



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 20, 2024 – 05:37 pm GMT

PDB ID : 7NB3
Title : Crystal structure of human choline alpha in complex with an inhibitor
Authors : Casale, E.; Fasolini, M.
Deposited on : 2021-01-25
Resolution : 2.00 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 : 4.02b-467
Mogul : 1.8.4, CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.36
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) : 2.36

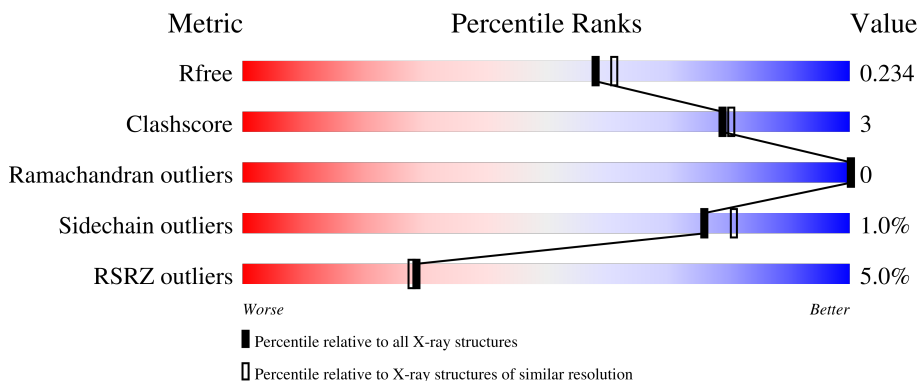
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

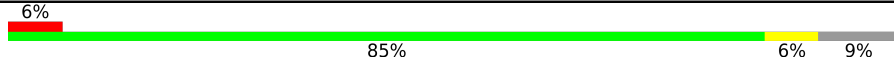
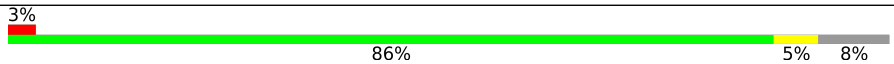
The reported resolution of this entry is 2.00 Å.

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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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	AAA	384	
1	BBB	384	

2 Entry composition [i](#)

There are 5 unique types of molecules in this entry. The entry contains 6175 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.

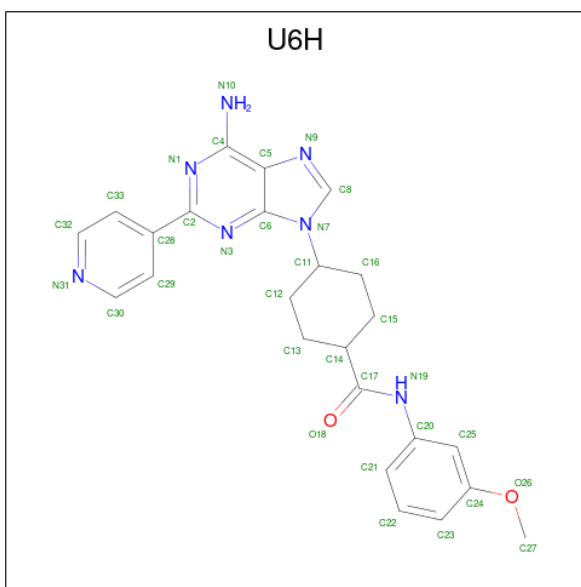
- Molecule 1 is a protein called Choline kinase alpha.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	AAA	348	Total 2883	C 1871	N 479	O 516	S 17	0	3	0
1	BBB	353	Total 2896	C 1878	N 490	O 512	S 16	0	2	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	74	GLY	-	expression tag	UNP P35790
BBB	74	GLY	-	expression tag	UNP P35790

- Molecule 2 is 4-(6-azanyl-2-pyridin-4-yl-purin-9-yl)- {N}-(3-methoxyphenyl)cyclohexane-1-carboxamide (three-letter code: U6H) (formula: C₂₄H₂₅N₇O₂) (labeled as "Ligand of Interest" by depositor).

