



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 19, 2022 – 06:11 am GMT

PDB ID : 7NRA
Title : The structure of the SBP TarP_Sse in complex with cinnamate
Authors : Bisson, C.; Salmon, R.C.; West, L.; Rafferty, J.B.; Hitchcock, A.; Thomas, G.H.; Kelly, D.J.
Deposited on : 2021-03-03
Resolution : 1.91 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 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 : 2.24
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0267
CCP4 : 7.1.010 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.24

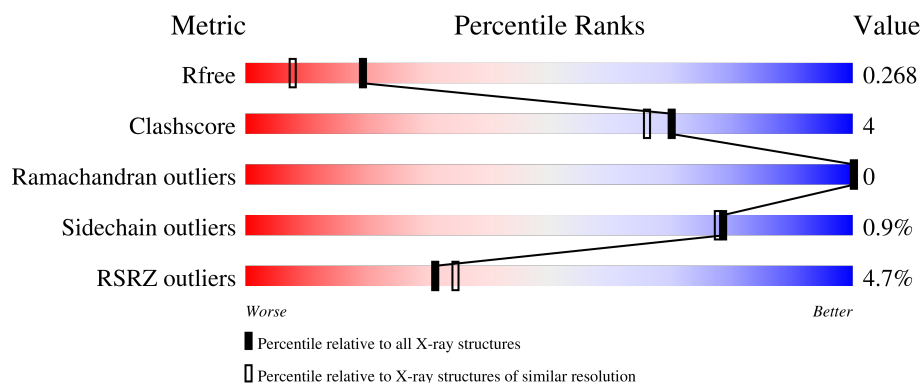
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.91 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	7937 (1.94-1.90)
Clashscore	141614	8644 (1.94-1.90)
Ramachandran outliers	138981	8530 (1.94-1.90)
Sidechain outliers	138945	8530 (1.94-1.90)
RSRZ outliers	127900	7793 (1.94-1.90)

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	337	<div> <div style="width: 90%;"></div> <div style="width: 7%;"></div> <div style="width: 3%;"></div> <div style="width: 2%;"></div> </div> 90% 7% •
1	BBB	337	<div> <div style="width: 9%;"></div> <div style="width: 87%;"></div> <div style="width: 10%;"></div> <div style="width: 4%;"></div> </div> 9% 87% 10% •

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5314 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.

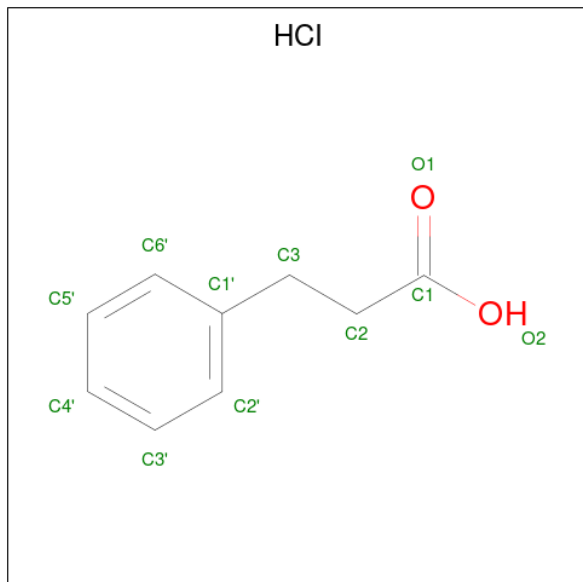
- Molecule 1 is a protein called TRAP dicarboxylate transporter, DctP subunit.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	AAA	327	Total	C	N	O	S	0	0	0
			2503	1587	405	499	12			
1	BBB	328	Total	C	N	O	S	0	0	0
			2512	1592	407	501	12			

