Full wwPDB X-ray Structure Validation Report (i)

Sep 1, 2022 – 02:15 PM EDT

PDB ID	:	5RM9
Title	:	PanDDA analysis group deposition – Crystal Structure of SARS-CoV-2 helicase in complex with Z2856434942
Authors	:	Newman, J.A.; Yosaatmadja, Y.; Douangamath, A.; Aimon, A.; Powell, A.J.; Dias, A.; Fearon, D.; Dunnett, L.; Brandao-Neto, J.; Krojer, T.; Skyner, R.; Gorrie-Stone, T.; Thompson, W.; von Delft, F.; Arrowsmith, C.H.; Edwards, A.; Bountra, C.; Gileadi, O.
Deposited on	:	2020-09-16
Resolution	:	2.08 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 (i) 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 (1)) were used in the production of this report:

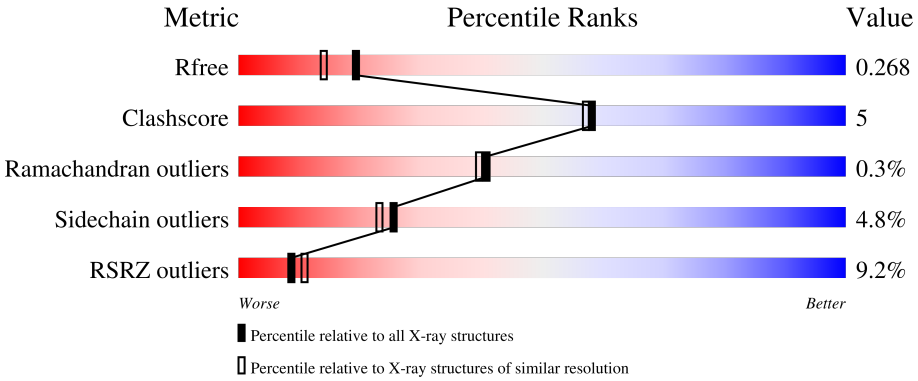
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.29
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.29

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 2.08 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	6189 (2.10-2.06)
Clashscore	141614	6738 (2.10-2.06)
Ramachandran outliers	138981	6663 (2.10-2.06)
Sidechain outliers	138945	6664 (2.10-2.06)
RSRZ outliers	127900	6057 (2.10-2.06)

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	601	15% 80% 15% • 5%
1	B	601	3% 83% 14% • •

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 9422 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.

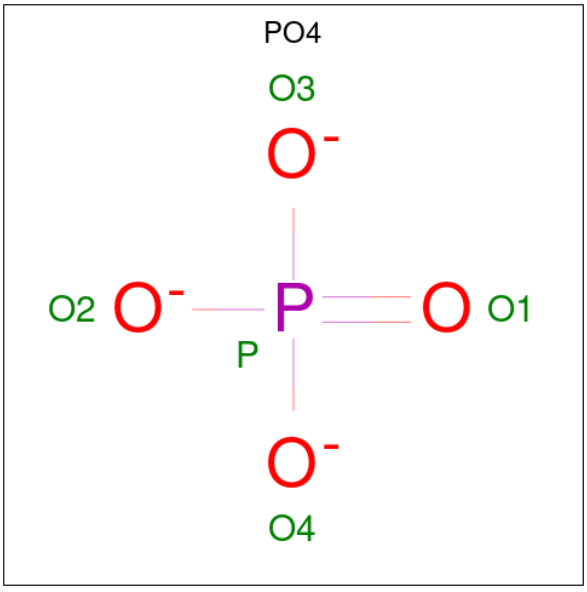
- Molecule 1 is a protein called Helicase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	572	Total	C	N	O	S	0	0	0
			4417	2816	737	832	32			
1	B	585	Total	C	N	O	S	0	1	0
			4508	2875	750	848	35			

- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

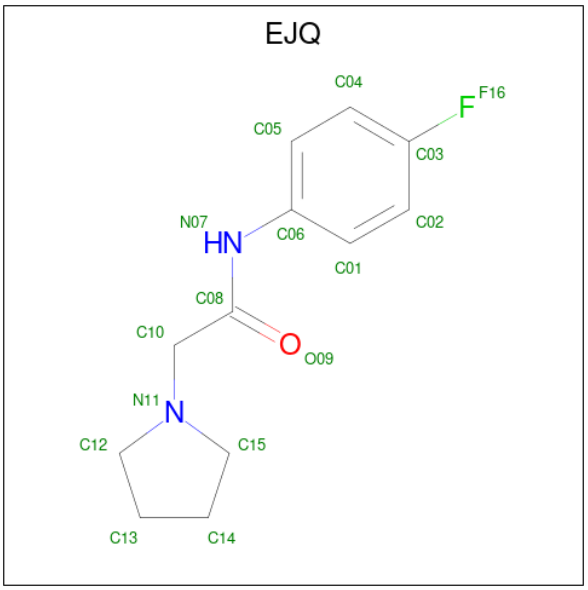
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	3	Total	Zn	0	0
			3	3		
2	B	3	Total	Zn	0	0
			3	3		

- Molecule 3 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	1	Total O P 5 4 1	0	0
3	A	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0
3	B	1	Total O P 5 4 1	0	0

- Molecule 4 is {N}-(4-fluorophenyl)-2-pyrrolidin-1-yl-ethanamide (three-letter code: EJQ) (formula: $C_{12}H_{15}FN_2O$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	B	1	Total C F N O 16 12 1 2 1	0	0

- Molecule 5 is water.

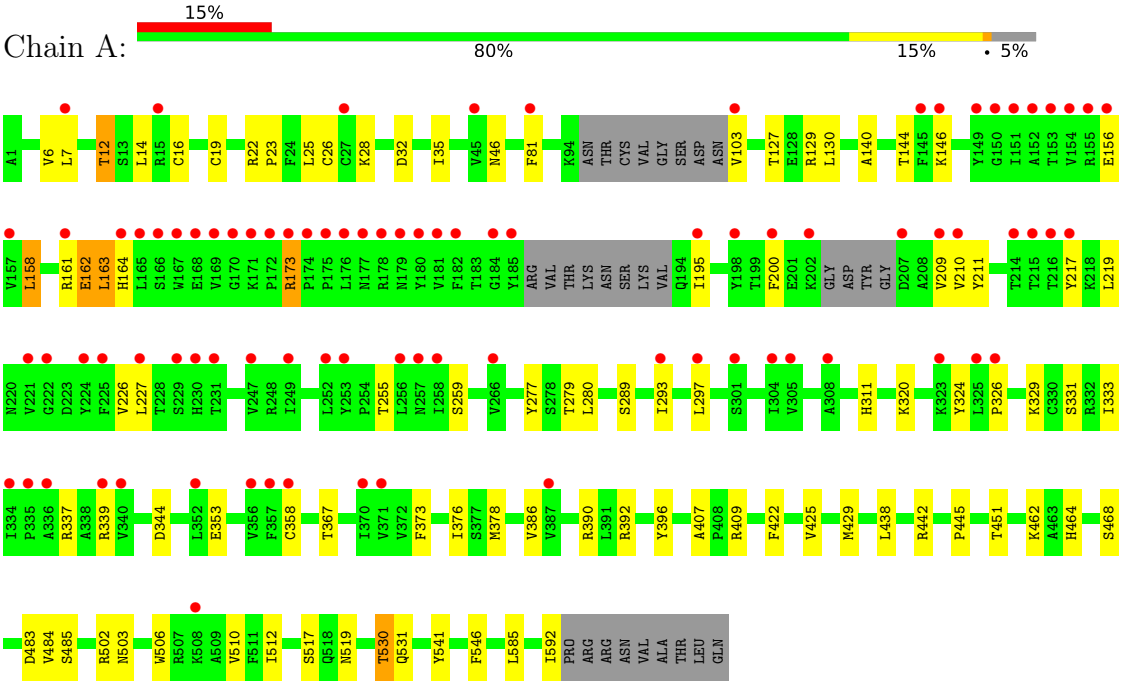
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	203	Total O 203 203	0	0
5	B	252	Total O 252 252	0	0

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.