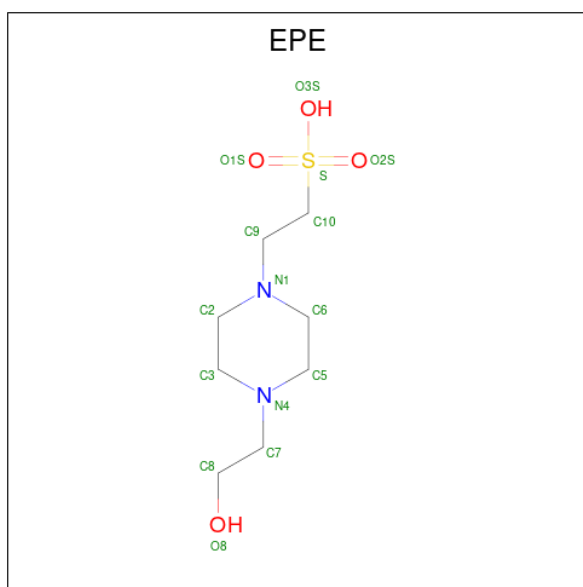


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	AAA	1	Total	C	N	O	0	0
			33	24	7	2		
2	BBB	1	Total	C	N	O	0	0
			33	24	7	2		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	1	Total	Mg	0	0
			1	1		
3	BBB	1	Total	Mg	0	0
			1	1		

- Molecule 4 is 4-(2-HYDROXYETHYL)-1-PIPERAZINE ETHANESULFONIC ACID (three-letter code: EPE) (formula: C₈H₁₈N₂O₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	AAA	1	Total	C	N	O	S	0	1
			15	8	2	4	1		
4	AAA	1	Total	C	N	O	S	0	1
			15	8	2	4	1		
4	BBB	1	Total	C	N	O	S	0	0
			15	8	2	4	1		

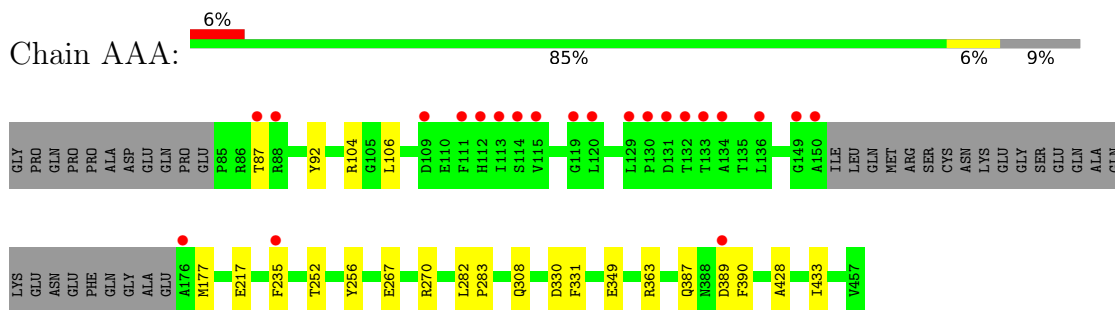
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	AAA	145	Total 145	O 145	0	0
5	BBB	138	Total 138	O 138	0	0

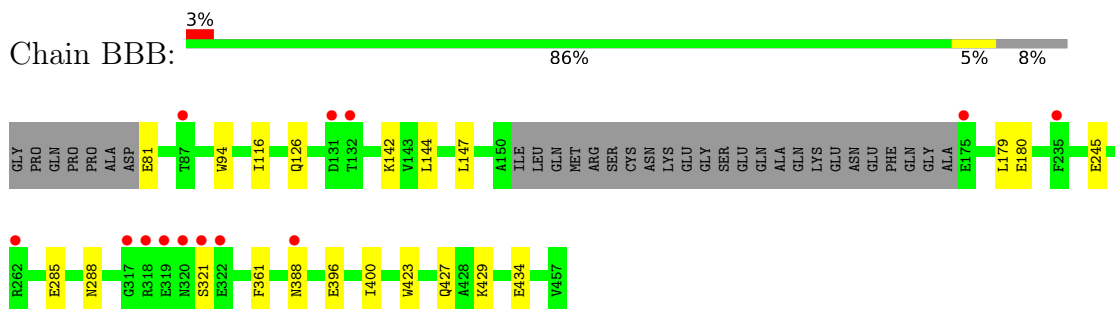
3 Residue-property plots [i](#)

