Full wwPDB X-ray Structure Validation Report (i)

Oct 26, 2023 – 08:29 AM EDT

PDB ID	:	3AHH
Title	:	H142A 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 (i) 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 (i)) were used in the production of this report:

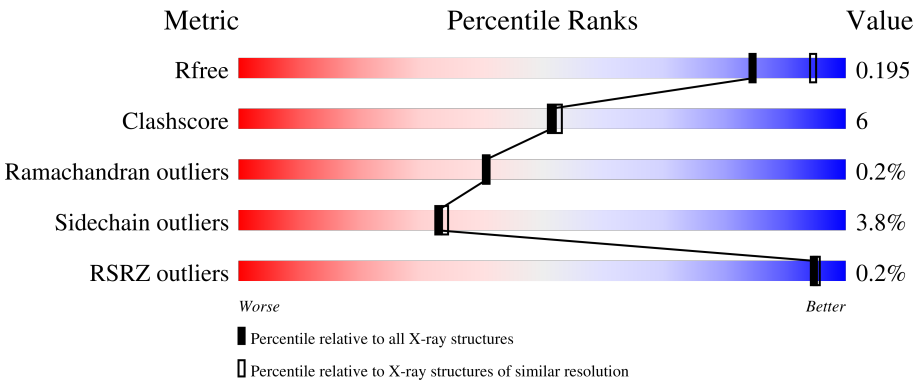
MolProbity	:	4.02b-467
Mogul	:	1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
buster-report	:	1.1.7 (2018)
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

1 Overall quality at a glance (i)

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}	130704	5197 (2.10-2.10)
Clashscore	141614	5710 (2.10-2.10)
Ramachandran outliers	138981	5647 (2.10-2.10)
Sidechain outliers	138945	5648 (2.10-2.10)
RSRZ outliers	127900	5083 (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 <=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	82% 10% • • 5%

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
5	EDO	A	836	-	-	X	-
6	PG4	A	837	-	-	X	-

2 Entry composition (i)

There are 7 unique types of molecules in this entry. The entry contains 7004 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
			Total	C	N	O	S			
1	A	802	6374	4050	1083	1217	24	0	0	0

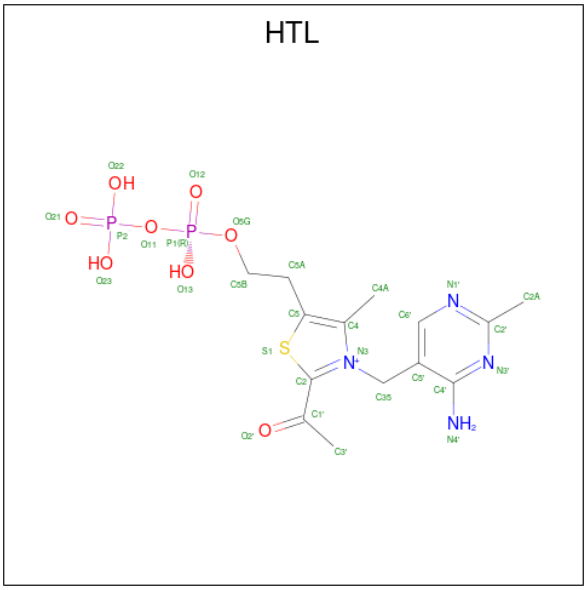
There are 21 discrepancies between the modelled and reference sequences:

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	142	ALA	HIS	engineered mutation	UNP D6PAH1

