



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 12:24 PM UTC

PDB ID : 3AHI / pdb_00003ahi
Title : H320A mutant of Phosphoketolase from Bifidobacterium Breve complexed with acetyl thiamine diphosphate
Authors : Suzuki, R.; Katayama, T.; Kim, B.-J.; Wakagi, T.; Shoun, H.; Ashida, H.; Yamamoto, K.; Fushinobu, S.
Deposited on : 2010-04-22
Resolution : 2.10 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

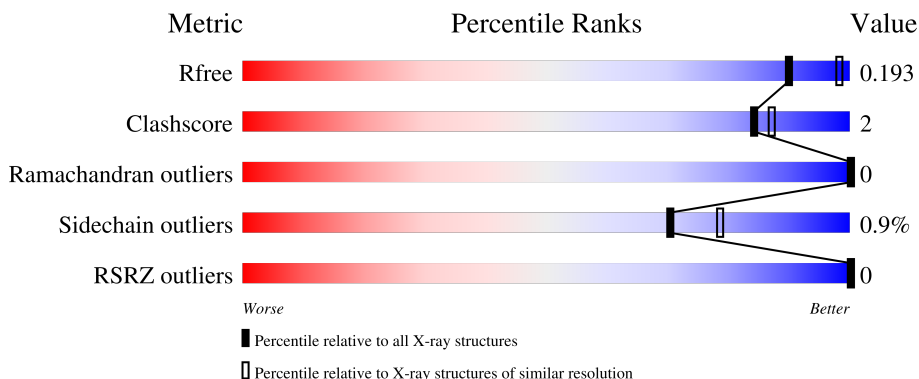
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	845	 83% 11% • 5%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 7093 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 Xylulose 5-phosphate/fructose 6-phosphate phosphoketolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	802	Total	C	N	O	S	0	0	0
			6374	4050	1083	1217	24			

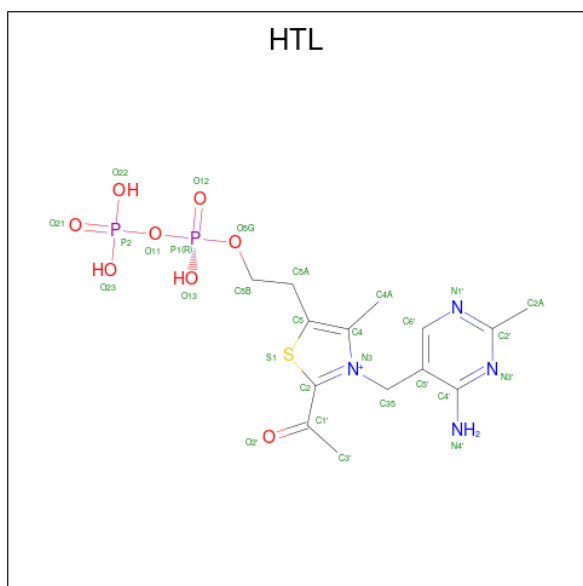
There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-19	MET	-	expression tag	UNP D6PAH1
A	-18	GLY	-	expression tag	UNP D6PAH1
A	-17	SER	-	expression tag	UNP D6PAH1
A	-16	SER	-	expression tag	UNP D6PAH1
A	-15	HIS	-	expression tag	UNP D6PAH1
A	-14	HIS	-	expression tag	UNP D6PAH1
A	-13	HIS	-	expression tag	UNP D6PAH1
A	-12	HIS	-	expression tag	UNP D6PAH1
A	-11	HIS	-	expression tag	UNP D6PAH1
A	-10	HIS	-	expression tag	UNP D6PAH1
A	-9	SER	-	expression tag	UNP D6PAH1
A	-8	SER	-	expression tag	UNP D6PAH1
A	-7	GLY	-	expression tag	UNP D6PAH1
A	-6	LEU	-	expression tag	UNP D6PAH1
A	-5	VAL	-	expression tag	UNP D6PAH1
A	-4	PRO	-	expression tag	UNP D6PAH1
A	-3	ARG	-	expression tag	UNP D6PAH1
A	-2	GLY	-	expression tag	UNP D6PAH1
A	-1	SER	-	expression tag	UNP D6PAH1
A	0	HIS	-	expression tag	UNP D6PAH1
A	320	ALA	HIS	engineered mutation	UNP D6PAH1

- Molecule 2 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is 2-ACETYL-THIAMINE DIPHOSPHATE (CCD ID: HTL) (formula: $C_{14}H_{21}N_4O_8P_2S$).



Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
3	A	1	Total	C	N	O	P	S	0	0
			29	14	4	8	2	1		

- Molecule 4 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Na	0	0
			1	1		

- Molecule 5 is 1,2-ETHANEDIOL (CCD ID: EDO) (formula: $C_2H_6O_2$).



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

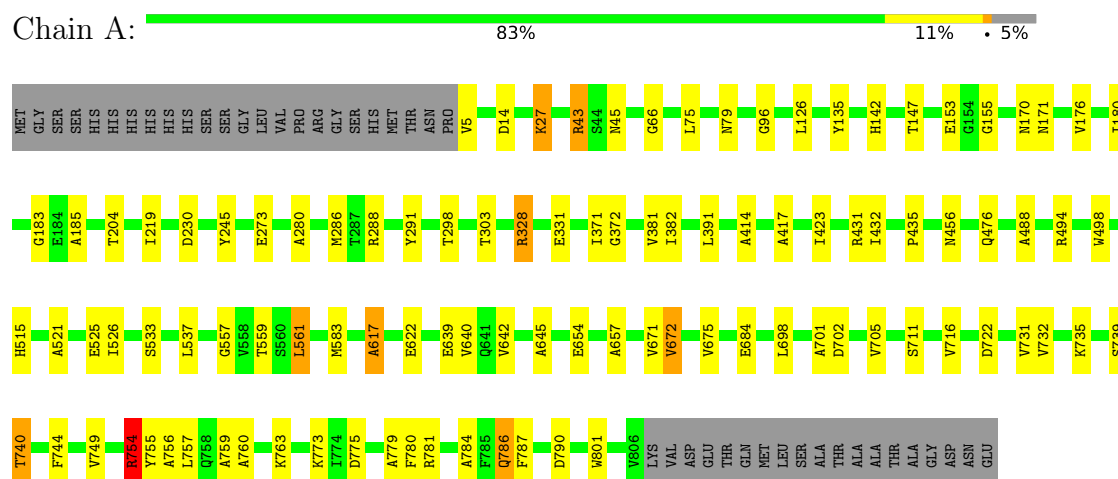
- Molecule 6 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	648	Total O 648 648	0	0

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: Xylulose 5-phosphate/fructose 6-phosphate phosphoketolase



4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	174.43Å 174.43Å 163.81Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.21 – 2.10 34.21 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.21-2.10) 99.9 (34.21-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	9.88 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.150 , 0.194 0.149 , 0.193	Depositor DCC
R_{free} test set	3692 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å ²)	23.8	Xtriage
Anisotropy	0.032	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 32.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	7093	wwPDB-VP
Average B, all atoms (Å ²)	25.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.49% 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: EDO, NA, HTL, MG

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	1.57	49/6547 (0.7%)	1.24	27/8901 (0.3%)