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: Choline kinase alpha



- Molecule 1: Choline kinase alpha



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	55.93Å 120.20Å 131.19Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	41.13 – 2.00 41.09 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.5 (41.13-2.00) 99.5 (41.09-2.00)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.18 (at 2.00Å)	Xtrriage
Refinement program	REFMAC 5.8.0267	Depositor
R, R_{free}	0.189 , 0.234 0.189 , 0.234	Depositor DCC
R_{free} test set	3047 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	34.5	Xtrriage
Anisotropy	0.428	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6175	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.39% 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: U6H, MG, EPE

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	AAA	0.45	0/2961	0.73	0/3990
1	BBB	0.42	0/2979	0.75	0/4020
All	All	0.43	0/5940	0.74	0/8010

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 [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	AAA	2883	0	2847	19	0
1	BBB	2896	0	2839	11	0
2	AAA	33	0	0	0	0
2	BBB	33	0	0	0	0
3	AAA	1	0	0	0	0
3	BBB	1	0	0	0	0
4	AAA	30	0	35	5	0
4	BBB	15	0	18	0	0
5	AAA	145	0	0	2	0
5	BBB	138	0	0	1	0
All	All	6175	0	5739	32	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 3.

All (32) 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)
4:AAA:503[A]:EPE:O8	4:AAA:503[A]:EPE:H32	1.38	1.10
4:AAA:503[A]:EPE:O8	4:AAA:503[A]:EPE:C3	2.24	0.86
4:AAA:503[A]:EPE:H32	4:AAA:503[A]:EPE:HO8	1.54	0.72
1:AAA:252:THR:HG22	1:AAA:256:TYR:CE2	2.32	0.65
1:AAA:270:ARG:NH2	1:AAA:428:ALA:O	2.31	0.63
1:AAA:267:GLU:H	1:AAA:267:GLU:CD	2.01	0.62
1:AAA:433:ILE:HG21	4:AAA:503[A]:EPE:H72	1.81	0.61
1:BBB:388:ASN:H	1:BBB:388:ASN:HD22	1.49	0.60
1:BBB:429:LYS:HE2	5:BBB:715:HOH:O	2.06	0.54
1:BBB:396:GLU:O	1:BBB:400:ILE:HG13	2.09	0.53
1:BBB:423:TRP:O	1:BBB:427:GLN:HG2	2.09	0.53
1:AAA:104:ARG:HH22	1:BBB:245:GLU:CD	2.13	0.53
1:AAA:267:GLU:HG2	1:AAA:270:ARG:HD3	1.92	0.51
1:BBB:388:ASN:H	1:BBB:388:ASN:ND2	2.09	0.49
1:BBB:285:GLU:O	1:BBB:288[A]:ASN:HB3	2.12	0.48
1:AAA:282:LEU:N	1:AAA:283:PRO:CD	2.77	0.48
1:BBB:126:GLN:NE2	1:BBB:142:LYS:HE3	2.29	0.48
1:AAA:92:TYR:OH	1:AAA:106:LEU:O	2.24	0.46
1:AAA:308:GLN:NE2	4:AAA:503[A]:EPE:O3S	2.48	0.46
1:AAA:387:GLN:HB3	1:AAA:390:PHE:HB2	1.97	0.45
1:AAA:217:GLU:H	1:AAA:217:GLU:CD	2.20	0.45
1:BBB:116:ILE:HD11	1:BBB:126:GLN:HB3	1.98	0.45
1:AAA:87:THR:HG23	5:AAA:736:HOH:O	2.17	0.45
1:AAA:235:PHE:HE2	1:AAA:331:PHE:CE1	2.36	0.43
1:AAA:252:THR:CG2	1:AAA:256:TYR:CE2	3.00	0.43
1:AAA:387:GLN:HG2	1:AAA:389:ASP:OD1	2.19	0.42
1:AAA:235:PHE:CZ	1:AAA:331:PHE:CD1	3.08	0.42
1:AAA:308:GLN:HB3	1:AAA:349:GLU:HG3	2.02	0.41
1:BBB:94:TRP:CZ3	1:BBB:147:LEU:HD21	2.55	0.41
1:AAA:363:ARG:NH1	5:AAA:611:HOH:O	2.53	0.41
1:BBB:361:PHE:CE2	1:BBB:434:GLU:HG2	2.56	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	AAA	347/384 (90%)	335 (96%)	12 (4%)	0	100	100
1	BBB	351/384 (91%)	341 (97%)	10 (3%)	0	100	100
All	All	698/768 (91%)	676 (97%)	22 (3%)	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 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	AAA	310/342 (91%)	309 (100%)	1 (0%)	92	95
1	BBB	306/342 (90%)	301 (98%)	5 (2%)	62	67
All	All	616/684 (90%)	610 (99%)	6 (1%)	76	81

