



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:24 AM UTC

PDB ID : 5ZI1 / pdb_00005zi1
Title : Crystal structure of Bacillus thuringiensis insecticidal crystal protein Cry7Ca1 (wild type)
Authors : Jing, X.; Gao, M.; Gong, P.
Deposited on : 2018-03-14
Resolution : 2.30 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

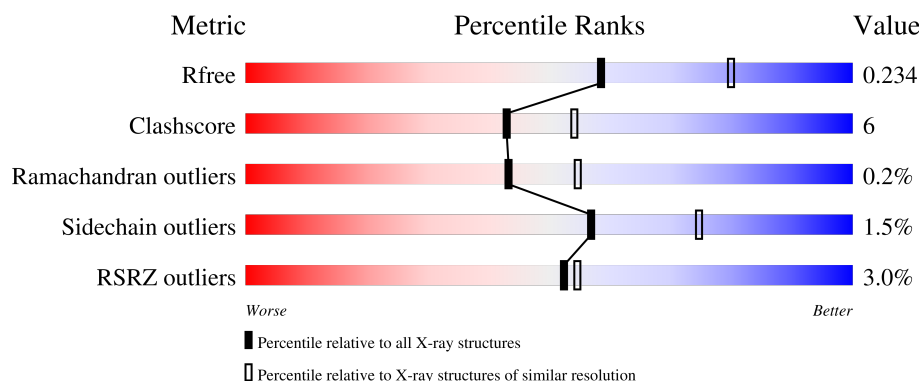
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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 (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	609	2% 87% 10% .
1	B	609	4% 80% 16% ..

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	ACT	A	701	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10151 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 insecticidal crystal protein Cry7Cal.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	590	Total	C	N	O	S	0	3	0
			4704	3023	766	899	16			
1	B	590	Total	C	N	O	S	0	1	0
			4690	3016	766	892	16			

There are 44 discrepancies between the modelled and reference sequences:

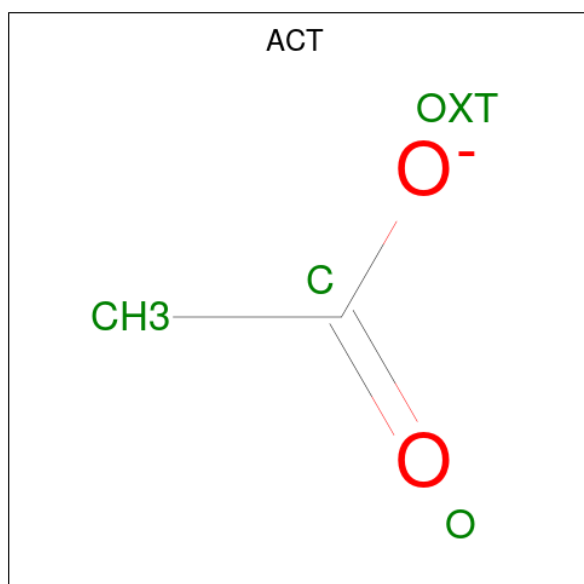
Chain	Residue	Modelled	Actual	Comment	Reference
A	42	MET	-	initiating methionine	UNP A9Q1Y3
A	43	ARG	-	expression tag	UNP A9Q1Y3
A	44	GLY	-	expression tag	UNP A9Q1Y3
A	45	SER	-	expression tag	UNP A9Q1Y3
A	46	HIS	-	expression tag	UNP A9Q1Y3
A	47	HIS	-	expression tag	UNP A9Q1Y3
A	48	HIS	-	expression tag	UNP A9Q1Y3
A	49	HIS	-	expression tag	UNP A9Q1Y3
A	50	HIS	-	expression tag	UNP A9Q1Y3
A	51	HIS	-	expression tag	UNP A9Q1Y3
A	52	GLY	-	expression tag	UNP A9Q1Y3
A	53	SER	-	expression tag	UNP A9Q1Y3
A	54	MET	-	expression tag	UNP A9Q1Y3
A	642	VAL	-	expression tag	UNP A9Q1Y3
A	643	ASP	-	expression tag	UNP A9Q1Y3
A	644	LEU	-	expression tag	UNP A9Q1Y3
A	645	GLN	-	expression tag	UNP A9Q1Y3
A	646	PRO	-	expression tag	UNP A9Q1Y3
A	647	SER	-	expression tag	UNP A9Q1Y3
A	648	LEU	-	expression tag	UNP A9Q1Y3
A	649	ILE	-	expression tag	UNP A9Q1Y3
A	650	SER	-	expression tag	UNP A9Q1Y3
B	42	MET	-	initiating methionine	UNP A9Q1Y3
B	43	ARG	-	expression tag	UNP A9Q1Y3
B	44	GLY	-	expression tag	UNP A9Q1Y3