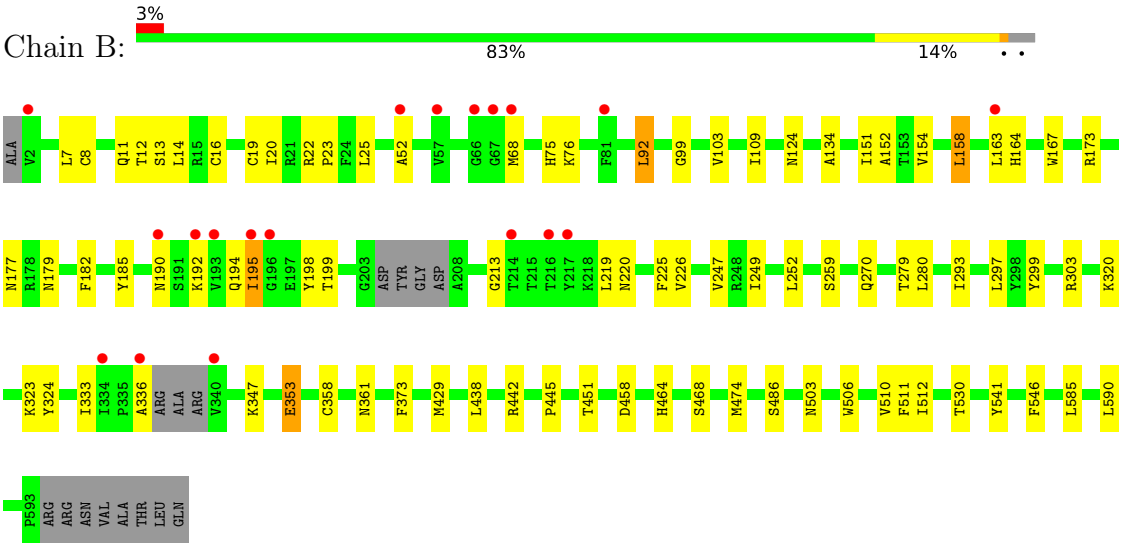
• Molecule 1: Helicase

Chain A:



• Molecule 1: Helicase

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α, β, γ	59.09Å 70.01Å 85.78Å 102.72° 96.48° 112.21°	Depositor
Resolution (Å)	62.11 – 2.08 62.11 – 2.08	Depositor EDS
% Data completeness (in resolution range)	96.1 (62.11-2.08) 96.0 (62.11-2.08)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	1.06 (at 2.08Å)	Xtriage
Refinement program	BUSTER 2.10.3 (20-MAY-2020)	Depositor
R, R_{free}	0.167 , 0.254 0.186 , 0.268	Depositor DCC
R_{free} test set	3610 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å^2)	44.8	Xtriage
Anisotropy	0.384	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.31 , 59.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	9422	wwPDB-VP
Average B, all atoms (Å^2)	79.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.87% 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: ZN, EJQ, PO4

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	0.52	0/4517	0.64	0/6156
1	B	0.54	0/4610	0.65	0/6283
All	All	0.53	0/9127	0.65	0/12439

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	4417	0	4321	47	0
1	B	4508	0	4425	39	0
2	A	3	0	0	0	0
2	B	3	0	0	0	0
3	A	10	0	0	0	0
3	B	10	0	0	0	0
4	B	16	0	0	0	0
5	A	203	0	0	1	0
5	B	252	0	0	0	0
All	All	9422	0	8746	85	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 5.