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

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

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

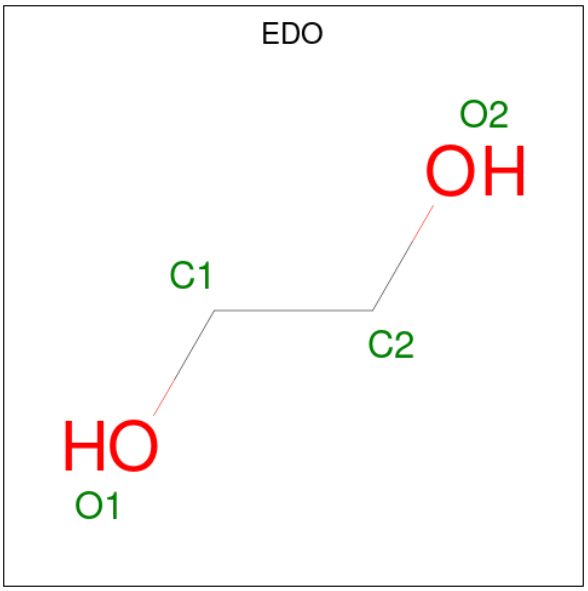


Mol	Chain	Residues	Atoms						ZeroOcc	AltConf
			Total	C	N	O	P	S		
3	A	1	29	14	4	8	2	1	0	0

- Molecule 4 is SODIUM ION (three-letter code: NA) (formula: Na).

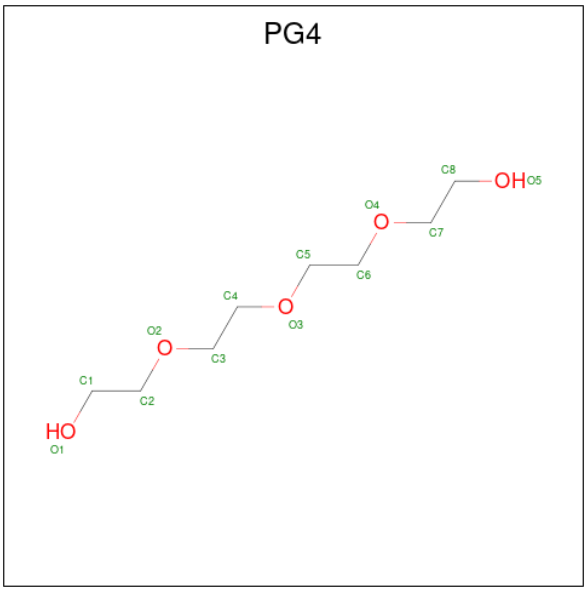
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Na		
4	A	2	2	2	0	0

- Molecule 5 is 1,2-ETHANEDIOL (three-letter code: EDO) (formula: $C_2H_6O_2$).



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

- Molecule 6 is TETRAETHYLENE GLYCOL (three-letter code: PG4) (formula: $C_8H_{18}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
6	A	1	13	8	5	0	0

- Molecule 7 is water.

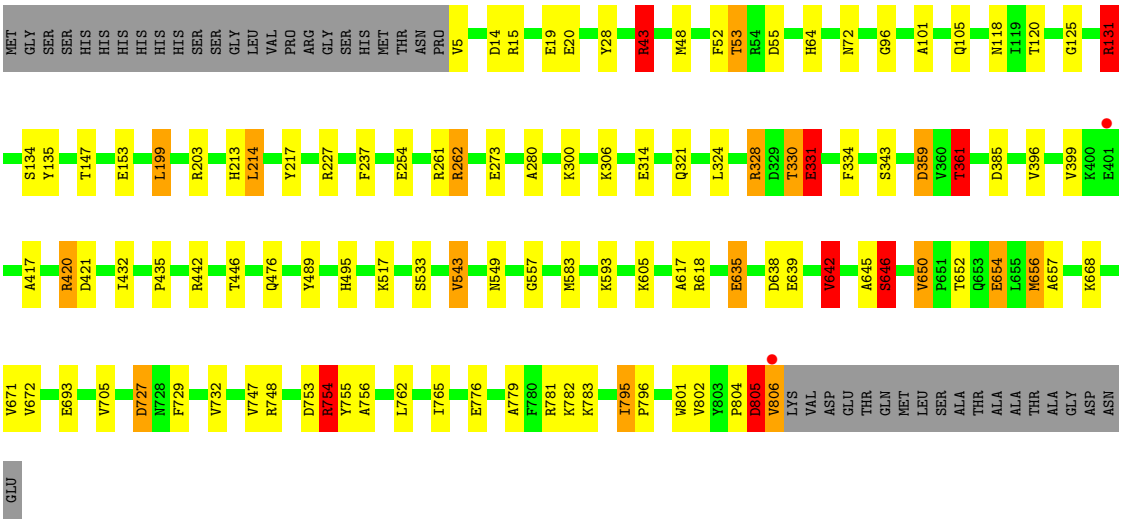
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
7	A	553	553	553	0	0