All (49) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	779	ALA	CA-CB	10.02	1.69	1.53
1	A	219	ILE	CA-CB	8.83	1.65	1.54
1	A	716	VAL	CA-CB	-7.79	1.44	1.54
1	A	617	ALA	CA-CB	7.50	1.65	1.53
1	A	732	VAL	CA-C	7.38	1.62	1.52
1	A	701	ALA	CA-CB	7.22	1.65	1.53
1	A	417	ALA	CA-CB	7.18	1.64	1.53
1	A	5	VAL	N-CA	7.11	1.59	1.46
1	A	180	ILE	CA-CB	-6.78	1.46	1.54
1	A	749	VAL	CA-CB	6.53	1.61	1.54
1	A	675	VAL	CA-CB	-6.40	1.48	1.55
1	A	185	ALA	CA-CB	6.30	1.64	1.53
1	A	559	THR	N-CA	6.29	1.54	1.46
1	A	515	HIS	CA-C	6.04	1.60	1.52
1	A	740	THR	CA-CB	5.92	1.60	1.53
1	A	183	GLY	N-CA	5.88	1.53	1.45
1	A	711	SER	CA-CB	5.86	1.60	1.53
1	A	775	ASP	CA-C	-5.83	1.45	1.52
1	A	488	ALA	CA-CB	5.81	1.62	1.53
1	A	787	PHE	N-CA	-5.73	1.39	1.46
1	A	303	THR	CA-CB	5.64	1.61	1.54
1	A	14	ASP	N-CA	5.64	1.54	1.46
1	A	382	ILE	CA-CB	5.61	1.62	1.54
1	A	280	ALA	CA-CB	5.61	1.62	1.53
1	A	640	VAL	CA-CB	5.58	1.62	1.54
1	A	759	ALA	C-O	5.51	1.30	1.24

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	298	THR	CA-C	5.51	1.57	1.52
1	A	757	LEU	CA-C	5.50	1.59	1.52
1	A	79	ASN	C-O	5.50	1.30	1.24
1	A	27	LYS	C-O	-5.50	1.17	1.24
1	A	780	PHE	CA-C	5.49	1.60	1.52
1	A	757	LEU	C-O	-5.43	1.17	1.24
1	A	671	VAL	CA-CB	-5.41	1.47	1.54
1	A	639	GLU	CA-C	5.34	1.59	1.52
1	A	684	GLU	CA-C	5.34	1.59	1.52
1	A	642	VAL	CA-CB	5.31	1.62	1.54
1	A	66	GLY	N-CA	5.30	1.52	1.45
1	A	672	VAL	CA-C	5.30	1.59	1.52
1	A	291	TYR	C-O	-5.29	1.16	1.24
1	A	754	ARG	CD-NE	-5.25	1.38	1.46
1	A	705	VAL	C-O	-5.20	1.18	1.24
1	A	533	SER	C-O	5.19	1.31	1.23
1	A	204	THR	N-CA	5.12	1.52	1.46
1	A	760	ALA	C-O	-5.06	1.17	1.24
1	A	731	VAL	N-CA	5.06	1.52	1.46
1	A	230	ASP	CG-OD1	5.04	1.34	1.25
1	A	372	GLY	N-CA	5.03	1.52	1.45
1	A	773	LYS	CA-C	5.03	1.59	1.52
1	A	45	ASN	CA-C	5.01	1.59	1.52

All (27) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	328	ARG	NE-CZ-NH2	-7.86	112.13	119.20
1	A	328	ARG	NE-CZ-NH1	6.99	128.49	121.50
1	A	126	LEU	N-CA-C	-6.91	103.19	111.69
1	A	328	ARG	CD-NE-CZ	6.90	134.06	124.40
1	A	176	VAL	N-CA-C	6.80	114.88	108.15
1	A	561	LEU	CB-CA-C	-6.13	101.25	110.88
1	A	328	ARG	CG-CD-NE	-6.02	98.76	112.00
1	A	382	ILE	CB-CA-C	-6.01	103.17	111.65
1	A	755	TYR	N-CA-C	-5.98	104.33	111.69
1	A	759	ALA	N-CA-C	5.95	117.77	111.28
1	A	219	ILE	CB-CA-C	-5.92	104.05	112.22
1	A	414	ALA	N-CA-C	-5.73	105.11	111.36
1	A	371	ILE	N-CA-C	-5.69	104.81	110.62
1	A	526	ILE	CA-C-N	-5.64	113.86	119.56
1	A	526	ILE	C-N-CA	-5.64	113.86	119.56