There are 24 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
AAA	0	MET	-	initiating methionine	UNP A3K0X1
AAA	326	ALA	-	expression tag	UNP A3K0X1
AAA	327	ALA	-	expression tag	UNP A3K0X1
AAA	328	ALA	-	expression tag	UNP A3K0X1
AAA	329	LEU	-	expression tag	UNP A3K0X1
AAA	330	GLU	-	expression tag	UNP A3K0X1
AAA	331	HIS	-	expression tag	UNP A3K0X1
AAA	332	HIS	-	expression tag	UNP A3K0X1
AAA	333	HIS	-	expression tag	UNP A3K0X1
AAA	334	HIS	-	expression tag	UNP A3K0X1
AAA	335	HIS	-	expression tag	UNP A3K0X1
AAA	336	HIS	-	expression tag	UNP A3K0X1
BBB	0	MET	-	initiating methionine	UNP A3K0X1
BBB	326	ALA	-	expression tag	UNP A3K0X1
BBB	327	ALA	-	expression tag	UNP A3K0X1
BBB	328	ALA	-	expression tag	UNP A3K0X1
BBB	329	LEU	-	expression tag	UNP A3K0X1
BBB	330	GLU	-	expression tag	UNP A3K0X1
BBB	331	HIS	-	expression tag	UNP A3K0X1
BBB	332	HIS	-	expression tag	UNP A3K0X1
BBB	333	HIS	-	expression tag	UNP A3K0X1
BBB	334	HIS	-	expression tag	UNP A3K0X1
BBB	335	HIS	-	expression tag	UNP A3K0X1
BBB	336	HIS	-	expression tag	UNP A3K0X1

- Molecule 2 is HYDROCINNAMIC ACID (three-letter code: HCI) (formula: $C_9H_{10}O_2$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	AAA	1	Total	C	O	0	0
			11	9	2		
2	BBB	1	Total	C	O	0	0
			11	9	2		

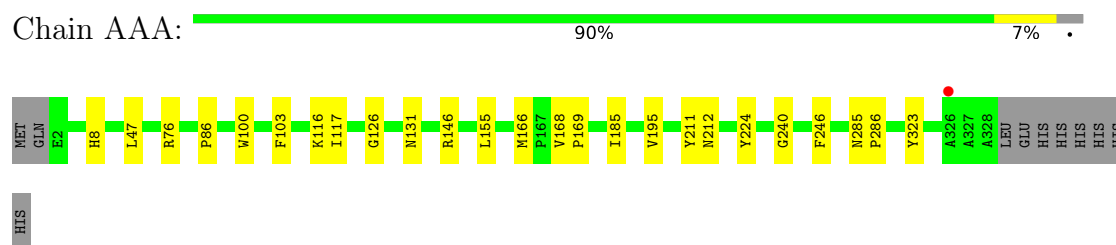
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	AAA	187	Total	O	0	0
			187	187		
3	BBB	90	Total	O	0	0
			90	90		

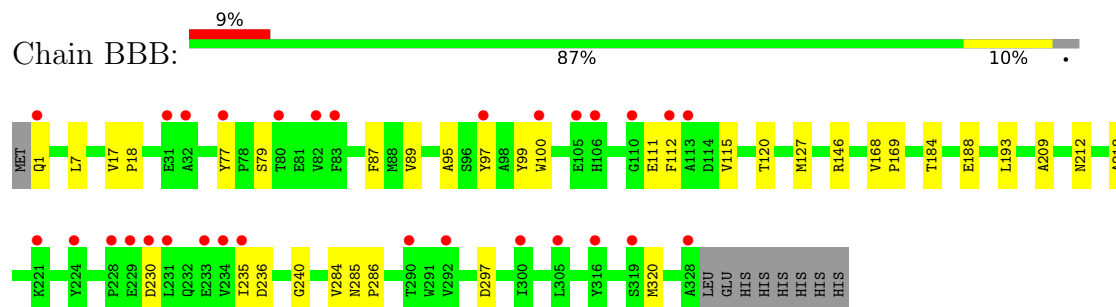
3 Residue-property plots [i](#)

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: TRAP dicarboxylate transporter, DctP subunit



- Molecule 1: TRAP dicarboxylate transporter, DctP subunit



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	64.12Å 70.20Å 85.01Å 90.00° 93.12° 90.00°	Depositor
Resolution (Å)	64.02 – 1.91 64.02 – 1.91	Depositor EDS
% Data completeness (in resolution range)	98.5 (64.02-1.91) 98.5 (64.02-1.91)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.01 (at 1.91Å)	Xtriage
Refinement program	REFMAC 5.8.0258	Depositor
R, R_{free}	0.200 , 0.261 0.210 , 0.268	Depositor DCC
R_{free} test set	2852 reflections (4.94%)	wwPDB-VP
Wilson B-factor (Å ²)	21.9	Xtriage
Anisotropy	0.805	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	(Not available) , (Not available)	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	5314	wwPDB-VP
Average B, all atoms (Å ²)	33.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.58% 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: HCl

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	0.74	0/2562	0.83	3/3495 (0.1%)
1	BBB	0.70	0/2571	0.79	0/3507
All	All	0.72	0/5133	0.81	3/7002 (0.0%)

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	AAA	76	ARG	NE-CZ-NH1	10.41	125.51	120.30
1	AAA	76	ARG	NE-CZ-NH2	-7.68	116.46	120.30
1	AAA	76	ARG	CB-CG-CD	5.69	126.39	111.60

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	AAA	2503	0	2411	15	0
1	BBB	2512	0	2422	21	0
2	AAA	11	0	9	1	0
2	BBB	11	0	9	0	0
3	AAA	187	0	0	1	0
3	BBB	90	0	0	1	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
All	All	5314	0	4851	36	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 4.