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	330	ASP
1	BBB	81	GLU
1	BBB	144	LEU
1	BBB	179	LEU
1	BBB	180	GLU
1	BBB	321	SER

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 7 ligands modelled in this entry, 2 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
4	EPE	AAA	504[A]	-	15,15,15	0.56	0	18,20,20	1.12	1 (5%)
2	U6H	BBB	501	-	34,37,37	1.64	7 (20%)	40,52,52	1.68	6 (15%)
4	EPE	BBB	503	-	15,15,15	0.74	1 (6%)	18,20,20	0.81	1 (5%)
2	U6H	AAA	501	-	34,37,37	1.59	9 (26%)	40,52,52	2.13	7 (17%)
4	EPE	AAA	503[A]	-	15,15,15	0.96	1 (6%)	18,20,20	0.97	1 (5%)

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	EPE	AAA	504[A]	-	-	5/9/19/19	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	U6H	BBB	501	-	-	4/14/28/28	0/5/5/5
4	EPE	BBB	503	-	-	3/9/19/19	0/1/1/1
2	U6H	AAA	501	-	-	0/14/28/28	0/5/5/5
4	EPE	AAA	503[A]	-	-	6/9/19/19	0/1/1/1

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	501	U6H	C14-C17	3.65	1.58	1.51
4	AAA	503[A]	EPE	O1S-S	3.49	1.55	1.45
2	BBB	501	U6H	C28-C2	-3.20	1.40	1.48
2	AAA	501	U6H	C28-C2	-2.88	1.41	1.48
2	AAA	501	U6H	C12-C13	2.88	1.60	1.52
2	BBB	501	U6H	C12-C11	2.87	1.59	1.52
2	AAA	501	U6H	C16-C11	2.78	1.59	1.52
2	BBB	501	U6H	C20-N19	-2.78	1.36	1.41
2	BBB	501	U6H	C13-C14	2.77	1.60	1.53
4	BBB	503	EPE	O3S-S	2.67	1.57	1.47
2	AAA	501	U6H	C20-N19	-2.60	1.36	1.41
2	BBB	501	U6H	C32-N31	2.56	1.41	1.33
2	BBB	501	U6H	C30-N31	2.28	1.40	1.33
2	AAA	501	U6H	C4-C5	-2.27	1.34	1.43
2	AAA	501	U6H	C16-C15	2.26	1.58	1.52
2	AAA	501	U6H	C12-C11	2.26	1.57	1.52
2	AAA	501	U6H	C30-N31	2.02	1.39	1.33
2	AAA	501	U6H	C5-N9	-2.01	1.32	1.39

