



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 10:13 AM UTC

PDB ID : 2XQ0 / pdb_00002xq0
Title : Structure of yeast LTA4 hydrolase in complex with Bestatin
Authors : Helgstrand, C.; Hasan, M.; Usyal, H.; Haeggstrom, J.Z.; Thunnissen, M.M.G.M.
Deposited on : 2010-08-31
Resolution : 1.96 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

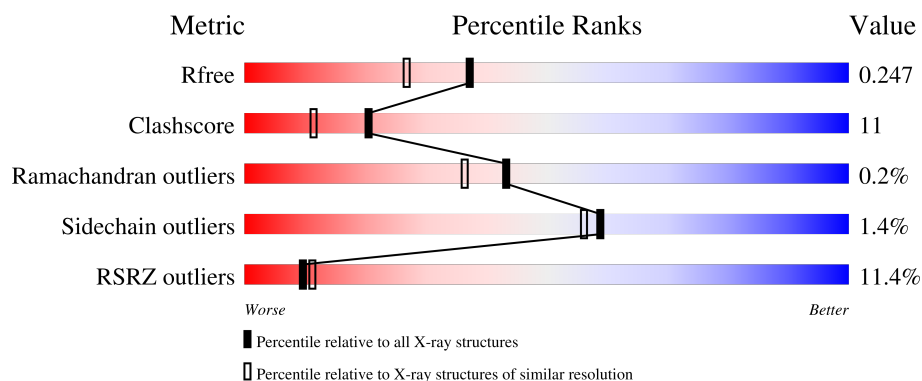
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.96 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	3494 (1.96-1.96)
Clashscore	190562	3612 (1.96-1.96)
Ramachandran outliers	187476	3587 (1.96-1.96)
Sidechain outliers	187428	3587 (1.96-1.96)
RSRZ outliers	180081	3495 (1.96-1.96)

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	632	11% 78% 20% ..

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	4	Total	Cl	0	0
			4	4		

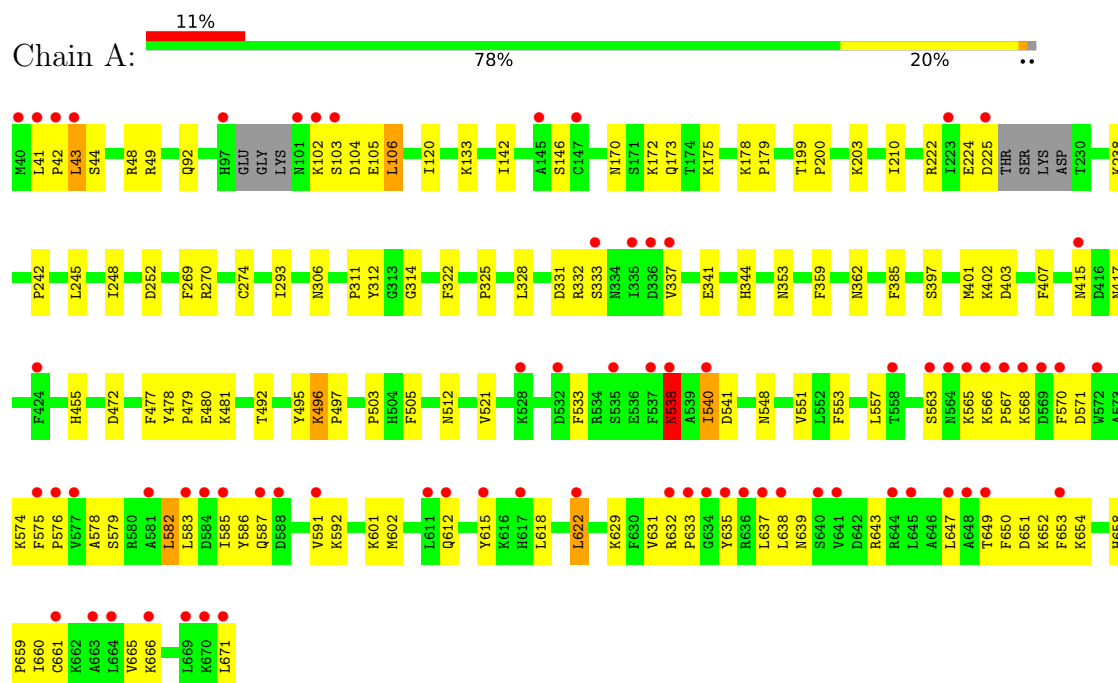
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	350	Total	O	0	0
			350	350		