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: Xylulose 5-phosphate/fructose 6-phosphate phosphoketolase

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α, β, γ	174.61Å 174.61Å 163.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.15 – 2.10 34.15 – 2.10	Depositor EDS
% Data completeness (in resolution range)	100.0 (34.15-2.10) 100.0 (34.15-2.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	9.74 (at 2.10Å)	Xtriage
Refinement program	REFMAC 5.5.0102	Depositor
R, R_{free}	0.158 , 0.196 0.157 , 0.195	Depositor DCC
R_{free} test set	3698 reflections (5.04%)	wwPDB-VP
Wilson B-factor (Å^2)	22.1	Xtriage
Anisotropy	0.030	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 35.7	EDS
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	7004	wwPDB-VP
Average B, all atoms (Å^2)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical values of $< |L| >$, $< L^2 >$ 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: MG, EDO, HTL, PG4, NA

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	1.39	26/6547 (0.4%)	1.17	42/8901 (0.5%)

All (26) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	646	SER	CB-OG	-8.81	1.30	1.42
1	A	359	ASP	CB-CG	-7.31	1.36	1.51
1	A	331	GLU	CG-CD	6.85	1.62	1.51
1	A	654	GLU	CB-CG	6.58	1.64	1.52
1	A	489	TYR	CD1-CE1	6.34	1.48	1.39
1	A	779	ALA	CA-CB	6.20	1.65	1.52
1	A	693	GLU	CG-CD	6.19	1.61	1.51
1	A	20	GLU	CG-CD	6.12	1.61	1.51
1	A	806	VAL	CB-CG1	6.02	1.65	1.52
1	A	261	ARG	CG-CD	5.84	1.66	1.51
1	A	28	TYR	CD1-CE1	5.82	1.48	1.39
1	A	237	PHE	CE2-CZ	5.79	1.48	1.37
1	A	776	GLU	CG-CD	5.72	1.60	1.51
1	A	14	ASP	CB-CG	5.67	1.63	1.51
1	A	755	TYR	CE2-CZ	-5.64	1.31	1.38
1	A	732	VAL	CB-CG2	5.61	1.64	1.52
1	A	343	SER	CB-OG	5.58	1.49	1.42
1	A	5	VAL	N-CA	5.56	1.57	1.46
1	A	805	ASP	N-CA	5.50	1.57	1.46
1	A	19	GLU	CG-CD	5.31	1.59	1.51
1	A	517	LYS	CD-CE	5.29	1.64	1.51
1	A	693	GLU	CB-CG	5.25	1.62	1.52
1	A	280	ALA	CA-CB	5.13	1.63	1.52
1	A	747	VAL	CB-CG1	5.11	1.63	1.52
1	A	417	ALA	CA-CB	5.04	1.63	1.52
1	A	134	SER	CB-OG	-5.03	1.35	1.42