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Chain	Residue	Modelled	Actual	Comment	Reference
B	45	SER	-	expression tag	UNP A9Q1Y3
B	46	HIS	-	expression tag	UNP A9Q1Y3
B	47	HIS	-	expression tag	UNP A9Q1Y3
B	48	HIS	-	expression tag	UNP A9Q1Y3
B	49	HIS	-	expression tag	UNP A9Q1Y3
B	50	HIS	-	expression tag	UNP A9Q1Y3
B	51	HIS	-	expression tag	UNP A9Q1Y3
B	52	GLY	-	expression tag	UNP A9Q1Y3
B	53	SER	-	expression tag	UNP A9Q1Y3
B	54	MET	-	expression tag	UNP A9Q1Y3
B	642	VAL	-	expression tag	UNP A9Q1Y3
B	643	ASP	-	expression tag	UNP A9Q1Y3
B	644	LEU	-	expression tag	UNP A9Q1Y3
B	645	GLN	-	expression tag	UNP A9Q1Y3
B	646	PRO	-	expression tag	UNP A9Q1Y3
B	647	SER	-	expression tag	UNP A9Q1Y3
B	648	LEU	-	expression tag	UNP A9Q1Y3
B	649	ILE	-	expression tag	UNP A9Q1Y3
B	650	SER	-	expression tag	UNP A9Q1Y3

- Molecule 2 is ACETATE ION (CCD ID: ACT) (formula: $C_2H_3O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	412	Total 412	O 412	0	0
3	B	341	Total 341	O 341	0	0

- Molecule 1: insecticidal crystal protein Cry7Cal



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	126.26Å 235.96Å 69.03Å 90.00° 116.53° 90.00°	Depositor
Resolution (Å)	40.80 – 2.30 40.80 – 2.30	Depositor EDS
% Data completeness (in resolution range)	99.3 (40.80-2.30) 99.4 (40.80-2.30)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.25 (at 2.29Å)	Xtriage
Refinement program	PHENIX 1.10_2155: ???	Depositor
R, R_{free}	0.189 , 0.233 0.192 , 0.234	Depositor DCC
R_{free} test set	3975 reflections (4.98%)	wwPDB-VP
Wilson B-factor (Å ²)	47.5	Xtriage
Anisotropy	0.652	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 45.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	10151	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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: 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	0.35	0/4826	0.53	0/6557
1	B	0.35	0/4806	0.53	0/6529
All	All	0.35	0/9632	0.53	0/13086

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	4704	0	4612	43	0
1	B	4690	0	4605	77	0
2	A	4	0	3	3	0
3	A	412	0	0	5	0
3	B	341	0	0	11	0
All	All	10151	0	9220	116	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 6.