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: LEUKOTRIENE A-4 HYDROLASE



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	58.64Å 99.87Å 112.65Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	28.66 – 1.96 28.66 – 1.96	Depositor EDS
% Data completeness (in resolution range)	98.9 (28.66-1.96) 99.2 (28.66-1.96)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.31 (at 1.95Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.190 , 0.247 0.189 , 0.247	Depositor DCC
R_{free} test set	976 reflections (2.03%)	wwPDB-VP
Wilson B-factor (Å ²)	29.0	Xtriage
Anisotropy	0.249	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 54.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	5489	wwPDB-VP
Average B, all atoms (Å ²)	42.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.43% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.49	0/5250	0.79	3/7121 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	224	GLU	N-CA-C	6.01	118.46	110.53
1	A	43	LEU	N-CA-C	5.47	116.93	110.97
1	A	538	ASN	N-CA-C	5.02	115.92	108.60

There are no chirality outliers.

There are no planarity outliers.

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	5112	0	4974	112	0
2	A	22	0	22	1	0
3	A	1	0	0	0	0
4	A	4	0	0	2	0
5	A	350	0	0	7	0
All	All	5489	0	4996	113	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 11.

All (113) 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:170:ASN:H	1:A:173:GLN:HE21	1.16	0.90
1:A:540:ILE:H	1:A:540:ILE:HD12	1.35	0.89
1:A:170:ASN:H	1:A:173:GLN:NE2	1.74	0.85
1:A:415:ASN:HB2	1:A:417:ASN:OD1	1.79	0.83
1:A:521:VAL:HG13	1:A:570:PHE:HZ	1.46	0.80
1:A:402:LYS:HG3	1:A:403:ASP:H	1.46	0.79
1:A:44:SER:HB3	4:A:1673:CL:CL	2.21	0.78
1:A:579:SER:O	1:A:583:LEU:HD13	1.85	0.74
1:A:306:ASN:O	1:A:325:PRO:HG3	1.89	0.72
1:A:541:ASP:HB3	5:A:2323:HOH:O	1.90	0.71
1:A:632:ARG:HB2	1:A:633:PRO:HD3	1.71	0.71
1:A:353:ASN:HD22	1:A:359:PHE:HA	1.55	0.69
1:A:633:PRO:O	1:A:637:LEU:HD23	1.92	0.69
1:A:242:PRO:HD2	1:A:245:LEU:HD12	1.77	0.67
1:A:103:SER:HB2	1:A:104:ASP:HA	1.78	0.66
1:A:402:LYS:CG	1:A:403:ASP:H	2.08	0.66
1:A:402:LYS:HE2	1:A:407:PHE:CD1	2.32	0.65
1:A:582:LEU:HD13	1:A:586:TYR:HD1	1.61	0.65
1:A:540:ILE:H	1:A:540:ILE:CD1	2.10	0.65
1:A:521:VAL:HG13	1:A:570:PHE:CZ	2.31	0.63
1:A:538:ASN:HB3	1:A:540:ILE:CD1	2.28	0.63
1:A:538:ASN:HB3	1:A:540:ILE:HD13	1.81	0.62
1:A:661:CYS:O	1:A:665:VAL:HG23	2.00	0.62
1:A:210:ILE:HD13	1:A:248:ILE:HD12	1.81	0.61
1:A:540:ILE:HD12	1:A:540:ILE:N	2.12	0.61
1:A:480:GLU:HB2	4:A:1676:CL:CL	2.38	0.60
1:A:639:ASN:HD21	1:A:643:ARG:HH21	1.51	0.59
1:A:643:ARG:NH1	1:A:647:LEU:HD11	2.18	0.59
1:A:238:LYS:HE2	5:A:2077:HOH:O	2.03	0.58
1:A:170:ASN:N	1:A:173:GLN:HE21	1.94	0.58
1:A:541:ASP:OD2	1:A:586:TYR:HE2	1.87	0.58
1:A:541:ASP:OD2	1:A:586:TYR:CE2	2.57	0.58
1:A:362[B]:ASN:ND2	5:A:2222:HOH:O	2.37	0.57
1:A:102:LYS:HB3	1:A:104:ASP:OD2	2.04	0.57
1:A:496:LYS:HG3	1:A:497:PRO:HD2	1.86	0.56
1:A:658:HIS:CG	1:A:659:PRO:HD2	2.41	0.56
1:A:629:LYS:O	1:A:633:PRO:HG2	2.07	0.54
1:A:270:ARG:HG2	1:A:274:CYS:SG	2.47	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:477:PHE:C	1:A:479:PRO:HD3	2.32	0.54
1:A:571:ASP:HA	5:A:2330:HOH:O	2.08	0.54
1:A:639:ASN:HD21	1:A:643:ARG:HG3	1.73	0.54