All (36) 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:AAA:131:ASN:HB2	3:AAA:643:HOH:O	1.76	0.85
1:BBB:285:ASN:N	1:BBB:286:PRO:CD	2.68	0.57
1:BBB:297:ASP:O	1:BBB:297:ASP:OD1	2.25	0.54
1:AAA:168:VAL:HG12	1:AAA:169:PRO:HD3	1.90	0.53
1:BBB:100:TRP:CH2	1:BBB:240:GLY:HA2	2.43	0.53
1:BBB:284:VAL:C	1:BBB:286:PRO:HD2	2.31	0.51
1:BBB:97:TYR:CE1	1:BBB:320:MET:SD	3.04	0.50
1:BBB:100:TRP:CZ2	1:BBB:240:GLY:HA2	2.48	0.49
1:AAA:103:PHE:CZ	1:AAA:117:ILE:HB	2.48	0.48
1:BBB:115:VAL:HG11	1:BBB:218:ALA:HB1	1.95	0.48
1:AAA:155:LEU:C	1:AAA:155:LEU:HD23	2.35	0.47
1:AAA:285:ASN:N	1:AAA:286:PRO:CD	2.78	0.46
1:BBB:87:PHE:HA	1:BBB:209:ALA:O	2.17	0.45
1:BBB:77:TYR:CD1	1:BBB:112:PHE:CE1	3.04	0.45
1:AAA:185:ILE:HD11	1:AAA:195:VAL:HG21	1.98	0.45
1:AAA:146:ARG:HH12	2:AAA:401:HCl:C1	2.30	0.45
1:BBB:168:VAL:N	1:BBB:169:PRO:CD	2.80	0.45
1:AAA:126:GLY:HA3	1:AAA:211:TYR:CE1	2.52	0.45
1:AAA:146:ARG:HG2	1:AAA:166:MET:HG2	1.99	0.44
1:AAA:116:LYS:HE2	1:AAA:224:TYR:CE1	2.52	0.44
1:AAA:8:HIS:CE1	1:AAA:47:LEU:HB2	2.53	0.43
1:AAA:168:VAL:N	1:AAA:169:PRO:CD	2.82	0.43
1:BBB:17:VAL:HB	1:BBB:18:PRO:HD3	1.99	0.43
1:BBB:127:MET:O	1:BBB:184:THR:HA	2.19	0.43
1:AAA:100:TRP:CH2	1:AAA:240:GLY:HA2	2.54	0.43
1:BBB:168:VAL:HG12	1:BBB:169:PRO:HD3	2.00	0.42
1:BBB:168:VAL:HG22	1:BBB:193:LEU:HD11	2.01	0.42
1:AAA:146:ARG:CG	1:AAA:166:MET:HG2	2.49	0.42
1:BBB:235:ILE:HG22	1:BBB:236:ASP:N	2.35	0.42
1:BBB:99:TYR:CG	1:BBB:120:THR:HB	2.54	0.42
1:BBB:89:VAL:HG13	1:BBB:95:ALA:HB2	2.02	0.42
1:BBB:1:GLN:HG3	3:BBB:555:HOH:O	2.19	0.41
1:BBB:7:LEU:C	1:BBB:7:LEU:HD23	2.40	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:AAA:246:PHE:HB2	1:AAA:323:TYR:HB3	2.02	0.41
1:BBB:79:SER:HB2	1:BBB:111:GLU:OE2	2.21	0.40
1:BBB:230:ASP:OD1	1:BBB:230:ASP:N	2.54	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	325/337 (96%)	321 (99%)	4 (1%)	0	100	100
1	BBB	326/337 (97%)	312 (96%)	14 (4%)	0	100	100
All	All	651/674 (97%)	633 (97%)	18 (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	266/276 (96%)	264 (99%)	2 (1%)	81	81
1	BBB	267/276 (97%)	264 (99%)	3 (1%)	73	72
All	All	533/552 (97%)	528 (99%)	5 (1%)	78	78

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	AAA	86	PRO
1	AAA	212	ASN
1	BBB	146	ARG
1	BBB	188	GLU
1	BBB	212	ASN

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

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no monosaccharides in this entry.