All (116) 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:156[A]:GLU:HG3	1:B:152:LEU:HD21	1.52	0.90
1:A:588:PHE:HB3	1:A:603:LEU:HD12	1.58	0.84
1:B:482:GLU:HG3	1:B:483:THR:HG23	1.65	0.79
1:B:481:LYS:NZ	1:B:486:GLY:O	2.21	0.73
1:B:549:GLN:NE2	3:B:702:HOH:O	2.21	0.70
1:A:152:LEU:O	1:A:156[A]:GLU:HG2	1.91	0.70
1:B:367:LYS:NZ	1:B:556:SER:OG	2.23	0.70
1:B:82:THR:HG22	1:B:86:ARG:HH11	1.56	0.69
1:B:150:LYS:NZ	3:B:706:HOH:O	2.25	0.69
1:A:616:LEU:HG	1:A:618:MET:HE1	1.75	0.68
1:A:588:PHE:HB3	1:A:603:LEU:CD1	2.27	0.65
1:A:530:SER:H	2:A:701:ACT:H3	1.62	0.64
1:A:506:PRO:HD3	1:A:561:GLN:HE22	1.64	0.63
1:A:519:GLU:HB3	1:A:552:ARG:HG3	1.82	0.62
1:A:308:LYS:HE3	1:A:405:ASN:HD21	1.65	0.62
1:B:562:LYS:HB3	1:B:641:VAL:CG2	2.30	0.62
1:A:209:GLN:NE2	3:A:804:HOH:O	2.33	0.61
1:A:391:LEU:O	1:A:392:SER:OG	2.22	0.57
1:B:152:LEU:O	1:B:156[B]:GLU:HG3	2.04	0.57
1:B:82:THR:O	1:B:86:ARG:HG3	2.05	0.56
1:B:562:LYS:HB3	1:B:641:VAL:HG22	1.87	0.56
1:A:529:ASP:HA	2:A:701:ACT:H3	1.88	0.55
1:B:140:ALA:HB1	1:B:150:LYS:HE3	1.88	0.55
1:A:156[A]:GLU:CG	1:B:152:LEU:HD21	2.31	0.55
1:B:338:THR:O	1:B:339:LYS:HD2	2.07	0.55
1:A:63:ARG:NH1	3:A:810:HOH:O	2.39	0.54
1:B:426:ASN:OD1	1:B:462:ILE:HA	2.07	0.54
1:B:562:LYS:HE2	1:B:641:VAL:CG2	2.38	0.54
1:B:337:LEU:HD21	1:B:340:ILE:HD11	1.90	0.54
1:B:218:ASN:ND2	3:B:703:HOH:O	2.22	0.54
1:B:511:GLN:HG3	1:B:637:GLU:HG2	1.90	0.54
1:B:482:GLU:OE1	3:B:701:HOH:O	2.19	0.53
1:B:128:ARG:NH2	1:B:132:GLU:OE2	2.41	0.53
1:B:428:LEU:HD21	1:B:461:PRO:HG2	1.89	0.53
1:A:545:LEU:O	1:A:623:LYS:HE3	2.09	0.53
1:A:144:ASN:HD22	1:A:150:LYS:NZ	2.07	0.53
1:B:112:ILE:HD11	1:B:180:PRO:HB2	1.90	0.52
1:B:588:PHE:HB3	1:B:603:LEU:HG	1.92	0.52
1:B:91:ASN:O	1:B:93:GLN:HG2	2.10	0.52
1:B:396:TYR:CE1	1:B:457:LEU:HD21	2.45	0.52
1:A:159:VAL:HG21	1:B:159:VAL:HG21	1.93	0.51
1:B:249:LYS:HD2	1:B:320:PHE:HB2	1.92	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:562:LYS:HE2	1:B:641:VAL:HG21	1.93	0.51
1:B:89:TRP:CE2	1:B:128:ARG:HB2	2.46	0.50
1:B:75:GLY:C	1:B:77:ILE:H	2.18	0.50
1:B:407:SER:OG	1:B:408:ALA:N	2.44	0.50
1:A:68:PHE:CD2	1:A:80:LEU:HD22	2.47	0.50
1:B:482:GLU:CG	1:B:483:THR:HG23	2.39	0.50
1:B:395:ILE:HB	1:B:473:LEU:HB3	1.94	0.49
1:B:111:GLU:HG3	1:B:112:ILE:H	1.78	0.49
1:B:621:ILE:HD12	1:B:631:ILE:HD13	1.94	0.49
1:B:483:THR:O	1:B:483:THR:OG1	2.31	0.49
1:B:403:ALA:HB1	1:B:439:ILE:HD12	1.94	0.49
1:B:330:LYS:HE2	3:B:883:HOH:O	2.12	0.48
1:A:81:PHE:HB3	1:A:135:THR:HG21	1.95	0.48
1:A:423:ASN:OD1	1:A:427:VAL:HG22	2.13	0.48
1:A:398:THR:HG22	1:A:419:LEU:HD22	1.96	0.48
1:A:330:LYS:NZ	3:A:827:HOH:O	2.47	0.47
1:B:457:LEU:HD12	1:B:468:GLU:HB3	1.95	0.47
1:A:317:SER:HA	1:A:482:GLU:HB2	1.96	0.47
