

Full wwPDB X-ray Structure Validation Report (i)

Nov 2, 2023 - 04:04 AM EDT

:	3P17
:	Thrombin Inhibition by Pyridin Derivatives
:	Biela, A.; Heine, A.; Klebe, G.
	2010-09-30
:	1.43 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 (1)) were used in the production of this report:

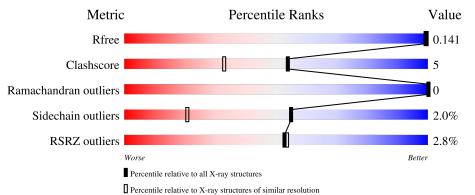
Xtriage (Phenix) EDS buster-report Percentile statistics Refmac CCP4 Ideal geometry (proteins) Ideal geometry (DNA, RNA)	:::::::::::::::::::::::::::::::::::::::	20191225.v01 (using entries in the PDB archive December 25th 2019) 5.8.0158 7.0.044 (Gargrove) Engh & Huber (2001) Parkinson et al. (1996)
Ideal geometry (DNA, RNA) Validation Pipeline (wwPDB-VP)		Parkinson et al. (1996) 2.36

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure: $X\text{-}RAY \, DIFFRACTION$

The reported resolution of this entry is 1.43 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	$\begin{array}{c} \textbf{Whole archive} \\ (\#\textbf{Entries}) \end{array}$	${f Similar\ resolution}\ (\#{ m Entries,\ resolution\ range}({ m \AA}))$
R_{free}	130704	2021 (1.46-1.42)
Clashscore	141614	2086 (1.46-1.42)
Ramachandran outliers	138981	2047 (1.46-1.42)
Sidechain outliers	138945	2047 (1.46-1.42)
RSRZ outliers	127900	1993 (1.46-1.42)

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	L	36	56%	17%	·	25%				
2	Н	259	^{2%} 84%			12% ••				
3	Ι	12	8%		8%	17%				



2 Entry composition (i)

There are 8 unique types of molecules in this entry. The entry contains 2734 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 thrombin light chain.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
1	L	27	Total 228	C 145	N 37	O 45	S 1	0	1	0

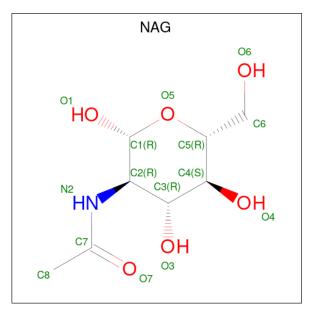
• Molecule 2 is a protein called thrombin heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	Н	251	Total 2096	C 1349	N 369	O 364	S 14	0	15	0

• Molecule 3 is a protein called Hirudin variant-2.

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace		
3	Ι	10	Total 87	C 55	N 10	0 21	S 1	0	0	0

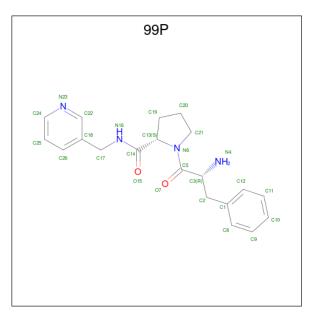
• Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).





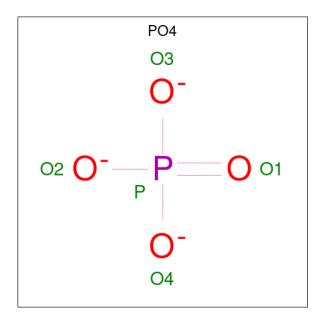
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	Н	1	Total 14	C 8	N 1	O 5	0	0

• Molecule 5 is D-phenylalanyl-N-(pyridin-3-ylmethyl)-L-prolinamide (three-letter code: 99P) (formula: $C_{20}H_{24}N_4O_2$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	Н	1	Total 26	C 20	N 4	O 2	0	0

• Molecule 6 is PHOSPHATE ION (three-letter code: PO4) (formula: O_4P).





Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	Н	1	Total 5	0 4	Р 1	0	0

• Molecule 7 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	Н	2	Total Na 2 2	0	0

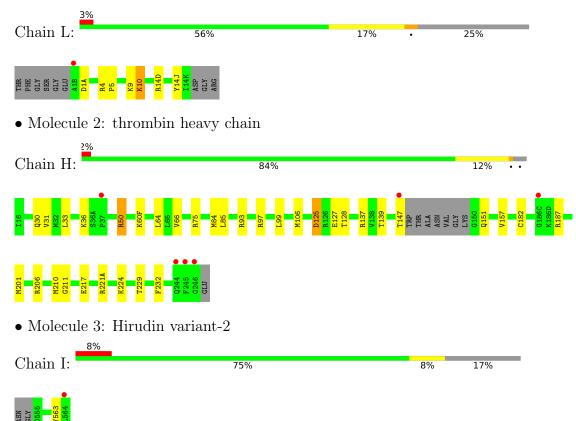
• Molecule 8 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	L	38	Total O 38 38	0	0
8	Н	230	Total O 230 230	0	0
8	Ι	8	Total O 8 8	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: thrombin light chain



4 Data and refinement statistics (i)

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants	70.00Å 71.40Å 72.50Å	Depositor
a, b, c, α , β , γ	90.00° 100.30° 90.00°	Depositor
Resolution (Å)	10.00 - 1.43	Depositor
Resolution (A)	30.90 - 1.43	EDS
% Data completeness	(Not available) (10.00-1.43)	Depositor
(in resolution range)	92.7 (30.90-1.43)	EDS
R _{merge}	(Not available)	Depositor
R _{sym}	0.05	Depositor
$< I/\sigma(I) > 1$	$2.38 (at 1.43 \text{\AA})$	Xtriage
Refinement program	SHELXL-97	Depositor
D D.	0.132 , 0.176	Depositor
R, R_{free}	0.136 , 0.141	DCC
R_{free} test set	3031 reflections $(5.04%)$	wwPDB-VP
Wilson B-factor $(Å^2)$	11.9	Xtriage
Anisotropy	0.305	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	0.37, 63.7	EDS
L-test for twinning ²	$ < L >=0.49, < L^2>=0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	2734	wwPDB-VP
Average B, all atoms $(Å^2)$	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 6.81% of the height of the origin peak. No significant pseudotranslation is detected.