5.6 Ligand geometry ⓘ

2 ligands are 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	HCI	AAA	401	-	8,11,11	1.36	1 (12%)	10,13,13	2.05	2 (20%)
2	HCI	BBB	401	-	8,11,11	1.24	1 (12%)	10,13,13	2.00	2 (20%)

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	HCI	AAA	401	-	-	2/3/5/5	0/1/1/1
2	HCI	BBB	401	-	-	2/3/5/5	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	BBB	401	HCI	C3-C2	-2.78	1.34	1.53
2	AAA	401	HCI	C3-C2	-2.51	1.36	1.53

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	AAA	401	HCI	C3-C2-C1	4.93	120.95	112.67
2	BBB	401	HCI	C3-C2-C1	4.41	120.07	112.67
2	BBB	401	HCI	C2-C3-C1'	3.37	125.10	113.28
2	AAA	401	HCI	C2-C3-C1'	3.35	125.06	113.28

There are no chirality outliers.

All (4) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	BBB	401	HCI	C2'-C1'-C3-C2
2	AAA	401	HCI	C6'-C1'-C3-C2
2	AAA	401	HCI	C2'-C1'-C3-C2
2	BBB	401	HCI	C6'-C1'-C3-C2

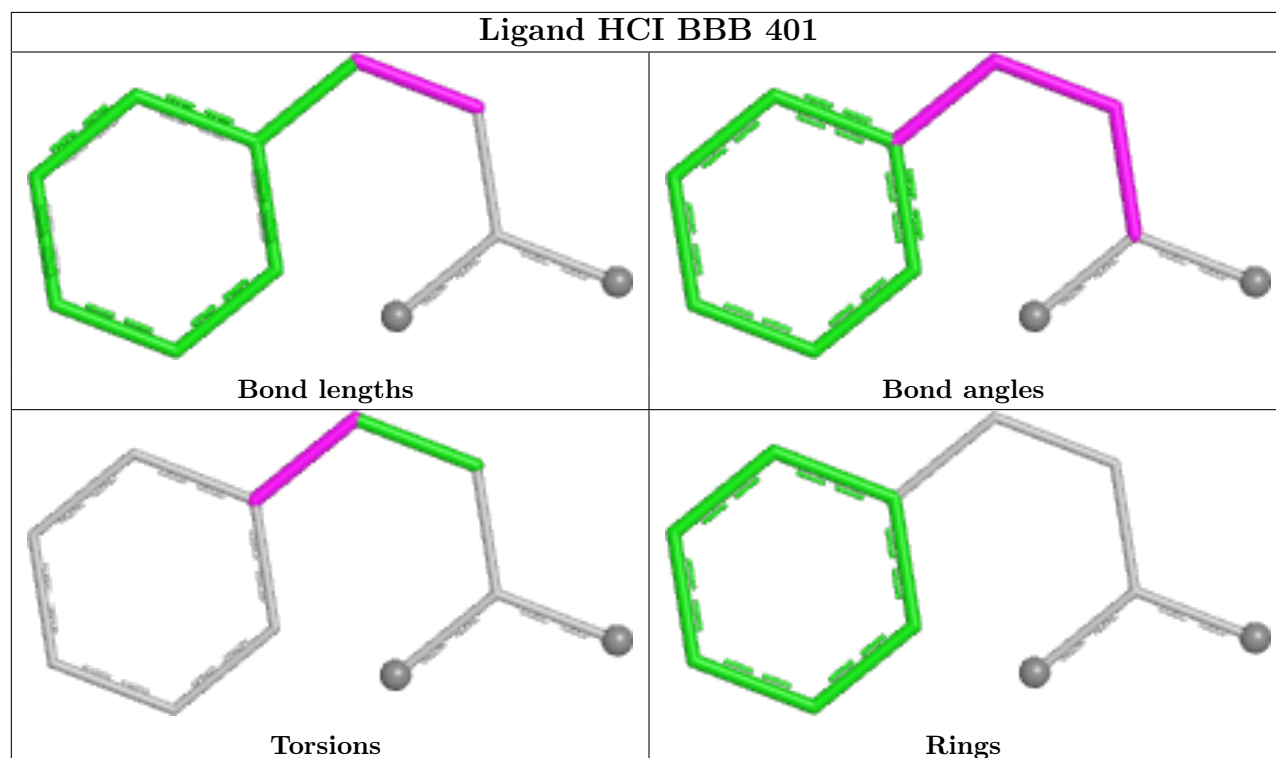
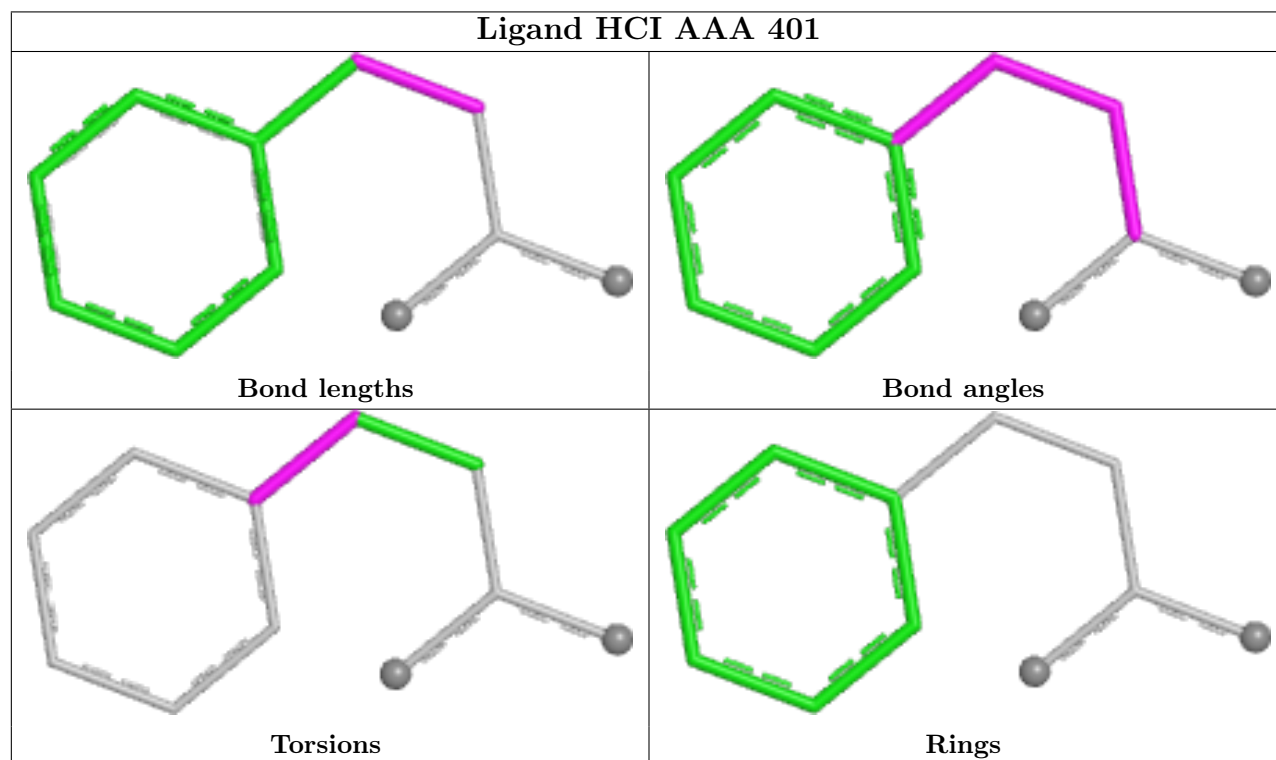