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	262	ARG	NE-CZ-NH2	-23.37	108.61	120.30
1	A	262	ARG	NE-CZ-NH1	20.47	130.53	120.30
1	A	359	ASP	CB-CG-OD1	-15.21	104.61	118.30
1	A	420	ARG	NE-CZ-NH1	14.69	127.64	120.30
1	A	328	ARG	NE-CZ-NH1	12.65	126.63	120.30
1	A	328	ARG	NE-CZ-NH2	-12.65	113.98	120.30
1	A	131	ARG	NE-CZ-NH1	-11.85	114.37	120.30
1	A	420	ARG	NE-CZ-NH2	-11.01	114.80	120.30
1	A	227	ARG	NE-CZ-NH1	10.26	125.43	120.30
1	A	43	ARG	NE-CZ-NH2	-9.16	115.72	120.30
1	A	131	ARG	NE-CZ-NH2	8.59	124.59	120.30
1	A	642	VAL	CG1-CB-CG2	8.32	124.22	110.90
1	A	262	ARG	CD-NE-CZ	8.21	135.10	123.60
1	A	543	VAL	CB-CA-C	-8.14	95.93	111.40
1	A	227	ARG	NE-CZ-NH2	-7.96	116.32	120.30
1	A	754	ARG	NE-CZ-NH1	-7.65	116.47	120.30
1	A	199	LEU	CB-CG-CD1	7.02	122.94	111.00
1	A	214	LEU	CB-CG-CD2	6.76	122.50	111.00
1	A	642	VAL	CB-CA-C	-6.74	98.59	111.40
1	A	359	ASP	CB-CG-OD2	6.69	124.32	118.30
1	A	330	THR	C-N-CA	-6.67	105.02	121.70
1	A	805	ASP	N-CA-C	6.60	128.81	111.00
1	A	727	ASP	CB-CG-OD1	6.54	124.19	118.30
1	A	650	VAL	CG1-CB-CG2	6.52	121.34	110.90
1	A	361	THR	N-CA-CB	-6.36	98.22	110.30
1	A	618	ARG	NE-CZ-NH1	6.26	123.43	120.30
1	A	43	ARG	NE-CZ-NH1	6.24	123.42	120.30
1	A	638	ASP	CB-CG-OD1	6.18	123.86	118.30
1	A	646	SER	CB-CA-C	-6.10	98.52	110.10
1	A	618	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	A	442	ARG	NE-CZ-NH1	5.94	123.27	120.30
1	A	203	ARG	NE-CZ-NH1	-5.50	117.55	120.30
1	A	328	ARG	CG-CD-NE	-5.41	100.45	111.80
1	A	324	LEU	CB-CG-CD2	-5.32	101.96	111.00
1	A	656	MET	CG-SD-CE	-5.29	91.73	100.20
1	A	593	LYS	CD-CE-NZ	5.23	123.73	111.70
1	A	15	ARG	NE-CZ-NH2	-5.21	117.70	120.30
1	A	557	GLY	N-CA-C	5.18	126.06	113.10
1	A	385	ASP	CB-CG-OD1	5.13	122.92	118.30
1	A	549	ASN	C-N-CA	-5.11	111.56	122.30
1	A	646	SER	N-CA-CB	-5.10	102.85	110.50
1	A	420	ARG	CD-NE-CZ	5.04	130.66	123.60

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	6374	0	6083	61	0
2	A	1	0	0	0	0
3	A	29	0	18	3	0
4	A	2	0	0	0	0
5	A	32	0	48	6	0
6	A	13	0	18	7	0
7	A	553	0	0	5	0
All	All	7004	0	6167	69	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 (69) 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:330:THR:O	1:A:331:GLU:CB	1.80	1.20
1:A:131:ARG:HH11	1:A:131:ARG:HG3	1.04	1.08
1:A:330:THR:O	1:A:331:GLU:HB3	1.51	1.04
1:A:131:ARG:HH11	1:A:131:ARG:CG	1.77	0.97
1:A:806:VAL:CG2	7:A:1017:HOH:O	2.16	0.92
1:A:330:THR:O	1:A:331:GLU:HB2	1.71	0.90
1:A:131:ARG:HG3	1:A:131:ARG:NH1	1.90	0.86
5:A:836:EDO:O2	6:A:837:PG4:H72	1.76	0.85
1:A:754:ARG:HH11	1:A:754:ARG:HG2	1.41	0.84
1:A:754:ARG:HH11	1:A:754:ARG:CG	1.94	0.79
6:A:837:PG4:H42	6:A:837:PG4:H82	1.63	0.79
1:A:254:GLU:OE2	1:A:262:ARG:HD3	1.83	0.78
1:A:53:THR:HG23	1:A:55:ASP:H	1.53	0.74
1:A:43:ARG:O	1:A:131:ARG:NH1	2.22	0.72
1:A:805:ASP:N	1:A:805:ASP:OD1	2.23	0.71
1:A:654:GLU:OE1	1:A:754:ARG:NH1	2.24	0.71