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	622	GLU	N-CA-C	5.56	117.34	111.28
1	A	557	GLY	N-CA-C	5.51	126.25	113.18
1	A	521	ALA	N-CA-C	-5.47	105.40	111.36
1	A	456	ASN	CA-C-N	-5.42	115.19	120.34
1	A	456	ASN	C-N-CA	-5.42	115.19	120.34
1	A	171	ASN	CA-C-N	-5.33	114.33	119.87
1	A	171	ASN	C-N-CA	-5.33	114.33	119.87
1	A	722	ASP	N-CA-C	-5.28	105.55	112.41
1	A	779	ALA	N-CA-C	-5.27	105.58	112.23
1	A	786	GLN	N-CA-C	-5.06	105.95	111.82
1	A	288	ARG	CA-C-N	-5.01	115.44	120.85
1	A	288	ARG	C-N-CA	-5.01	115.44	120.85

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	6374	0	6083	29	1
2	A	1	0	0	0	0
3	A	29	0	18	0	0
4	A	1	0	0	0	0
5	A	40	0	60	1	0
6	A	648	0	0	4	1
All	All	7093	0	6161	29	1

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 2.

All (29) 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:735:LYS:HD3	6:A:1433:HOH:O	2.05	0.57
1:A:170:ASN:HD21	1:A:431:ARG:HH11	1.54	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:435:PRO:HA	1:A:476:GLN:O	2.07	0.54
1:A:27:LYS:HE2	6:A:949:HOH:O	2.08	0.53
1:A:654:GLU:OE1	1:A:754:ARG:HD3	2.09	0.52
1:A:328:ARG:O	1:A:328:ARG:HG2	2.09	0.51
1:A:423:ILE:HD11	1:A:432:ILE:HD12	1.93	0.49
1:A:43:ARG:NH2	1:A:135:TYR:OH	2.47	0.48
1:A:583:MET:HA	1:A:617:ALA:HB1	1.96	0.47
1:A:756:ALA:HB2	1:A:781:ARG:CZ	2.45	0.47
1:A:654:GLU:OE1	1:A:754:ARG:CD	2.62	0.47
1:A:525:GLU:HB3	6:A:1349:HOH:O	2.15	0.47
1:A:657:ALA:HA	1:A:801:TRP:CZ2	2.50	0.46
1:A:423:ILE:HD11	1:A:432:ILE:CD1	2.44	0.46
1:A:763:LYS:HE3	1:A:763:LYS:HB2	1.70	0.46
1:A:494:ARG:N	1:A:494:ARG:HD3	2.32	0.44
1:A:331:GLU:HG2	6:A:1442:HOH:O	2.16	0.43
1:A:702:ASP:OD1	5:A:829:EDO:O1	2.34	0.43
1:A:498:TRP:CE2	1:A:537:LEU:HD13	2.54	0.43
1:A:96:GLY:HA3	1:A:153:GLU:O	2.19	0.42
1:A:645:ALA:HA	1:A:672:VAL:O	2.20	0.42
1:A:698:LEU:HD23	1:A:698:LEU:HA	1.92	0.41
1:A:744:PHE:CE1	1:A:784:ALA:HB3	2.55	0.41
1:A:786:GLN:HE21	1:A:790:ASP:CG	2.28	0.41
1:A:754:ARG:HH22	1:A:801:TRP:HB3	1.84	0.41
1:A:142:HIS:CD2	1:A:155:GLY:HA2	2.56	0.40
1:A:75:LEU:HD23	1:A:75:LEU:HA	1.99	0.40
1:A:245:TYR:OH	1:A:273:GLU:OE2	2.35	0.40
1:A:739:SER:OG	1:A:740:THR:N	2.55	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:286:MET:CE	6:A:1071:HOH:O[6_565]	2.10	0.10

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	800/845 (95%)	765 (96%)	35 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	676/711 (95%)	670 (99%)	6 (1%)	70	78

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

Mol	Chain	Res	Type
1	A	43	ARG
1	A	147	THR
1	A	381	VAL
1	A	391	LEU
1	A	561	LEU
1	A	754	ARG

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	39	GLN
1	A	79	ASN
1	A	105	GLN
1	A	118	ASN
1	A	132	GLN
1	A	170	ASN
1	A	321	GLN
1	A	441	ASN