1:A:571:ASP:O	1:A:574:LYS:HG2	2.08	0.53
1:A:503:PRO:HG2	1:A:505:PHE:CE2	2.45	0.52
1:A:385:PHE:HE2	1:A:548:ASN:HB3	1.75	0.52
1:A:503:PRO:HG2	1:A:505:PHE:CZ	2.45	0.52
1:A:538:ASN:HA	1:A:585:ILE:CG2	2.40	0.51
1:A:658:HIS:ND1	1:A:659:PRO:HD2	2.25	0.51
1:A:331:ASP:CG	1:A:333:SER:HG	2.18	0.51
1:A:48:ARG:HD2	1:A:495:TYR:CZ	2.47	0.49
1:A:274:CYS:SG	1:A:328:LEU:HD21	2.52	0.49
1:A:210:ILE:HD13	1:A:248:ILE:CD1	2.42	0.49
1:A:353:ASN:ND2	1:A:359:PHE:HA	2.24	0.49
1:A:538:ASN:HA	1:A:585:ILE:HG23	1.94	0.48
1:A:175:LYS:HB2	1:A:269:PHE:CE2	2.48	0.48
1:A:402:LYS:HG3	1:A:403:ASP:N	2.21	0.48
1:A:566:LYS:HE2	1:A:568:LYS:HB2	1.96	0.48
1:A:331:ASP:O	1:A:332:ARG:HB2	2.12	0.48
1:A:397:SER:O	1:A:401:MET:HG3	2.14	0.48
1:A:622:LEU:HD12	1:A:635:TYR:CE2	2.50	0.47
1:A:639:ASN:ND2	1:A:643:ARG:HG3	2.29	0.47
1:A:631:VAL:HG11	1:A:661:CYS:SG	2.54	0.47
1:A:178:LYS:HB3	1:A:179:PRO:HD2	1.96	0.47
2:A:901:BES:H163	2:A:901:BES:H4	1.75	0.47
1:A:612:GLN:HA	1:A:615:TYR:CZ	2.50	0.47
1:A:103:SER:HB2	1:A:104:ASP:CA	2.43	0.46
1:A:533:PHE:CZ	1:A:578:ALA:HB2	2.49	0.46
1:A:601:LYS:NZ	5:A:2336:HOH:O	2.49	0.46
1:A:120:ILE:HG21	1:A:146:SER:HB3	1.98	0.46
1:A:622:LEU:CD1	1:A:635:TYR:CE2	2.99	0.46
1:A:344:HIS:CE1	1:A:362[B]:ASN:OD1	2.69	0.45
1:A:344:HIS:HE1	1:A:362[B]:ASN:OD1	1.98	0.45
1:A:402:LYS:CG	1:A:403:ASP:N	2.74	0.45
1:A:43:LEU:HD12	1:A:43:LEU:N	2.31	0.45
1:A:618:LEU:HD23	1:A:638:LEU:HD13	1.99	0.45
1:A:314:GLY:HA2	1:A:322:PHE:O	2.17	0.45
1:A:666:LYS:O	1:A:671:LEU:HB2	2.16	0.45
1:A:103:SER:HB2	1:A:105:GLU:N	2.31	0.44
1:A:103:SER:CB	1:A:104:ASP:HA	2.40	0.44
1:A:639:ASN:ND2	1:A:643:ARG:HH21	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:178:LYS:HD2	1:A:252:ASP:HB2	1.99	0.44
1:A:649:THR:HG23	1:A:653:PHE:CE2	2.53	0.43
1:A:172:LYS:HB3	1:A:172:LYS:HE2	1.81	0.43
1:A:478:TYR:HB3	1:A:481:LYS:HB2	2.00	0.43
1:A:133:LYS:O	1:A:133:LYS:HG3	2.16	0.43
1:A:311:PRO:HG2	1:A:312:TYR:CD2	2.53	0.43
1:A:49:ARG:HH22	1:A:472:ASP:CG	2.26	0.43
1:A:650:PHE:O	1:A:654:LYS:N	2.49	0.43
1:A:103:SER:N	1:A:104:ASP:HA	2.33	0.43
1:A:203:LYS:HD2	1:A:242:PRO:HD3	1.99	0.43
1:A:612:GLN:HG2	1:A:615:TYR:CE1	2.54	0.42
1:A:455:HIS:HE1	5:A:2285:HOH:O	2.03	0.42
1:A:575:PHE:N	1:A:576:PRO:CD	2.82	0.42
1:A:649:THR:HG23	1:A:653:PHE:HE2	1.84	0.42
1:A:639:ASN:HD21	1:A:643:ARG:CG	2.31	0.42
1:A:200:PRO:HB2	1:A:353:ASN:O	2.19	0.42
1:A:651:ASP:HA	1:A:654:LYS:HD3	2.02	0.42
1:A:563:SER:OG	1:A:565:LYS:HE3	2.20	0.41
1:A:649:THR:O	1:A:652:LYS:HB3	2.20	0.41
1:A:337:VAL:O	1:A:341:GLU:HG2	2.21	0.41
1:A:551:VAL:HG13	1:A:601:LYS:HE3	2.03	0.41
1:A:582:LEU:HD13	1:A:586:TYR:CD1	2.47	0.41
1:A:591:VAL:HA	1:A:602:MET:SD	2.60	0.41
1:A:222:ARG:NH2	1:A:225:ASP:OD2	2.54	0.41
1:A:565:LYS:O	1:A:567:PRO:HD3	2.20	0.41
1:A:41:LEU:HB2	1:A:42:PRO:HD2	2.03	0.41
1:A:49:ARG:NH2	1:A:472:ASP:OD1	2.53	0.41
1:A:106:LEU:HB2	1:A:142:ILE:HB	2.01	0.41
1:A:652:LYS:HD3	1:A:653:PHE:CZ	2.56	0.41
1:A:658:HIS:ND1	1:A:660:ILE:HG12	2.36	0.41
1:A:492:THR:HA	1:A:496:LYS:HB2	2.03	0.41
1:A:553:PHE:CZ	1:A:557:LEU:HD11	2.56	0.40
1:A:92:GLN:HG2	5:A:2057:HOH:O	2.21	0.40
1:A:587:GLN:HE21	1:A:592:LYS:NZ	2.20	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	620/632 (98%)	596 (96%)	23 (4%)	1 (0%)	43	36