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	AAA	401	HCI	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	AAA	327/337 (97%)	-0.01	1 (0%) 94 94	14, 23, 42, 73	0
1	BBB	328/337 (97%)	0.55	30 (9%) 9 11	14, 36, 78, 106	0
All	All	655/674 (97%)	0.27	31 (4%) 31 34	14, 27, 70, 106	0

All (31) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	BBB	300	ILE	5.7
1	BBB	328	ALA	4.6
1	BBB	1	GLN	4.6
1	BBB	112	PHE	4.0
1	BBB	221	LYS	3.8
1	BBB	80	THR	3.5
1	AAA	326	ALA	3.4
1	BBB	113	ALA	3.4
1	BBB	100	TRP	3.3
1	BBB	224	TYR	3.0
1	BBB	305	LEU	2.9
1	BBB	233	GLU	2.8
1	BBB	234	VAL	2.8
1	BBB	106	HIS	2.7
1	BBB	235	ILE	2.6
1	BBB	82	VAL	2.5
1	BBB	228	PRO	2.5
1	BBB	316	TYR	2.5
1	BBB	31	GLU	2.4
1	BBB	110	GLY	2.3
1	BBB	319	SER	2.3
1	BBB	32	ALA	2.3
1	BBB	229	GLU	2.3
1	BBB	77	TYR	2.3

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Mol	Chain	Res	Type	RSRZ
1	BBB	83	PHE	2.3
1	BBB	231	LEU	2.3
1	BBB	290	THR	2.2
1	BBB	292	VAL	2.2
1	BBB	230	ASP	2.1
1	BBB	97	TYR	2.1
1	BBB	105	GLU	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 monosaccharides in this entry.