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:754:ARG:HG2	1:A:754:ARG:NH1	2.09	0.65
1:A:273:GLU:OE1	7:A:1303:HOH:O	2.15	0.64
1:A:635:GLU:OE1	1:A:635:GLU:HA	2.00	0.62
1:A:118:ASN:HB2	7:A:1047:HOH:O	2.00	0.61
1:A:635:GLU:HB2	1:A:639:GLU:OE2	2.03	0.59
1:A:656:MET:CE	1:A:671:VAL:HG11	2.32	0.59
1:A:53:THR:CG2	1:A:55:ASP:H	2.15	0.58
1:A:806:VAL:HG22	7:A:1017:HOH:O	1.94	0.57
1:A:654:GLU:CD	1:A:754:ARG:HH12	2.08	0.57
1:A:420:ARG:HD2	1:A:421:ASP:OD1	2.04	0.56
1:A:328:ARG:HG2	1:A:328:ARG:O	2.05	0.56
1:A:321:GLN:HE22	6:A:837:PG4:H51	1.74	0.52
1:A:432:ILE:CD1	1:A:446:THR:HG21	2.40	0.52
1:A:331:GLU:HA	1:A:334:PHE:HB3	1.90	0.52
1:A:96:GLY:HA3	1:A:153:GLU:O	2.10	0.52
1:A:646:SER:OG	1:A:652:THR:HA	2.10	0.52
1:A:583:MET:HA	1:A:617:ALA:HB1	1.93	0.51
3:A:827:HTL:H4'2	3:A:827:HTL:C1'	2.24	0.50
1:A:642:VAL:HG22	1:A:765:ILE:HD11	1.94	0.50
1:A:43:ARG:NH2	1:A:135:TYR:OH	2.45	0.49
1:A:805:ASP:C	1:A:806:VAL:HG23	2.33	0.49
1:A:321:GLN:OE1	6:A:837:PG4:H71	2.12	0.49
3:A:827:HTL:C1'	5:A:836:EDO:C2	2.92	0.48
1:A:756:ALA:HB2	1:A:781:ARG:CZ	2.44	0.48
1:A:795:ILE:HD13	1:A:796:PRO:HD2	1.96	0.47
5:A:836:EDO:O2	6:A:837:PG4:C7	2.57	0.47
1:A:43:ARG:HB2	1:A:131:ARG:HH12	1.79	0.47
1:A:254:GLU:OE2	1:A:262:ARG:CD	2.59	0.47
1:A:306:LYS:CE	1:A:314:GLU:OE1	2.63	0.46
1:A:656:MET:HE1	1:A:671:VAL:HG11	1.97	0.46
3:A:827:HTL:C1'	5:A:836:EDO:H21	2.45	0.46
1:A:131:ARG:CG	1:A:131:ARG:NH1	2.55	0.46
1:A:656:MET:HE3	1:A:671:VAL:HG11	1.97	0.46
1:A:306:LYS:HE2	1:A:314:GLU:OE1	2.14	0.46
1:A:361:THR:HG21	7:A:1084:HOH:O	2.16	0.46
1:A:435:PRO:HA	1:A:476:GLN:O	2.15	0.45
1:A:657:ALA:HA	1:A:801:TRP:CZ2	2.52	0.45
1:A:495:HIS:CE1	1:A:533:SER:HG	2.34	0.45
6:A:837:PG4:H42	6:A:837:PG4:H62	1.46	0.44
1:A:43:ARG:HB2	1:A:131:ARG:NH1	2.33	0.44
6:A:837:PG4:H82	6:A:837:PG4:C4	2.39	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:TYR:HB2	1:A:300:LYS:HD3	2.01	0.43
1:A:748:ARG:HA	1:A:753:ASP:OD2	2.19	0.43
1:A:120:THR:O	1:A:125:GLY:HA3	2.19	0.42
1:A:754:ARG:HH11	1:A:754:ARG:CB	2.32	0.42
1:A:72:ASN:HD21	1:A:101:ALA:HA	1.83	0.42
1:A:48:MET:HE3	1:A:52:PHE:CE2	2.54	0.42
1:A:645:ALA:HA	1:A:672:VAL:O	2.20	0.42
1:A:654:GLU:CD	1:A:754:ARG:NH1	2.70	0.42
1:A:705:VAL:HB	1:A:729:PHE:HA	2.01	0.41
1:A:64:HIS:NE2	5:A:836:EDO:H11	2.35	0.41
1:A:64:HIS:NE2	5:A:836:EDO:C1	2.84	0.41
1:A:762:LEU:HD23	1:A:762:LEU:HA	1.92	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	A	800/845 (95%)	759 (95%)	39 (5%)	2 (0%)	41 41