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Mol	Chain	Res	Type
1	A	472	GLN
1	A	549	ASN
1	A	554	GLN
1	A	728	ASN
1	A	758	GLN
1	A	786	GLN

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 13 ligands modelled in this entry, 2 are monoatomic - leaving 11 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	$\# Z > 2$
5	EDO	A	833	-	3,3,3	0.52	0	2,2,2	0.71	0
5	EDO	A	831	-	3,3,3	0.54	0	2,2,2	0.51	0
5	EDO	A	830	-	3,3,3	0.72	0	2,2,2	0.38	0
5	EDO	A	837	-	3,3,3	0.70	0	2,2,2	0.94	0
3	HTL	A	827	2	29,30,30	1.65	8 (27%)	35,45,45	2.09	9 (25%)
5	EDO	A	829	-	3,3,3	0.67	0	2,2,2	0.24	0
5	EDO	A	836	-	3,3,3	0.20	0	2,2,2	0.96	0
5	EDO	A	838	-	3,3,3	0.53	0	2,2,2	0.49	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	EDO	A	834	-	3,3,3	0.74	0	2,2,2	1.31	0
5	EDO	A	835	-	3,3,3	0.40	0	2,2,2	0.68	0
5	EDO	A	832	-	3,3,3	0.71	0	2,2,2	0.22	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
5	EDO	A	833	-	-	1/1/1/1	-
5	EDO	A	831	-	-	0/1/1/1	-
5	EDO	A	830	-	-	1/1/1/1	-
5	EDO	A	837	-	-	0/1/1/1	-
3	HTL	A	827	2	-	4/19/21/21	0/2/2/2
5	EDO	A	829	-	-	0/1/1/1	-
5	EDO	A	836	-	-	1/1/1/1	-
5	EDO	A	838	-	-	0/1/1/1	-
5	EDO	A	834	-	-	0/1/1/1	-
5	EDO	A	835	-	-	1/1/1/1	-
5	EDO	A	832	-	-	0/1/1/1	-

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	827	HTL	C35-C5'	3.57	1.57	1.51
3	A	827	HTL	C1'-C2	3.23	1.52	1.48
3	A	827	HTL	C4'-N3'	3.02	1.39	1.35
3	A	827	HTL	P1-O13	-2.81	1.42	1.55
3	A	827	HTL	C3'-C1'	2.61	1.55	1.50
3	A	827	HTL	C35-N3	2.25	1.50	1.47
3	A	827	HTL	C5-C4	2.25	1.39	1.35
3	A	827	HTL	C2-S1	2.06	1.78	1.71

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	827	HTL	C35-C5'-C4'	4.88	131.26	122.36
3	A	827	HTL	O2'-C1'-C2	4.48	123.36	118.80
3	A	827	HTL	C2A-C2'-N1'	4.38	121.86	117.20
3	A	827	HTL	C6'-N1'-C2'	3.72	122.19	116.07
3	A	827	HTL	N1'-C2'-N3'	-3.47	119.75	125.53

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	827	HTL	C35-C5'-C6'	-3.18	114.70	120.69
3	A	827	HTL	C5A-C5-C4	3.18	136.15	128.17
3	A	827	HTL	C3'-C1'-C2	-3.00	115.14	118.17
3	A	827	HTL	C4-C5-S1	-2.09	108.40	110.56

There are no chirality outliers.

All (8) torsion outliers are listed below:

