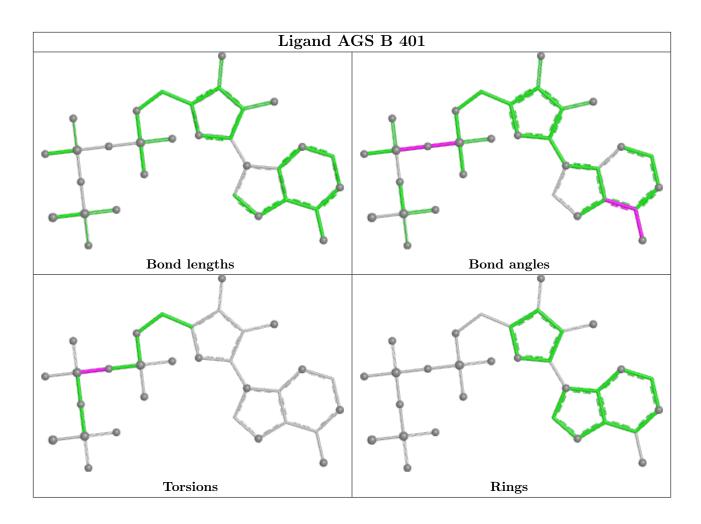
The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less 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



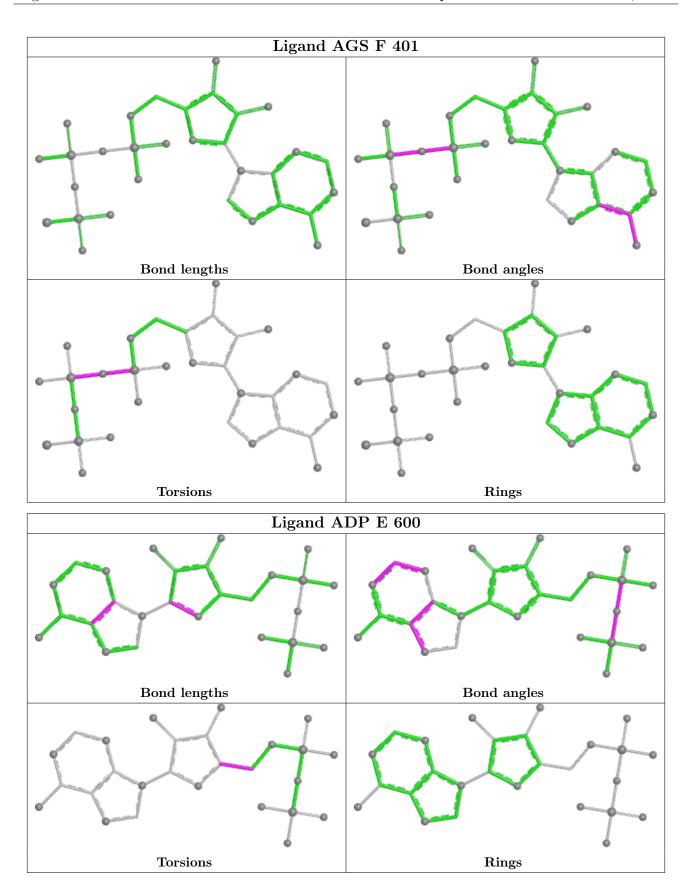
equivalents in the CSD to analyse the geometry.



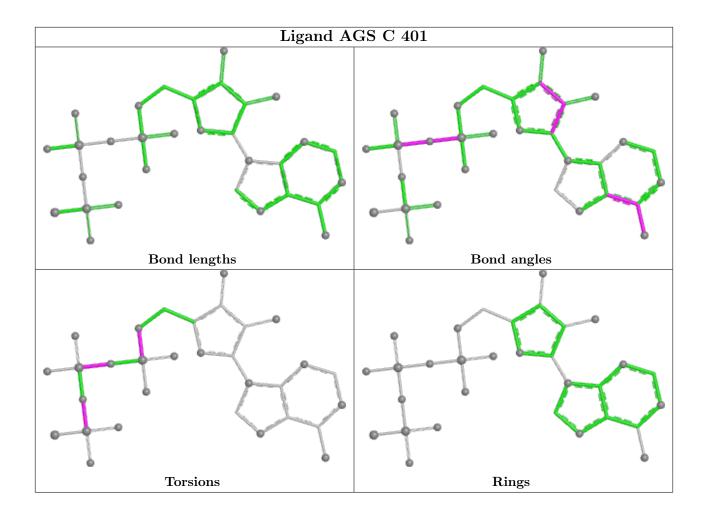




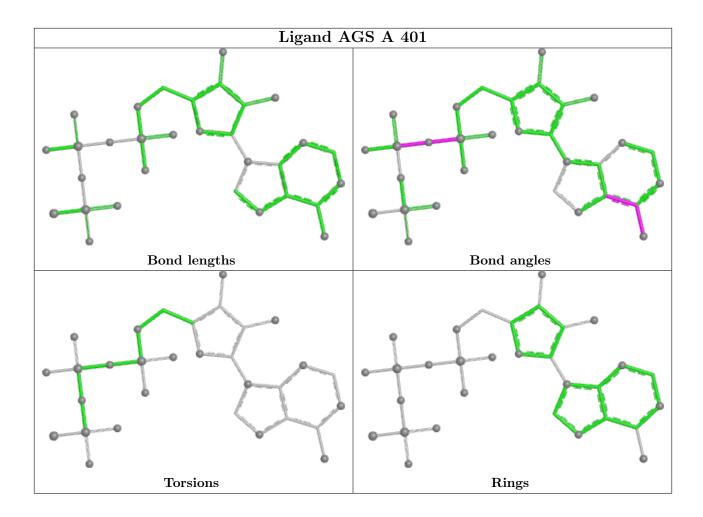












5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

There are no chain breaks in this entry.



6 Map visualisation (i)

This section contains visualisations of the EMDB entry EMD-13301. These allow visual inspection of the internal detail of the map and identification of artifacts.

No raw map or half-maps were deposited for this entry and therefore no images, graphs, etc. pertaining to the raw map can be shown.

6.1 Orthogonal projections (i)

This section was not generated.

6.2 Central slices (i)

This section was not generated.

6.3 Largest variance slices (i)

This section was not generated.

6.4 Orthogonal surface views (i)

This section was not generated.

6.5 Mask visualisation (i)

This section was not generated. No masks/segmentation were deposited.



7 Map analysis (i)

This section contains the results of statistical analysis of the map.

7.1 Map-value distribution (i)

This section was not generated.

7.2 Volume estimate versus contour level (i)

This section was not generated.

7.3 Rotationally averaged power spectrum (i)

This section was not generated. The rotationally averaged power spectrum had issues being displayed.



8 Fourier-Shell correlation (i)

This section was not generated. No FSC curve or half-maps provided.



9 Map-model fit (i)

This section was not generated.