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AAA	501	U6H	N3-C2-N1	-9.18	118.90	126.11
2	BBB	501	U6H	N3-C2-N1	-5.63	121.69	126.11
2	AAA	501	U6H	C2-N3-C6	5.57	122.03	115.08
2	BBB	501	U6H	C6-C5-N9	-3.60	105.64	109.40
2	BBB	501	U6H	C2-N3-C6	3.59	119.56	115.08
2	BBB	501	U6H	C33-C32-N31	-2.99	118.41	123.62
4	AAA	503[A]	EPE	O3S-S-O2S	2.90	118.35	111.27
2	AAA	501	U6H	C20-C25-C24	2.73	123.45	119.17
2	AAA	501	U6H	C33-C32-N31	-2.51	119.26	123.62
4	BBB	503	EPE	O3S-S-O2S	-2.44	105.30	111.27
2	AAA	501	U6H	C4-N1-C2	2.27	119.79	116.63

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	AAA	504[A]	EPE	O3S-S-C10	2.26	109.43	105.77
2	BBB	501	U6H	C29-C30-N31	-2.05	120.05	123.62
2	BBB	501	U6H	C5-C4-N1	-2.04	119.67	121.01
2	AAA	501	U6H	C5-C4-N10	-2.03	117.27	120.35
2	AAA	501	U6H	C28-C2-N1	2.00	120.70	117.33

There are no chirality outliers.

All (18) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	AAA	503[A]	EPE	S-C10-C9-N1
4	AAA	503[A]	EPE	C9-C10-S-O1S
4	AAA	503[A]	EPE	C9-C10-S-O3S
4	AAA	504[A]	EPE	C10-C9-N1-C6
4	AAA	504[A]	EPE	S-C10-C9-N1
4	BBB	503	EPE	C8-C7-N4-C5
4	AAA	503[A]	EPE	C8-C7-N4-C3
4	AAA	503[A]	EPE	N4-C7-C8-O8
4	AAA	504[A]	EPE	N4-C7-C8-O8
4	BBB	503	EPE	N4-C7-C8-O8
4	AAA	503[A]	EPE	C9-C10-S-O2S
4	BBB	503	EPE	C9-C10-S-O2S
2	BBB	501	U6H	C23-C24-O26-C27
2	BBB	501	U6H	C25-C24-O26-C27
4	AAA	504[A]	EPE	C9-C10-S-O3S
2	BBB	501	U6H	C13-C14-C17-N19
2	BBB	501	U6H	C13-C14-C17-O18
4	AAA	504[A]	EPE	C9-C10-S-O2S