All (85) 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:331:SER:HB2	1:A:353:GLU:HG3	1.58	0.86
1:B:12:THR:HG22	1:B:14:LEU:H	1.40	0.84
1:B:12:THR:HG21	1:B:25:LEU:O	1.82	0.80
1:A:146:LYS:HE2	1:A:227:LEU:HB3	1.80	0.64
1:A:163:LEU:HG	1:A:211:TYR:HB3	1.79	0.62
1:A:163:LEU:HD11	1:A:200:PHE:HE2	1.67	0.59
1:B:13:SER:HB2	1:B:92:LEU:HB2	1.84	0.58
1:A:326:PRO:HG2	1:A:329:LYS:NZ	2.17	0.58
1:B:510:VAL:HG21	1:B:541:TYR:CD1	2.40	0.57
1:B:279:THR:HB	1:B:429:MET:CE	2.36	0.56
1:A:326:PRO:HG2	1:A:329:LYS:HZ1	1.71	0.55
1:A:140:ALA:O	1:A:144:THR:HG23	2.06	0.54
1:A:279:THR:HB	1:A:429:MET:CE	2.38	0.53
1:A:510:VAL:HG21	1:A:541:TYR:CD1	2.42	0.53
1:B:279:THR:HB	1:B:429:MET:HE3	1.89	0.53
1:A:445:PRO:HB3	1:A:468:SER:HB3	1.90	0.53
1:B:151:ILE:HG12	1:B:226:VAL:HG22	1.92	0.52
1:B:167:TRP:CD1	1:B:173:ARG:NH1	2.77	0.52
1:B:445:PRO:HB3	1:B:468:SER:HB3	1.90	0.52
1:B:7:LEU:HD13	1:B:103:VAL:HG22	1.93	0.51
1:A:6:VAL:HA	1:A:129:ARG:HD2	1.94	0.50
1:A:297:LEU:HD11	1:A:324:TYR:HB3	1.93	0.50
1:A:326:PRO:CG	1:A:329:LYS:NZ	2.74	0.50
1:B:8:CYS:SG	1:B:99:GLY:O	2.70	0.50
1:B:511:PHE:HB3	1:B:530:THR:HG22	1.95	0.49
1:B:451:THR:HG21	1:B:585:LEU:HD23	1.95	0.49
1:A:280:LEU:HD11	1:A:438:LEU:HG	1.94	0.49
1:A:293:ILE:HG13	1:A:320:LYS:HB3	1.94	0.49
1:A:28:LYS:O	1:A:32:ASP:OD2	2.30	0.48
1:B:16:CYS:O	1:B:22:ARG:HA	2.12	0.48
1:A:158:LEU:HD11	1:A:164:HIS:CE1	2.49	0.48
1:A:158:LEU:HD21	1:A:164:HIS:CE1	2.49	0.47
1:A:451:THR:HG21	1:A:585:LEU:HD23	1.96	0.47
1:B:297:LEU:HD11	1:B:324:TYR:HB3	1.95	0.47
1:B:182:PHE:HB3	1:B:225:PHE:HB3	1.95	0.47
1:A:279:THR:HB	1:A:429:MET:HE3	1.97	0.47
1:B:474[B]:MET:HG2	1:B:590:LEU:HB2	1.95	0.47
1:A:512:ILE:O	1:A:546:PHE:HA	2.15	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:154:VAL:HG13	1:B:163:LEU:HD22	1.97	0.47
1:B:195:ILE:HG23	1:B:195:ILE:O	2.14	0.47
1:B:198:TYR:HA	1:B:213:GLY:HA2	1.97	0.46
1:B:320:LYS:HE3	1:B:323:LYS:NZ	2.29	0.46
1:A:14:LEU:HB2	1:A:25:LEU:O	2.15	0.46
1:A:333:ILE:HB	1:A:358:CYS:HB2	1.98	0.46
1:B:333:ILE:HB	1:B:358:CYS:HB2	1.97	0.46
1:B:185:TYR:CE2	1:B:194:GLN:HG2	2.50	0.46
1:A:311:HIS:HE2	1:A:339:ARG:NH2	2.14	0.46
1:A:503:ASN:HB3	1:A:506:TRP:CD1	2.51	0.45
1:B:442:ARG:HA	1:B:464:HIS:HB3	1.98	0.45
1:A:442:ARG:HA	1:A:464:HIS:HB3	1.98	0.45
1:B:512:ILE:O	1:B:546:PHE:HA	2.16	0.45
1:B:293:ILE:HG13	1:B:320:LYS:HB3	1.97	0.45
1:A:16:CYS:O	1:A:22:ARG:HA	2.16	0.45
1:A:311:HIS:HE2	1:A:339:ARG:HH21	1.64	0.45
1:B:154:VAL:HG22	1:B:163:LEU:HD13	1.98	0.44
1:A:519:ASN:HB3	1:A:530:THR:CG2	2.48	0.44
1:A:462:LYS:HA	1:A:462:LYS:HD3	1.87	0.44
1:B:109:ILE:HD13	1:B:134:ALA:HB2	1.99	0.44
1:B:252:LEU:HB3	1:B:299:TYR:CD1	2.53	0.44
1:B:158:LEU:CD1	1:B:164:HIS:ND1	2.81	0.44
1:B:280:LEU:HD11	1:B:438:LEU:HG	2.00	0.43
1:A:462:LYS:NZ	5:A:811:HOH:O	2.52	0.43
1:A:279:THR:HB	1:A:429:MET:HE2	2.01	0.43
1:A:386:VAL:HG13	1:A:390:ARG:HE	1.84	0.43
1:B:303:ARG:NH1	1:B:353:GLU:O	2.53	0.42
1:B:503:ASN:HB3	1:B:506:TRP:CD1	2.54	0.42
1:A:158:LEU:HD12	1:A:162:GLU:HB3	2.02	0.42
1:A:19:CYS:CB	1:A:23:PRO:HD2	2.50	0.42
1:A:161:ARG:O	1:A:210:VAL:HG13	2.20	0.42
1:A:337:ARG:NH1	1:B:336:ALA:O	2.53	0.41
1:A:163:LEU:HD11	1:A:200:PHE:CE2	2.52	0.41
1:A:277:TYR:HA	1:A:396:TYR:O	2.19	0.41
1:B:474[B]:MET:CG	1:B:590:LEU:HB2	2.50	0.41
1:A:409:ARG:NH2	1:A:422:PHE:O	2.51	0.41
1:A:7:LEU:HD13	1:A:103:VAL:HG22	2.02	0.41
1:A:12:THR:HG21	1:A:26:CYS:HA	2.03	0.41
1:A:173:ARG:H	1:A:173:ARG:NH1	2.19	0.41
1:A:376:ILE:HG12	1:A:425:VAL:HG11	2.02	0.41
1:A:378:MET:O	1:A:407:ALA:HB2	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:152:ALA:HB2	1:B:167:TRP:CZ3	2.56	0.41
1:A:127:THR:HG23	1:A:130:LEU:H	1.86	0.41
1:B:52:ALA:CB	1:B:75:HIS:CG	3.04	0.40
1:B:19:CYS:CB	1:B:23:PRO:HD2	2.50	0.40
1:A:367:THR:HG22	1:A:392:ARG:HB3	2.02	0.40
1:B:249:ILE:HD11	1:B:270:GLN:HG2	2.02	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	564/601 (94%)	541 (96%)	20 (4%)	3 (0%)	29 25
1	B	580/601 (96%)	556 (96%)	24 (4%)	0	100 100
All	All	1144/1202 (95%)	1097 (96%)	44 (4%)	3 (0%)	41 39