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	331	GLU
1	A	804	PRO

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	A	676/711 (95%)	650 (96%)	26 (4%)	33 34

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	43	ARG
1	A	53	THR
1	A	105	GLN
1	A	131	ARG
1	A	147	THR
1	A	199	LEU
1	A	213	HIS
1	A	214	LEU
1	A	359	ASP
1	A	361	THR
1	A	396	VAL
1	A	399	VAL
1	A	543	VAL
1	A	605	LYS
1	A	635	GLU
1	A	642	VAL
1	A	646	SER
1	A	650	VAL
1	A	668	LYS
1	A	727	ASP
1	A	754	ARG
1	A	782	LYS
1	A	783	LYS
1	A	795	ILE
1	A	802	VAL
1	A	805	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	33	ASN
1	A	39	GLN
1	A	72	ASN
1	A	441	ASN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	A	554	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 13 ligands modelled in this entry, 3 are monoatomic - leaving 10 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	834	-	3,3,3	0.87	0	2,2,2	0.73	0
6	PG4	A	837	-	12,12,12	1.06	0	11,11,11	1.07	1 (9%)
5	EDO	A	835	-	3,3,3	0.47	0	2,2,2	0.44	0
5	EDO	A	831	-	3,3,3	0.64	0	2,2,2	0.64	0
5	EDO	A	836	-	3,3,3	0.24	0	2,2,2	1.03	0
5	EDO	A	832	-	3,3,3	0.39	0	2,2,2	0.49	0
5	EDO	A	829	-	3,3,3	0.68	0	2,2,2	0.28	0
5	EDO	A	830	-	3,3,3	0.60	0	2,2,2	0.21	0
5	EDO	A	833	-	3,3,3	0.61	0	2,2,2	0.71	0
3	HTL	A	827	2	23,30,30	1.72	7 (30%)	31,45,45	2.81	10 (32%)

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	834	-	-	0/1/1/1	-
6	PG4	A	837	-	-	7/10/10/10	-
5	EDO	A	835	-	-	1/1/1/1	-
5	EDO	A	831	-	-	0/1/1/1	-
5	EDO	A	836	-	-	1/1/1/1	-
5	EDO	A	832	-	-	0/1/1/1	-
5	EDO	A	829	-	-	1/1/1/1	-
5	EDO	A	830	-	-	0/1/1/1	-
5	EDO	A	833	-	-	0/1/1/1	-
3	HTL	A	827	2	-	5/16/21/21	0/2/2/2

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	827	HTL	C5A-C5	5.05	1.53	1.50
3	A	827	HTL	C35-C5'	2.65	1.56	1.51
3	A	827	HTL	C5-S1	-2.53	1.69	1.74
3	A	827	HTL	C2'-N1'	2.38	1.38	1.34
3	A	827	HTL	C4'-N3'	2.27	1.38	1.35
3	A	827	HTL	P1-O13	-2.10	1.45	1.55
3	A	827	HTL	C6'-N1'	-2.06	1.30	1.34

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	827	HTL	C5A-C5-C4	9.56	135.10	127.43
3	A	827	HTL	C4-N3-C2	7.16	112.62	108.64
3	A	827	HTL	C5-C4-N3	4.68	117.44	107.66
3	A	827	HTL	C5'-C35-N3	-4.40	105.99	113.26
3	A	827	HTL	C4A-C4-C5	-3.00	121.05	127.60
3	A	827	HTL	C2A-C2'-N1'	2.96	120.39	117.14
3	A	827	HTL	C35-C5'-C6'	-2.91	115.12	120.69
3	A	827	HTL	C35-C5'-C4'	2.68	129.73	121.83
3	A	827	HTL	N1'-C2'-N3'	-2.45	121.32	125.54
3	A	827	HTL	C6'-N1'-C2'	2.11	119.56	115.96
6	A	837	PG4	O3-C4-C3	2.01	119.45	110.39

There are no chirality outliers.