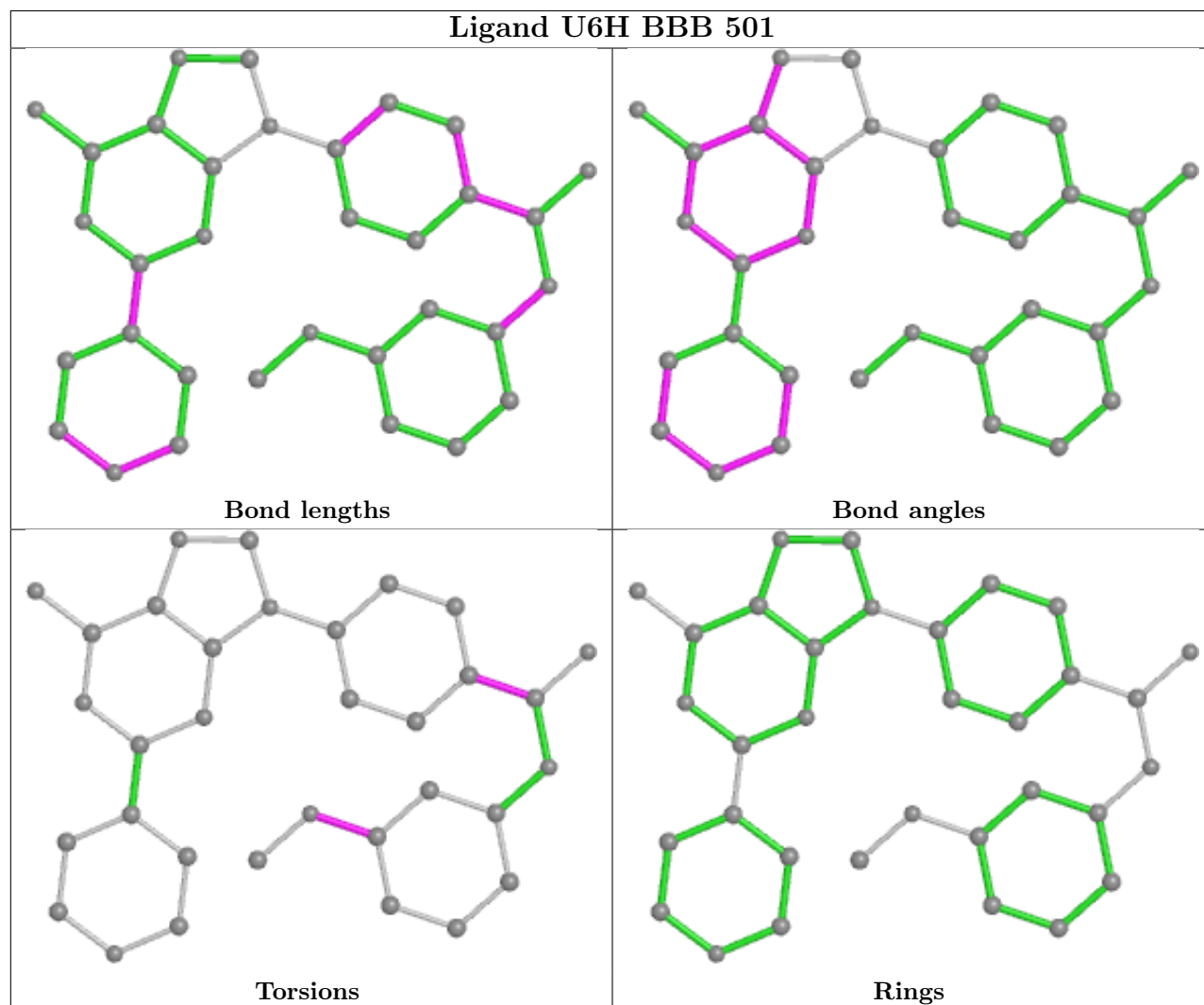
There are no ring outliers.