1:A:208:MET:HE1	1:A:216:PHE:HD2	1.80	0.47
1:B:111:GLU:HG3	1:B:112:ILE:N	2.30	0.47
1:B:518:PHE:CZ	1:B:552:ARG:HD3	2.50	0.47
1:A:80:LEU:HD23	1:A:194:PHE:CZ	2.50	0.47
1:B:86:ARG:NH2	3:B:732:HOH:O	2.48	0.46
1:B:220:GLN:O	1:B:224:VAL:HG23	2.15	0.46
1:B:70:GLY:O	1:B:508:LYS:HE3	2.17	0.46
1:B:208:MET:HE3	1:B:212:GLU:HG2	1.98	0.46
1:A:156[A]:GLU:HG2	1:A:156[A]:GLU:H	1.59	0.45
1:B:89:TRP:CG	1:B:128:ARG:HD3	2.51	0.45
1:A:356:TRP:HB2	1:A:487:THR:HB	1.98	0.45
1:B:291:THR:OG1	1:B:535:GLY:HA3	2.17	0.45
1:B:572:THR:OG1	1:B:629:CYS:HB2	2.16	0.45
1:B:153:LEU:O	1:B:157:ARG:HG2	2.18	0.44
1:B:338:THR:C	1:B:339:LYS:HD2	2.42	0.44
1:B:482:GLU:HG3	1:B:483:THR:CG2	2.43	0.44
1:B:358:GLY:HA2	3:B:824:HOH:O	2.17	0.44
1:A:307:THR:HG23	3:A:1039:HOH:O	2.17	0.44
1:B:481:LYS:NZ	1:B:486:GLY:C	2.76	0.44
1:A:89:TRP:CE2	1:A:128:ARG:HB2	2.52	0.43
1:B:147:ASP:HB3	1:B:150:LYS:HB2	1.99	0.43
1:A:144:ASN:HD22	1:A:150:LYS:HZ2	1.66	0.43
1:B:423:ASN:O	1:B:463:TYR:HB2	2.19	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:243:LYS:NZ	3:B:738:HOH:O	2.50	0.43
1:A:152:LEU:HB3	1:B:152:LEU:HD11	2.00	0.43
1:A:249:LYS:NZ	3:A:842:HOH:O	2.51	0.43
1:A:290:LEU:HD12	1:A:495:HIS:CE1	2.54	0.43
1:A:388:PHE:HB3	1:A:390:LEU:HD21	2.00	0.42
1:B:200:GLU:HG2	1:B:279:ALA:HB3	2.01	0.42
1:B:239:LEU:HD12	1:B:239:LEU:HA	1.92	0.42
1:B:335:GLN:NE2	3:B:743:HOH:O	2.52	0.42
1:B:239:LEU:HD13	1:B:259:PHE:HD2	1.84	0.42
1:A:506:PRO:HD3	1:A:561:GLN:NE2	2.34	0.42
1:B:543:ASN:HB3	1:B:628:ASN:OD1	2.19	0.42
1:B:71:HIS:HD2	3:B:1011:HOH:O	2.02	0.42
1:B:239:LEU:HG	1:B:256:TYR:CE1	2.55	0.42
1:B:343:ARG:HG2	1:B:385:SER:HB2	2.02	0.42
1:A:94[B]:ASN:HB2	1:A:121:LEU:HD22	2.02	0.41
1:A:68:PHE:CD2	1:A:68:PHE:O	2.73	0.41
1:A:81:PHE:O	1:A:85:LEU:HD12	2.20	0.41
1:A:530:SER:H	2:A:701:ACT:CH3	2.30	0.41
1:B:75:GLY:C	1:B:77:ILE:N	2.78	0.41
1:B:94:ASN:HB2	3:B:943:HOH:O	2.20	0.41
1:B:384:LEU:HD13	1:B:435:PHE:CD1	2.55	0.41
1:B:592:MET:SD	1:B:598:LEU:HA	2.60	0.41
1:A:54:MET:HE1	1:A:103:GLU:HG2	2.03	0.41
1:B:343:ARG:HB2	1:B:357:THR:OG1	2.21	0.41
1:B:466:LEU:HA	1:B:466:LEU:HD23	1.82	0.41
1:A:239:LEU:HD23	1:A:239:LEU:HA	1.80	0.41
1:A:339:LYS:HB2	1:A:362:VAL:HB	2.03	0.41
1:B:401:ILE:HG12	1:B:416:LEU:HD22	2.02	0.40
1:B:519:GLU:HB3	1:B:552:ARG:HD2	2.04	0.40
1:A:186:ALA:HB1	1:A:270:LEU:HD12	2.04	0.40
1:B:472:ARG:NH2	1:B:496:VAL:HA	2.37	0.40
1:B:481:LYS:HE2	1:B:481:LYS:HB2	1.87	0.40
1:B:523:ALA:HB3	1:B:546:PRO:HD3	2.03	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	591/609 (97%)	575 (97%)	15 (2%)	1 (0%)	43	55
1	B	589/609 (97%)	565 (96%)	23 (4%)	1 (0%)	43	55
All	All	1180/1218 (97%)	1140 (97%)	38 (3%)	2 (0%)	43	55