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	195	ILE
1	A	219	LEU
1	A	484	VAL

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	485/523 (93%)	461 (95%)	24 (5%)	25 22
1	B	498/523 (95%)	475 (95%)	23 (5%)	27 25
All	All	983/1046 (94%)	936 (95%)	47 (5%)	25 23

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	12	THR
1	A	35	ILE
1	A	46	ASN
1	A	81	PHE
1	A	156	GLU
1	A	158	LEU
1	A	162	GLU
1	A	163	LEU
1	A	173	ARG
1	A	209	VAL
1	A	217	TYR
1	A	226	VAL
1	A	255	THR
1	A	259	SER
1	A	289	SER
1	A	344	ASP
1	A	373	PHE
1	A	483	ASP
1	A	485	SER
1	A	502	ARG
1	A	517	SER
1	A	530	THR
1	A	531	GLN
1	A	592	ILE
1	B	11	GLN
1	B	20	ILE
1	B	68	MET
1	B	76	LYS
1	B	92	LEU
1	B	124	ASN
1	B	158	LEU
1	B	177	ASN
1	B	179	ASN
1	B	190	ASN
1	B	192	LYS

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Mol	Chain	Res	Type
1	B	195	ILE
1	B	199	THR
1	B	219	LEU
1	B	220	ASN
1	B	247	VAL
1	B	259	SER
1	B	347	LYS
1	B	353	GLU
1	B	361	ASN
1	B	373	PHE
1	B	458	ASP
1	B	486	SER