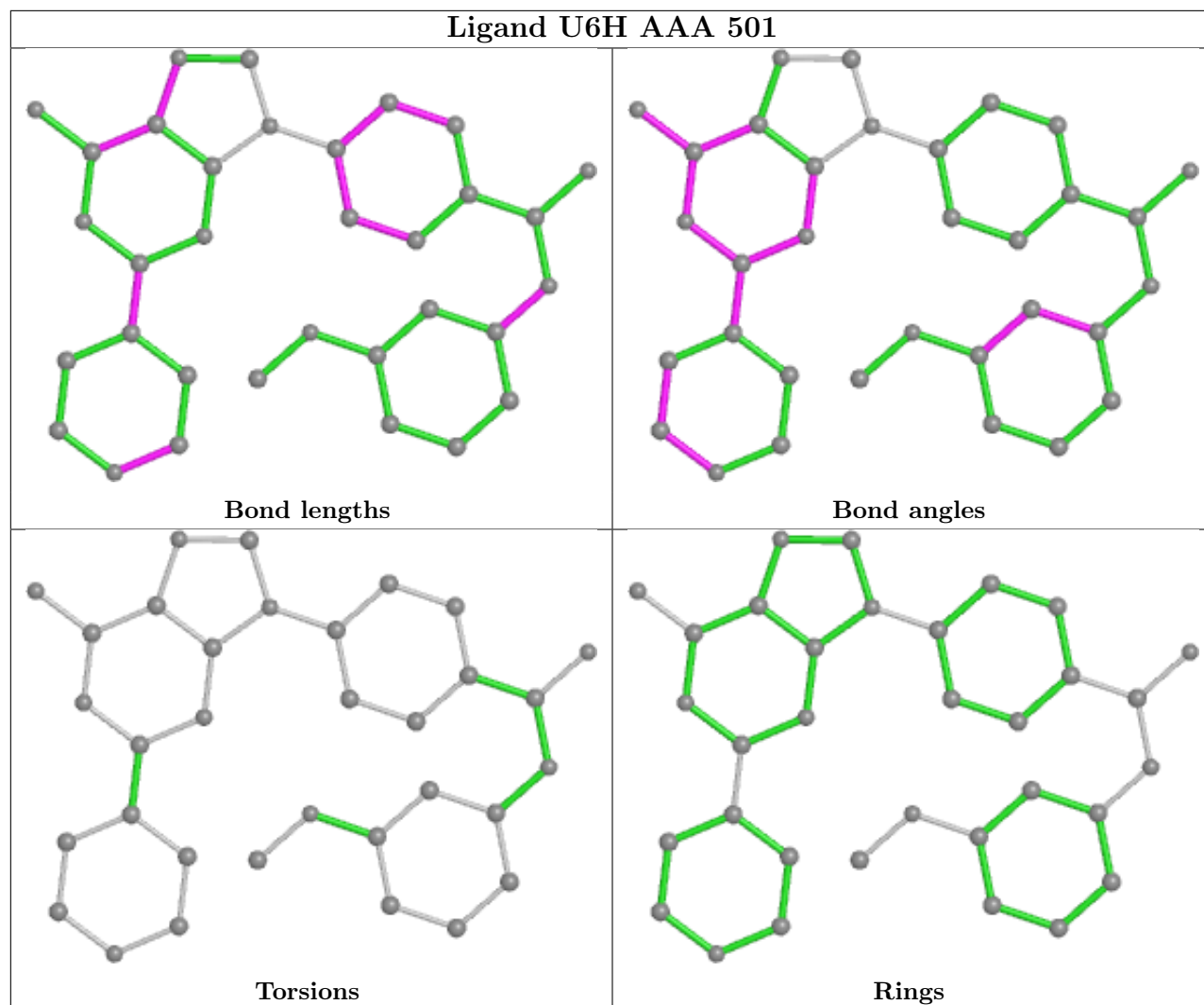
1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	AAA	503[A]	EPE	5	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	AAA	348/384 (90%)	0.30	22 (6%) 20 19	22, 36, 74, 89	0
1	BBB	353/384 (91%)	0.06	13 (3%) 41 41	24, 37, 66, 98	0
All	All	701/768 (91%)	0.18	35 (4%) 28 28	22, 37, 71, 98	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	AAA	87	THR	4.6
1	BBB	321	SER	4.3
1	AAA	132	THR	4.2
1	BBB	317	GLY	4.1
1	AAA	130	PRO	3.9
1	AAA	120	LEU	3.6
1	AAA	136	LEU	3.5
1	BBB	320	ASN	3.4
1	BBB	87	THR	3.4
1	AAA	88	ARG	3.3
1	BBB	131	ASP	3.3
1	AAA	150	ALA	3.1
1	AAA	129	LEU	3.1
1	BBB	132	THR	3.0
1	AAA	133	THR	2.9
1	AAA	149	GLY	2.9
1	AAA	111	PHE	2.9
1	AAA	176	ALA	2.9
1	AAA	235	PHE	2.7
1	AAA	115	VAL	2.7
1	AAA	113	ILE	2.6
1	AAA	114	SER	2.5
1	BBB	322	GLU	2.5
1	AAA	109	ASP	2.5

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Mol	Chain	Res	Type	RSRZ
1	BBB	318	ARG	2.4
1	AAA	131	ASP	2.4
1	BBB	319	GLU	2.4
1	AAA	389	ASP	2.3
1	AAA	119	GLY	2.3
1	BBB	262	ARG	2.2
1	BBB	388	ASN	2.2
1	BBB	175	GLU	2.2
1	AAA	134	ALA	2.2
1	BBB	235	PHE	2.1
1	AAA	112	HIS	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](#)