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	350	ASN
1	B	546	PRO

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	512/529 (97%)	503 (98%)	9 (2%)	51	70
1	B	509/529 (96%)	501 (98%)	8 (2%)	55	73
All	All	1021/1058 (96%)	1004 (98%)	17 (2%)	57	72

All (17) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	156[A]	GLU
1	A	156[B]	GLU
1	A	174	SER
1	A	198	ASN

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Mol	Chain	Res	Type
1	A	350	ASN
1	A	424	SER
1	A	481	LYS
1	A	485	SER
1	A	618	MET
1	B	156[A]	GLU
1	B	156[B]	GLU
1	B	301	LEU
1	B	350	ASN
1	B	424	SER
1	B	438	ASN
1	B	457	LEU
1	B	603	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (10) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	144	ASN
1	A	198	ASN
1	A	405	ASN
1	A	625	ASN
1	B	71	HIS
1	B	142	GLN
1	B	293	GLN
1	B	335	GLN
1	B	350	ASN
1	B	405	ASN

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

1 ligand is 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	$\# Z > 2$
2	ACT	A	701	-	3,3,3	0.78	0	3,3,3	1.04	0

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

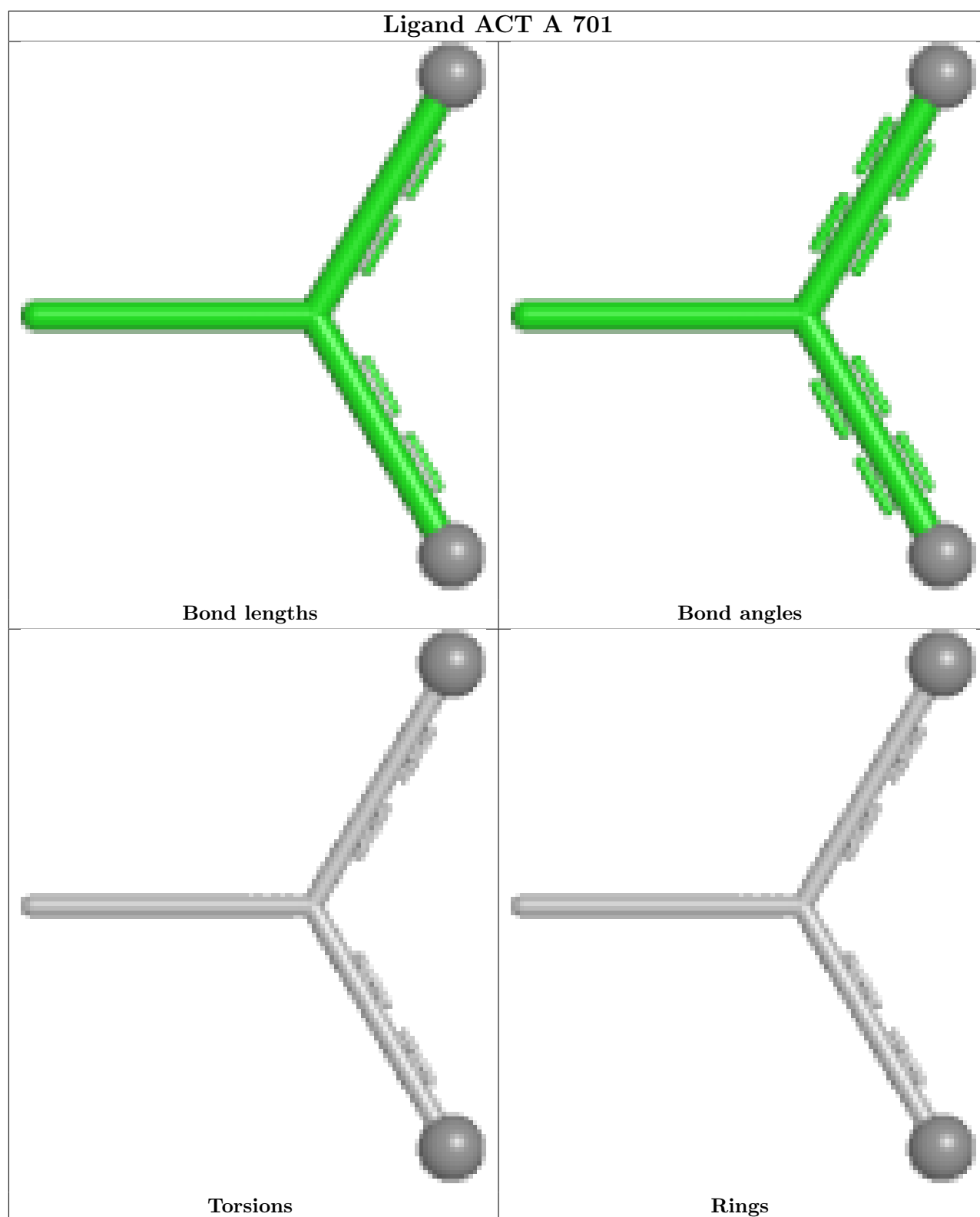
There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	ACT	3	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 ⓘ

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	590/609 (96%)	0.15	11 (1%) 66 68	33, 53, 68, 97	3 (0%)
1	B	590/609 (96%)	0.49	24 (4%) 41 43	35, 58, 81, 98	1 (0%)
All	All	1180/1218 (96%)	0.32	35 (2%) 52 54	33, 55, 77, 98	4 (0%)

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	642	VAL	5.7
1	B	384	LEU	5.0
1	A	642	VAL	4.0
1	B	73	THR	3.6
1	B	378	THR	3.2
1	A	68	PHE	3.2
1	B	248	VAL	3.2
1	B	594	GLU	2.9
1	B	483	THR	2.9
1	B	74	ALA	2.8
1	B	609	TYR	2.7
1	A	73	THR	2.7
1	B	380	SER	2.6
1	A	74	ALA	2.6
1	A	609	TYR	2.6
1	A	149	LEU	2.5
1	B	411	TYR	2.5
1	B	405	ASN	2.5
1	B	458	LEU	2.4
1	B	383	THR	2.4
1	A	392	SER	2.4
1	B	342	VAL	2.4
1	B	507	ASP	2.3
1	B	75	GLY	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	409	THR	2.3
1	B	641	VAL	2.3
1	B	148	LYS	2.3
1	A	94[A]	ASN	2.2
1	B	344	ALA	2.2
1	B	414	VAL	2.2
1	B	316	ALA	2.2
1	A	466	LEU	2.2
1	A	543	ASN	2.2
1	B	416	LEU	2.1
1	A	641	VAL	2.1