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	164	HIS
1	A	179	ASN
1	A	245	HIS
1	B	179	ASN
1	B	268	ASN
1	B	404	GLN
1	B	464	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 11 ligands modelled in this entry, 6 are monoatomic - leaving 5 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	PO4	A	704	-	4,4,4	1.88	0	6,6,6	0.59	0
4	EJQ	B	701	-	17,17,17	0.30	0	22,22,22	0.73	1 (4%)
3	PO4	A	705	-	4,4,4	2.47	1 (25%)	6,6,6	0.67	0
3	PO4	B	706	-	4,4,4	2.40	1 (25%)	6,6,6	0.71	0
3	PO4	B	705	-	4,4,4	2.44	1 (25%)	6,6,6	0.76	0

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
4	EJQ	B	701	-	-	2/8/15/15	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	B	705	PO4	P-O1	4.10	1.60	1.50
3	B	706	PO4	P-O1	4.09	1.60	1.50
3	A	705	PO4	P-O1	4.07	1.60	1.50

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	B	701	EJQ	C12-N11-C15	-2.55	101.56	104.04

There are no chirality outliers.

All (2) torsion outliers are listed below:

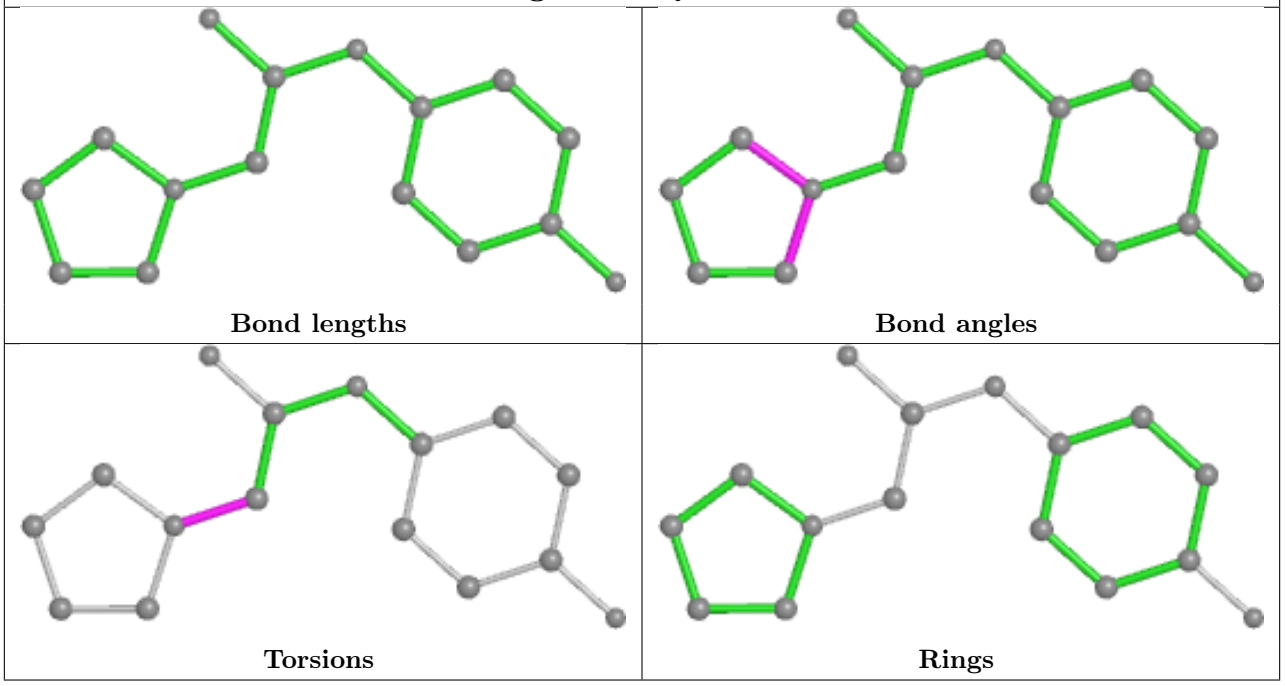
Mol	Chain	Res	Type	Atoms
4	B	701	EJQ	C08-C10-N11-C15
4	B	701	EJQ	C08-C10-N11-C12

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 EJQ B 701



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	572/601 (95%)	0.77	88 (15%) 2 2	41, 84, 160, 191	0
1	B	585/601 (97%)	0.17	19 (3%) 47 53	40, 62, 123, 154	0
All	All	1157/1202 (96%)	0.47	107 (9%) 9 11	40, 73, 150, 191	0