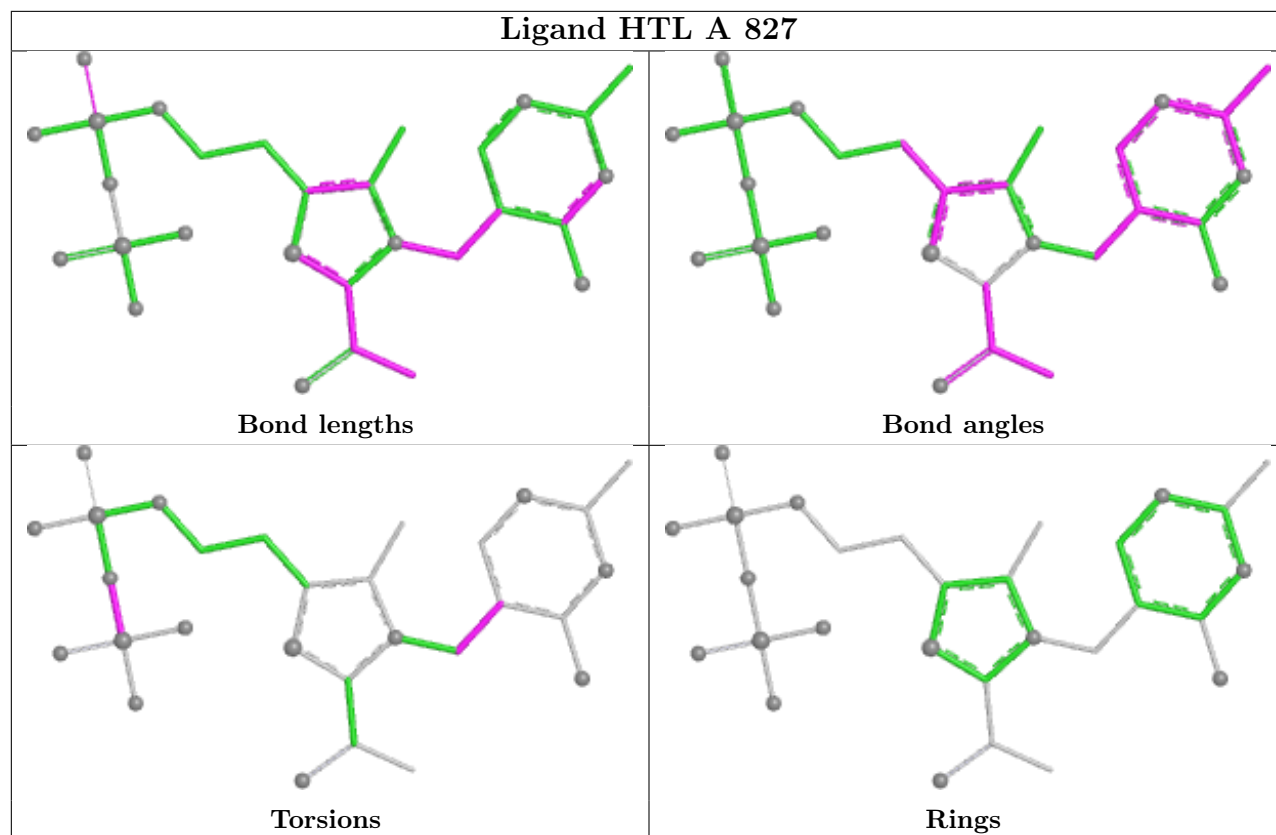
Mol	Chain	Res	Type	Atoms
3	A	827	HTL	N3-C35-C5'-C4'
5	A	833	EDO	O1-C1-C2-O2
3	A	827	HTL	N3-C35-C5'-C6'
5	A	835	EDO	O1-C1-C2-O2
3	A	827	HTL	P1-O11-P2-O22
5	A	836	EDO	O1-C1-C2-O2
3	A	827	HTL	P1-O11-P2-O23
5	A	830	EDO	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	829	EDO	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	802/845 (94%)	-0.69	0 100 100	14, 22, 37, 56	0

There are no RSRZ outliers to report.

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.