6.4 Ligands [i](#)

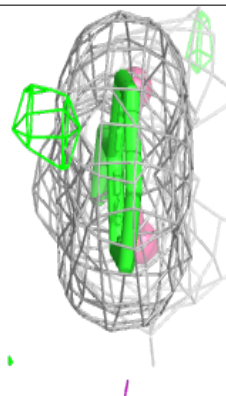
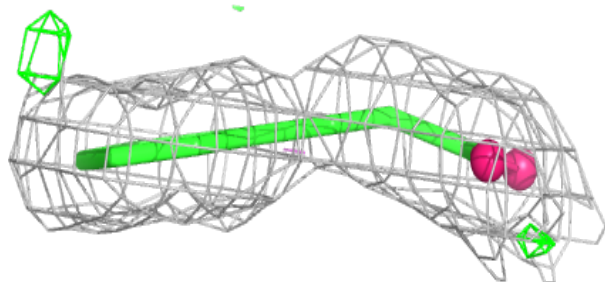
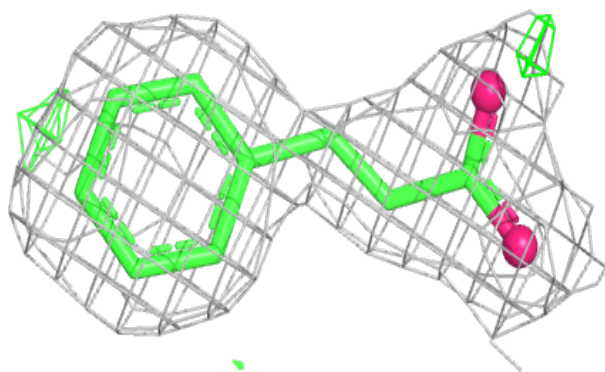
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	HCI	BBB	401	11/11	0.93	0.11	13,25,46,50	0
2	HCI	AAA	401	11/11	0.95	0.12	8,21,34,55	0

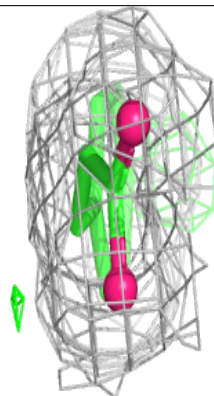
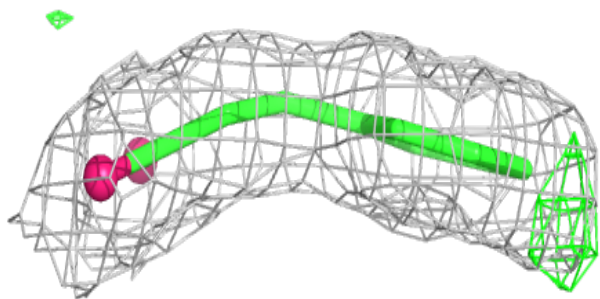
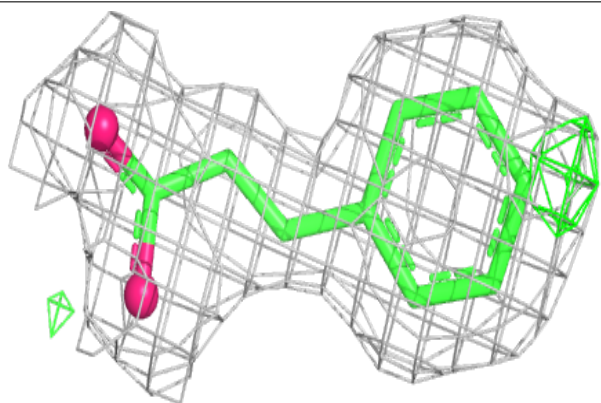
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation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

Electron density around HCI BBB 401:

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

**Electron density around HCI AAA 401:**

$2mF_o-DF_c$ (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.