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	293	ILE

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	566/571 (99%)	558 (99%)	8 (1%)	59	56

All (8) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	106	LEU
1	A	199	THR
1	A	496	LYS
1	A	512	ASN
1	A	538	ASN
1	A	540	ILE
1	A	582	LEU
1	A	622	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (14) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	97	HIS
1	A	128	GLN
1	A	131	GLN
1	A	154	ASN
1	A	167	GLN
1	A	173	GLN
1	A	330	HIS
1	A	353	ASN
1	A	395	GLN
1	A	412	GLN
1	A	504	HIS
1	A	587	GLN
1	A	589	ASN
1	A	639	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 [i](#)

Of 6 ligands modelled in this entry, 5 are monoatomic - leaving 1 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	$\# Z > 2$
2	BES	A	901	3	22,22,22	0.68	0	26,29,29	1.61	5 (19%)

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
2	BES	A	901	3	-	7/24/24/24	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	901	BES	C2-C3-N1	-4.28	110.42	116.22
2	A	901	BES	C13-C4-N1	-3.21	103.33	110.58
2	A	901	BES	C4-N1-C3	3.10	128.31	121.65
2	A	901	BES	O3-C3-N1	2.80	127.98	122.96
2	A	901	BES	O2-C2-C1	2.47	114.73	109.64

There are no chirality outliers.