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](#)

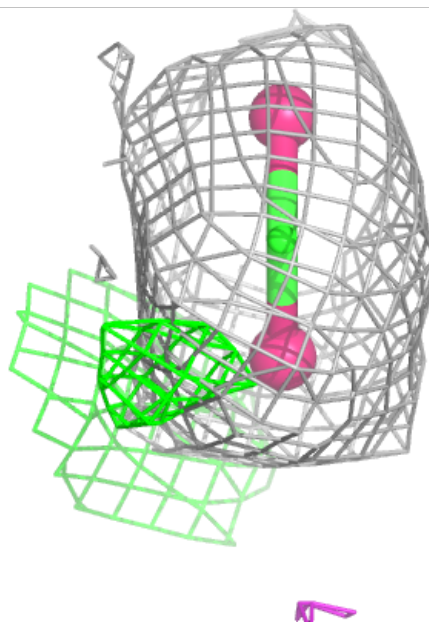
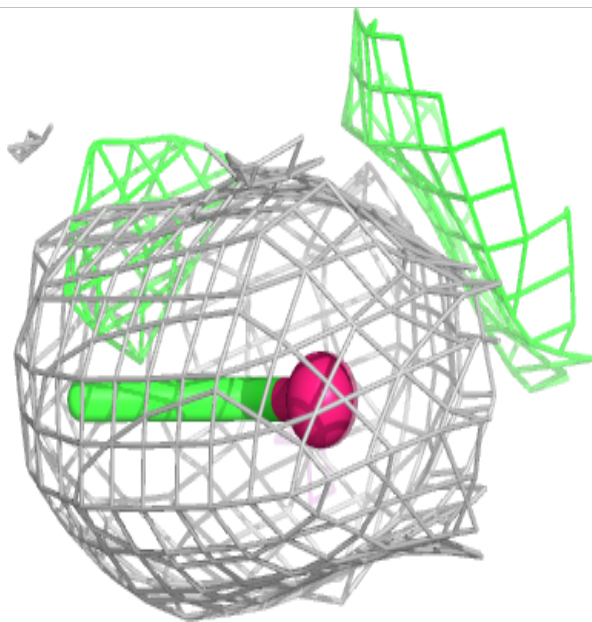
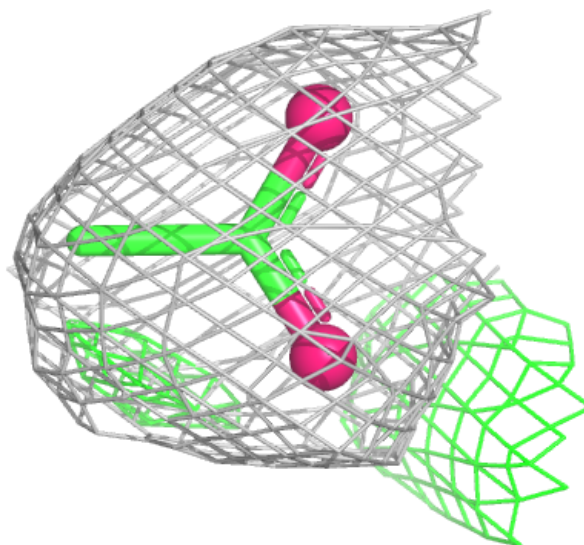
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists 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
2	ACT	A	701	4/4	0.89	0.14	49,52,59,67	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 ACT 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 ⓘ

There are no such residues in this entry.