All (15) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	827	HTL	N3-C35-C5'-C4'
6	A	837	PG4	C6-C5-O3-C4
6	A	837	PG4	O3-C5-C6-O4
6	A	837	PG4	C8-C7-O4-C6
6	A	837	PG4	O1-C1-C2-O2
5	A	836	EDO	O1-C1-C2-O2
6	A	837	PG4	O2-C3-C4-O3
6	A	837	PG4	C5-C6-O4-C7
5	A	829	EDO	O1-C1-C2-O2
5	A	835	EDO	O1-C1-C2-O2
6	A	837	PG4	C1-C2-O2-C3
3	A	827	HTL	P1-O11-P2-O21
3	A	827	HTL	P1-O11-P2-O22
3	A	827	HTL	P1-O11-P2-O23
3	A	827	HTL	N3-C35-C5'-C6'

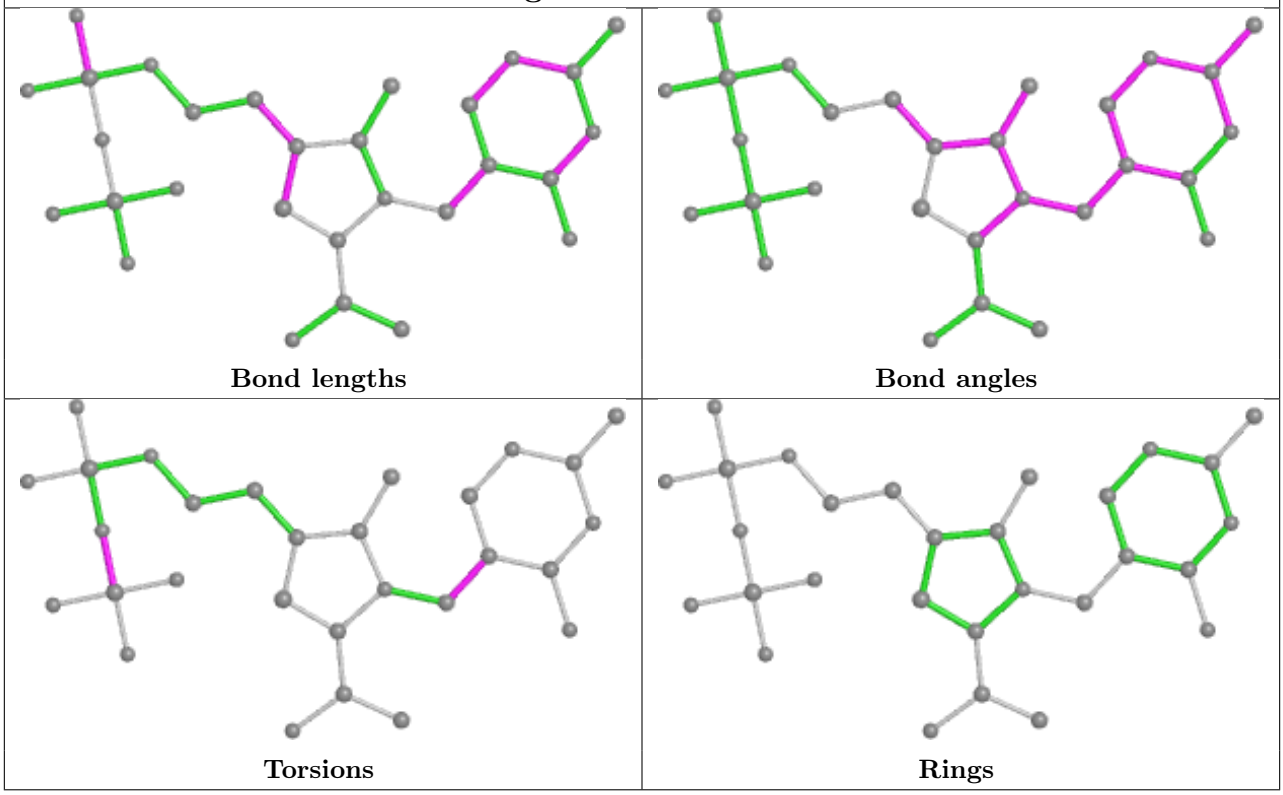
There are no ring outliers.