All (7) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	901	BES	C14-C13-C4-C5
2	A	901	BES	C14-C13-C4-N1
2	A	901	BES	O2-C2-C3-N1
2	A	901	BES	C4-C13-C14-C16
2	A	901	BES	O2-C2-C3-O3
2	A	901	BES	C1-C6-C7-C8
2	A	901	BES	C1-C6-C7-C12

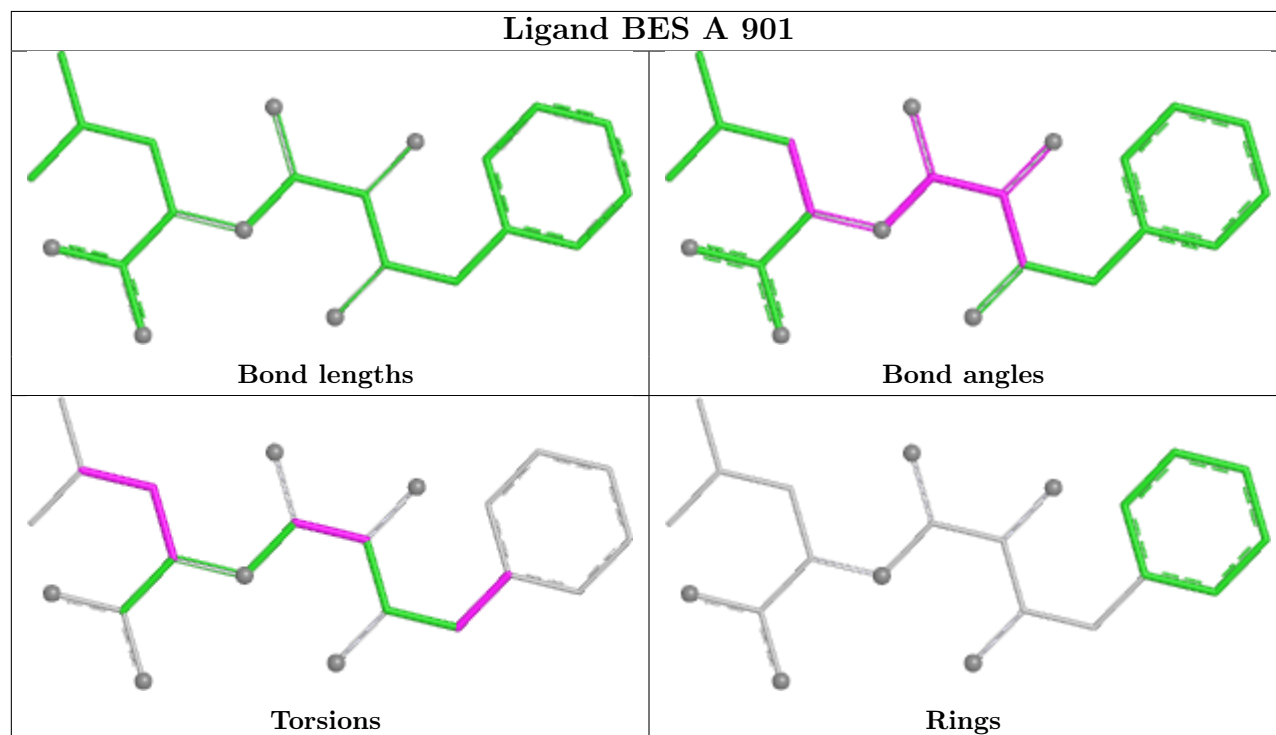
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	901	BES	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	625/632 (98%)	0.35	71 (11%)	10 11	10, 35, 85, 160	1 (0%)

All (71) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	570	PHE	5.6
1	A	669	LEU	4.6
1	A	622	LEU	4.2
1	A	563	SER	4.1
1	A	648	ALA	4.0
1	A	43	LEU	4.0
1	A	671	LEU	4.0
1	A	670	LYS	3.8
1	A	568	LYS	3.7
1	A	577	VAL	3.7
1	A	637	LEU	3.6
1	A	663	ALA	3.5
1	A	225	ASP	3.5
1	A	564	ASN	3.5
1	A	644	ARG	3.4
1	A	572	TRP	3.3
1	A	103	SER	3.3
1	A	40	MET	3.2
1	A	41	LEU	3.2
1	A	634	GLY	3.1
1	A	617	HIS	3.1
1	A	615	TYR	2.9
1	A	567	PRO	2.9
1	A	535	SER	2.9
1	A	102	LYS	2.9
1	A	336	ASP	2.8
1	A	576	PRO	2.8