All (107) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	170	GLY	16.0
1	A	152	ALA	10.1
1	A	202	LYS	10.0
1	A	154	VAL	9.7
1	A	225	PHE	9.4
1	A	167	TRP	9.1
1	B	196	GLY	8.5
1	A	181	VAL	7.9
1	A	229	SER	7.6
1	A	169	VAL	7.6
1	A	149	TYR	7.1
1	A	176	LEU	6.9
1	B	217	TYR	6.8
1	B	340	VAL	6.8
1	A	224	TYR	6.6
1	A	165	LEU	6.5
1	A	247	VAL	6.2
1	A	214	THR	5.8
1	A	178	ARG	5.8
1	A	146	LYS	5.6
1	A	215	THR	5.5
1	A	340	VAL	5.2
1	A	210	VAL	4.9
1	A	166	SER	4.9

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Mol	Chain	Res	Type	RSRZ
1	A	151	ILE	4.9
1	A	195	ILE	4.9
1	A	249	ILE	4.9
1	A	182	PHE	4.7
1	B	193	VAL	4.7
1	B	57	VAL	4.6
1	A	304	ILE	4.6
1	A	103	VAL	4.5
1	A	339	ARG	4.5
1	A	230	HIS	4.4
1	A	252	LEU	4.3
1	A	305	VAL	4.3
1	A	27	CYS	4.3
1	A	184	GLY	4.2
1	B	52	ALA	4.2
1	A	200	PHE	4.0
1	A	256	LEU	3.8
1	A	352	LEU	3.7
1	B	81	PHE	3.6
1	A	180	TYR	3.6
1	B	216	THR	3.5
1	B	66	GLY	3.5
1	A	150	GLY	3.5
1	A	172	PRO	3.4
1	A	257	ASN	3.3
1	A	357	PHE	3.3
1	B	214	THR	3.2
1	A	207	ASP	3.2
1	A	155	ARG	3.2
1	A	253	TYR	3.1
1	A	387	VAL	3.1
1	A	168	GLU	3.1
1	A	185	TYR	3.1
1	A	161	ARG	3.0
1	B	336	ALA	2.9
1	A	334	ILE	2.9
1	A	221	VAL	2.8
1	A	179	ASN	2.8
1	B	190	ASN	2.7
1	A	156	GLU	2.7
1	B	2	VAL	2.7
1	A	217	TYR	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	164	HIS	2.7
1	A	370	ILE	2.7
1	A	198	TYR	2.6
1	A	145	PHE	2.6
1	B	68	MET	2.6
1	A	356	VAL	2.6
1	A	258	ILE	2.5
1	A	336	ALA	2.5
1	A	266	VAL	2.5
1	A	508	LYS	2.5
1	A	371	VAL	2.4
1	A	323	LYS	2.4
1	A	177	ASN	2.4
1	B	195	ILE	2.4
1	A	171	LYS	2.3
1	A	174	PRO	2.3
1	A	222	GLY	2.3
1	A	7	LEU	2.3
1	A	81	PHE	2.3
1	A	173	ARG	2.3
1	A	297	LEU	2.3
1	A	231	THR	2.3
1	A	335	PRO	2.3
1	A	308	ALA	2.2
1	A	227	LEU	2.2
1	A	326	PRO	2.2
1	A	209	VAL	2.2
1	A	216	THR	2.1
1	A	358	CYS	2.1
1	A	15	ARG	2.1
1	A	301	SER	2.1
1	A	153	THR	2.1
1	B	334	ILE	2.1
1	A	45	VAL	2.1
1	B	163	LEU	2.1
1	A	175	PRO	2.1
1	A	157	VAL	2.0
1	B	67	GLY	2.0
1	B	192	LYS	2.0
1	A	293	ILE	2.0
1	A	325	LEU	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)