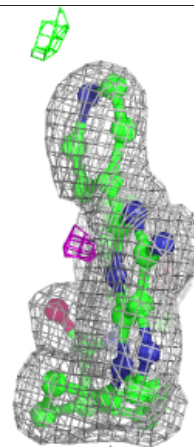
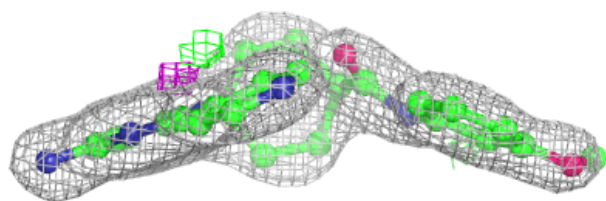
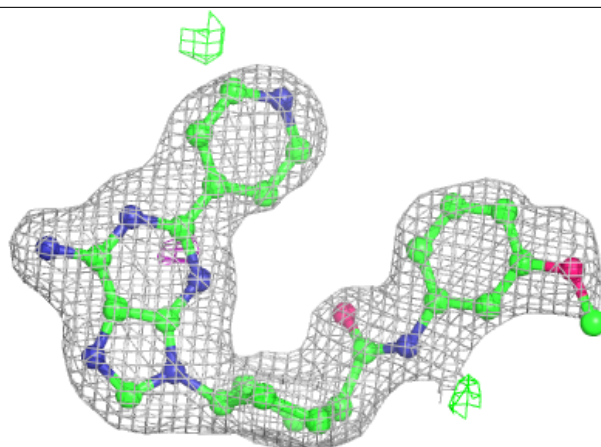
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q<0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
3	MG	BBB	502	1/1	0.69	0.31	70,70,70,70	0
4	EPE	BBB	503	15/15	0.77	0.28	57,87,100,117	0
4	EPE	AAA	503[A]	15/15	0.91	0.22	59,65,81,85	15
2	U6H	BBB	501	33/33	0.93	0.18	33,50,64,65	0
4	EPE	AAA	504[A]	15/15	0.94	0.19	42,57,69,70	15
3	MG	AAA	502	1/1	0.95	0.04	45,45,45,45	0
2	U6H	AAA	501	33/33	0.96	0.12	34,39,48,57	0

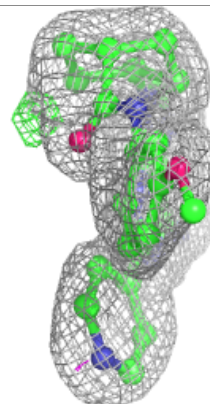
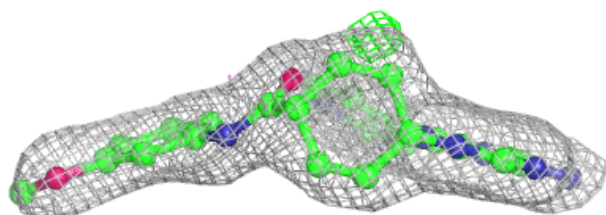
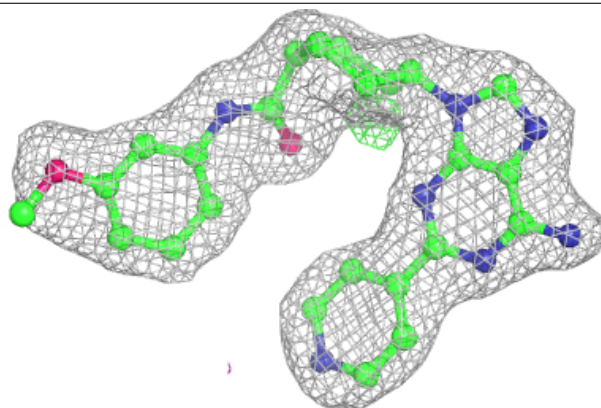
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around U6H BBB 501:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)

**Electron density around U6H AAA 501:**

$2mF_o-DF_c$ (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.