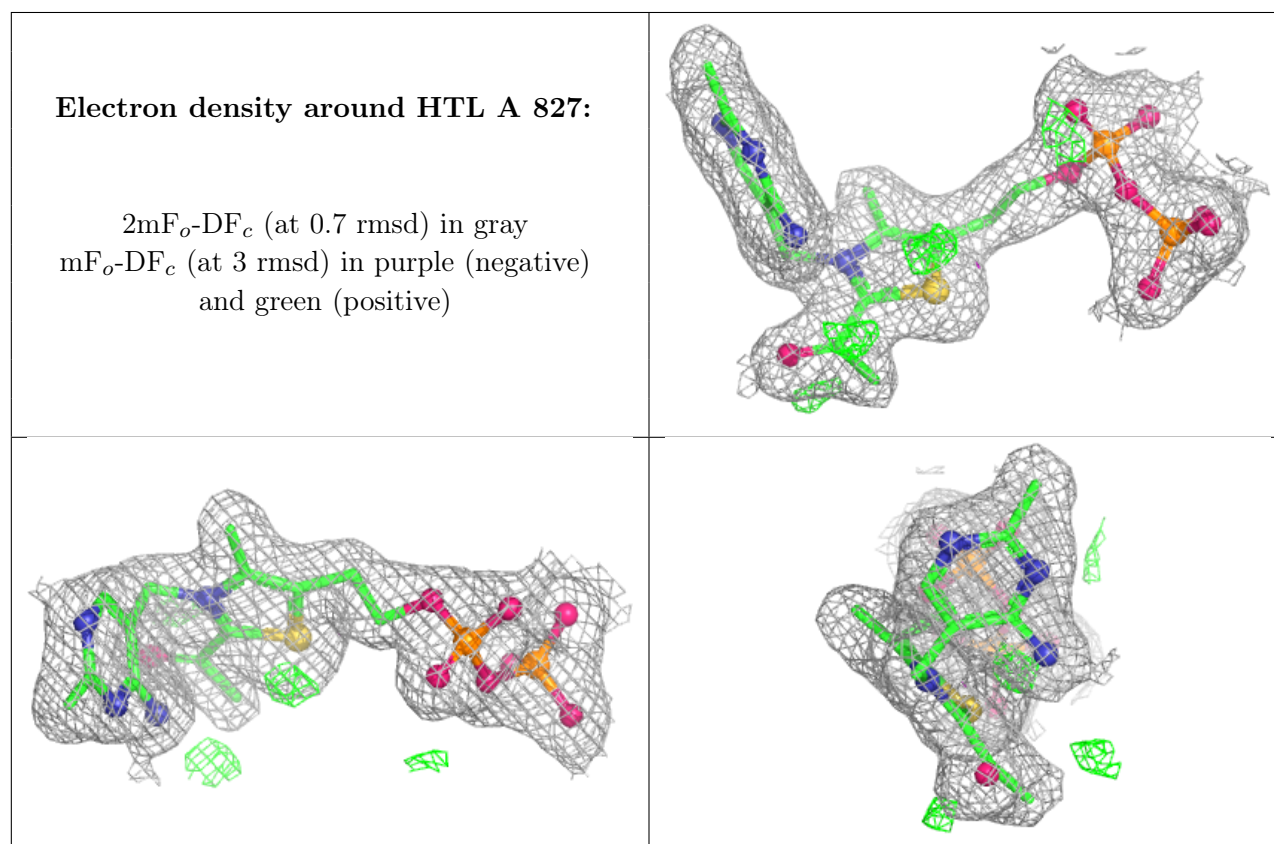
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	EDO	A	835	4/4	0.84	0.20	55,57,57,59	0
5	EDO	A	830	4/4	0.86	0.13	50,50,51,53	0
5	EDO	A	831	4/4	0.88	0.17	59,60,61,63	0
5	EDO	A	829	4/4	0.89	0.12	41,46,48,52	0
5	EDO	A	834	4/4	0.91	0.14	39,40,41,45	0
5	EDO	A	833	4/4	0.92	0.11	37,40,40,47	0
5	EDO	A	836	4/4	0.93	0.14	39,43,46,49	0
5	EDO	A	832	4/4	0.94	0.10	43,48,48,49	0
4	NA	A	828	1/1	0.96	0.04	34,34,34,34	1

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
5	EDO	A	837	4/4	0.96	0.08	21,21,23,28	0
5	EDO	A	838	4/4	0.97	0.09	30,35,37,37	0
3	HTL	A	827	29/29	0.99	0.04	12,17,26,33	0
2	MG	A	826	1/1	1.00	0.01	16,16,16,16	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.



6.5 Other polymers ⓘ

There are no such residues in this entry.