3 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	A	837	PG4	7	0
5	A	836	EDO	6	0
3	A	827	HTL	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 then 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.

Ligand HTL A 827



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%)	-0.73	2 (0%) 95 95	13, 21, 36, 55	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	806	VAL	2.5
1	A	401	GLU	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
4	NA	A	828	1/1	0.80	0.28	21,21,21,21	1
6	PG4	A	837	13/13	0.80	0.18	41,51,57,58	0
5	EDO	A	829	4/4	0.87	0.16	53,54,54,54	0
5	EDO	A	830	4/4	0.89	0.23	51,52,52,53	0
5	EDO	A	836	4/4	0.93	0.17	31,43,44,45	0

Continued on next page...

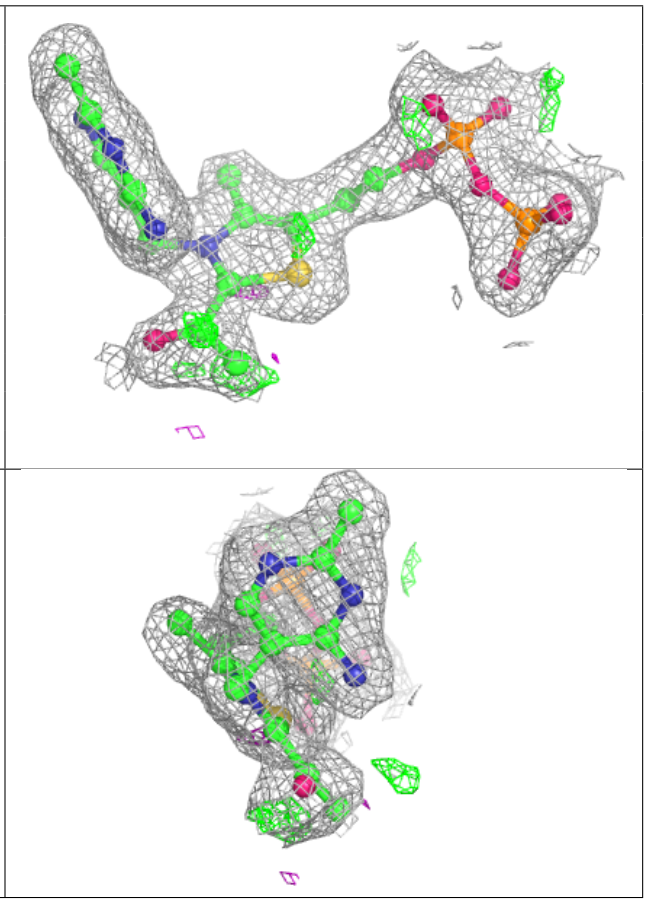
Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å^2)	Q<0.9
5	EDO	A	833	4/4	0.94	0.13	37,37,42,44	0
5	EDO	A	832	4/4	0.95	0.16	34,35,35,36	0
5	EDO	A	831	4/4	0.96	0.13	40,45,45,46	0
2	MG	A	826	1/1	0.97	0.10	16,16,16,16	0
5	EDO	A	835	4/4	0.97	0.09	24,30,32,32	0
5	EDO	A	834	4/4	0.98	0.05	22,23,24,25	0
4	NA	A	1397	1/1	0.99	0.06	22,22,22,22	1
3	HTL	A	827	29/29	0.99	0.07	13,17,33,38	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 HTL A 827:

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.