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Mol	Chain	Res	Type	RSRZ
1	A	645	LEU	2.8
1	A	661	CYS	2.7
1	A	635	TYR	2.6
1	A	591	VAL	2.6
1	A	638	LEU	2.6
1	A	540	ILE	2.6
1	A	666	LYS	2.6
1	A	581	ALA	2.6
1	A	528	LYS	2.5
1	A	649	THR	2.5
1	A	583	LEU	2.5
1	A	101	ASN	2.5
1	A	641	VAL	2.5
1	A	636	ARG	2.4
1	A	42	PRO	2.4
1	A	335	ILE	2.4
1	A	653	PHE	2.3
1	A	611	LEU	2.3
1	A	538	ASN	2.3
1	A	664	LEU	2.3
1	A	565	LYS	2.3
1	A	575	PHE	2.3
1	A	147	CYS	2.3
1	A	415	ASN	2.3
1	A	647	LEU	2.3
1	A	640	SER	2.2
1	A	223	ILE	2.2
1	A	585	ILE	2.2
1	A	566	LYS	2.2
1	A	588	ASP	2.2
1	A	584	ASP	2.2
1	A	633	PRO	2.2
1	A	145	ALA	2.2
1	A	97	HIS	2.1
1	A	424	PHE	2.1
1	A	587	GLN	2.1
1	A	558	THR	2.1
1	A	632	ARG	2.1
1	A	612	GLN	2.1
1	A	537	PHE	2.1
1	A	532	ASP	2.1
1	A	569	ASP	2.1

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Mol	Chain	Res	Type	RSRZ
1	A	333	SER	2.1
1	A	337	VAL	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](#)

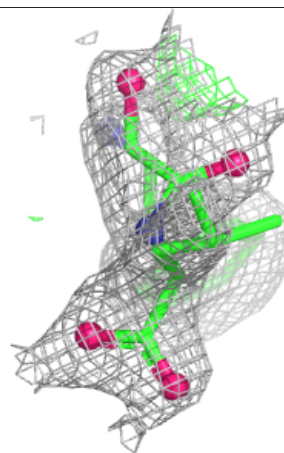
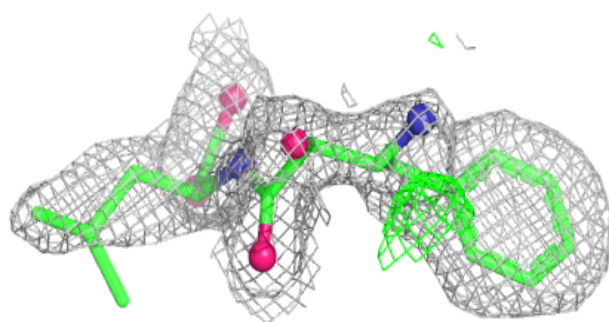
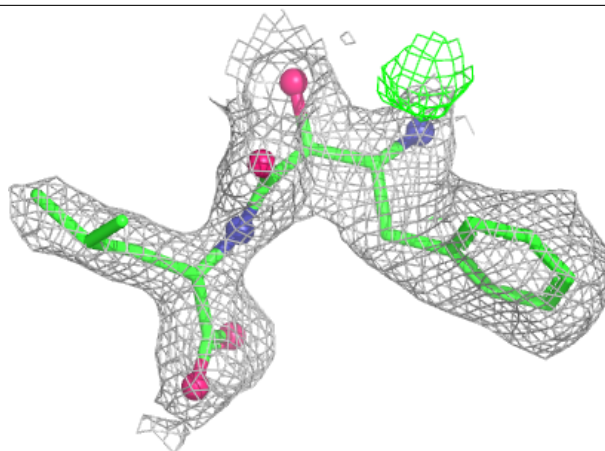
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
4	CL	A	1676	1/1	0.87	0.13	71,71,71,71	0
2	BES	A	901	22/22	0.88	0.10	32,48,58,59	0
4	CL	A	1673	1/1	0.93	0.10	69,69,69,69	0
4	CL	A	1675	1/1	0.94	0.08	68,68,68,68	0
4	CL	A	1674	1/1	0.94	0.23	59,59,59,59	0
3	ZN	A	1672	1/1	1.00	0.02	30,30,30,30	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 BES A 901:

$2mF_o-DF_c$ (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.