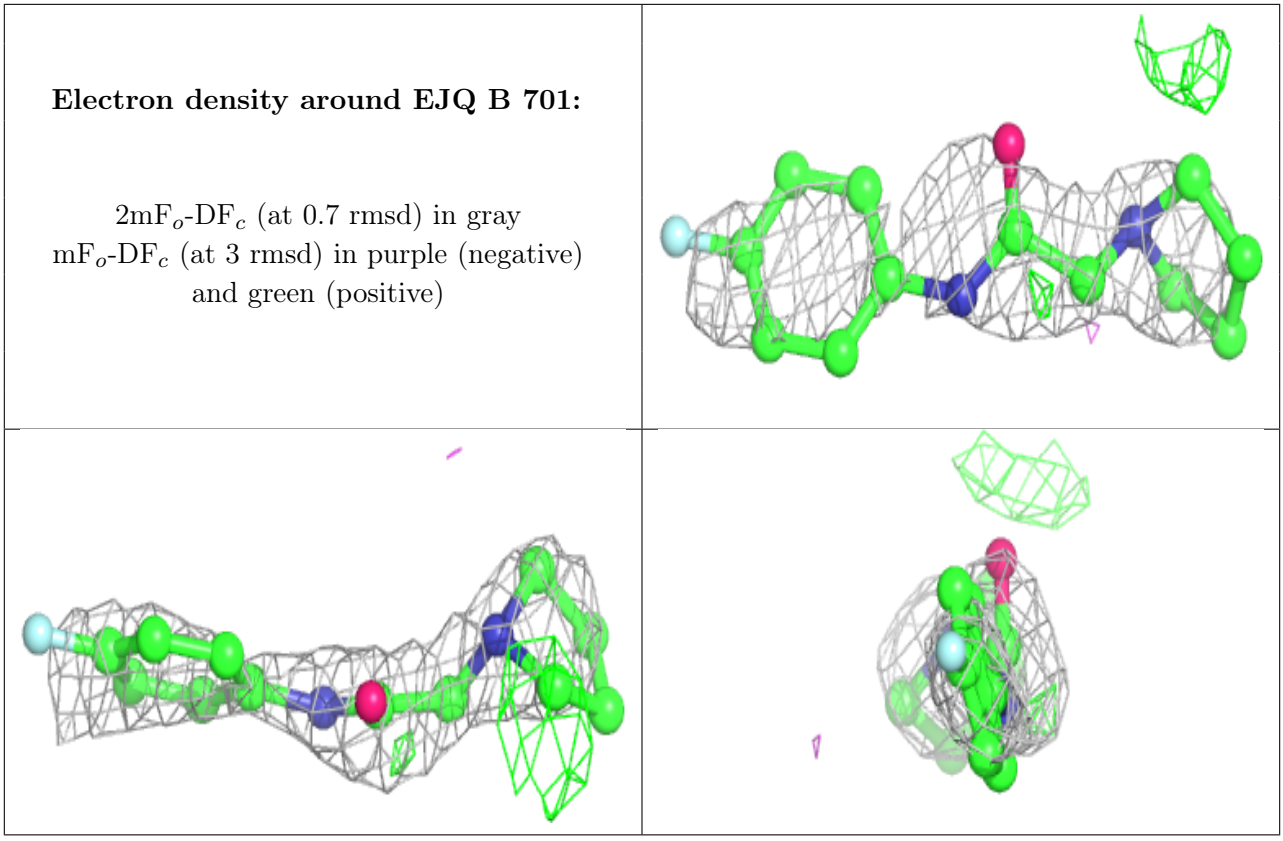
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' 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
4	EJQ	B	701	16/16	0.85	0.37	60,63,66,66	16
2	ZN	B	704	1/1	0.97	0.09	99,99,99,99	0
3	PO4	B	705	5/5	0.98	0.17	56,57,59,62	0
2	ZN	A	702	1/1	0.99	0.10	73,73,73,73	0
3	PO4	A	704	5/5	0.99	0.14	71,73,79,80	0
3	PO4	A	705	5/5	0.99	0.12	67,67,74,75	0
2	ZN	A	703	1/1	0.99	0.07	126,126,126,126	0
3	PO4	B	706	5/5	0.99	0.14	52,55,57,59	0
2	ZN	B	703	1/1	0.99	0.16	87,87,87,87	0
2	ZN	B	702	1/1	1.00	0.14	61,61,61,61	0
2	ZN	A	701	1/1	1.00	0.14	78,78,78,78	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 EJQ B 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.