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.



¹Intensities estimated from amplitudes.

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: PO4, NAG, TYS, 99P, 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	Mol Chain		nd lengths	Bond angles		
MOI	Unam	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	L	0.77	0/233	1.35	4/309~(1.3%)	
2	Н	0.58	1/2193~(0.0%)	1.15	9/2965~(0.3%)	
3	Ι	0.44	0/71	0.90	0/93	
All	All	0.60	1/2497~(0.0%)	1.17	13/3367~(0.4%)	

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
2	Н	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	$\mathrm{Ideal}(\mathrm{\AA})$
2	Н	60(F)	LYS	C-N	-6.24	1.19	1.34

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$\mathbf{Ideal}(^{o})$
1	L	1(A)	ASP	CB-CG-OD2	-7.63	111.44	118.30
1	L	4	ARG	NE-CZ-NH1	6.36	123.48	120.30
2	Н	221(A)	ARG	NE-CZ-NH1	6.33	123.47	120.30
2	Н	93	ARG	NE-CZ-NH2	-6.25	117.17	120.30
2	Н	50	ARG	CD-NE-CZ	6.17	132.24	123.60
1	L	10	LYS	CA-CB-CG	5.90	126.38	113.40
2	Н	137	ARG	NE-CZ-NH2	5.76	123.18	120.30
2	Н	206	ARG	NE-CZ-NH2	-5.66	117.47	120.30
2	Н	93	ARG	NE-CZ-NH1	5.52	123.06	120.30

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Mol	Chain	Res	Type	Atoms	Z	$Observed(^{o})$	$Ideal(^{o})$
1	L	14(J)	TYR	CB-CG-CD2	-5.47	117.72	121.00
2	Н	125	ASP	CB-CG-OD1	5.38	123.14	118.30
2	Н	232	PHE	CB-CG-CD1	-5.20	117.16	120.80
2	Н	147	THR	CA-CB-CG2	-5.16	105.18	112.40

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There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
2	Н	75[A]	ARG	Sidechain
2	Н	75[B]	ARG	Sidechain

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	L	228	0	238	4	0
2	Н	2096	0	2122	17	0
3	Ι	87	0	65	0	0
4	Н	14	0	13	5	0
5	Н	26	0	24	0	0
6	Η	5	0	0	0	0
7	Н	2	0	0	0	0
8	Η	230	0	0	5	0
8	Ι	8	0	0	0	0
8	L	38	0	0	1	0
All	All	2734	0	2462	26	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 5.

All (26) close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-1 Atom-2		Clash overlap (Å)
4:H:600:NAG:H3	4:H:600:NAG:H83	1.13	1.08

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A + a ma 1	A + a	Interatomic	Clash
Atom-1	Atom-2	distance (\AA)	overlap (Å)
4:H:600:NAG:H3	4:H:600:NAG:C8	1.97	0.95
2:H:139:THR:HG22	2:H:157[A]:VAL:HG12	1.49	0.93
1:L:14(D):ARG:HG3	1:L:14(D):ARG:HH11	1.50	0.77
4:H:600:NAG:C1	4:H:600:NAG:H82	2.17	0.74
2:H:84:MET:HE3	8:H:249:HOH:O	1.89	0.71
1:L:14(D):ARG:HG3	1:L:14(D):ARG:NH1	2.11	0.64
4:H:600:NAG:H83	4:H:600:NAG:C3	2.01	0.63
4:H:600:NAG:C8	4:H:600:NAG:C1	2.79	0.58
2:H:97[A]:ARG:HG3	8:H:288:HOH:O	2.09	0.53
2:H:31:VAL:HG13	2:H:66:VAL:HG13	1.92	0.52
2:H:64:LEU:HB2	2:H:85[B]:LEU:HD22	1.91	0.52
2:H:31:VAL:CG1	2:H:66:VAL:HG13	2.40	0.51
1:L:5:PRO:HA	1:L:9[B]:LYS:HD3	1.93	0.49
2:H:139:THR:CG2	2:H:157[A]:VAL:HG12	2.33	0.49
1:L:14(D):ARG:HD3	8:L:165:HOH:O	2.12	0.48
2:H:211:GLY:HA2	2:H:229:THR:O	2.15	0.45
2:H:127:GLU:HG3	8:H:270:HOH:O	2.16	0.45
2:H:125:ASP:OD1	2:H:128[B]:THR:HG22	2.18	0.44
2:H:217:GLU:HB2	2:H:224:LYS:HE3	2.01	0.43
2:H:151:GLN:HG2	8:H:393:HOH:O	2.18	0.43
2:H:30:GLN:NE2	2:H:139:THR:OG1	2.50	0.43
2:H:125:ASP:H	2:H:128[B]:THR:CG2	2.32	0.43
2:H:36:LYS:NZ	8:H:249:HOH:O	2.49	0.42
2:H:201:MET:SD	2:H:210:MET:HG3	2.60	0.42
2:H:33[A]:LEU:HD11	2:H:106:MET:HE1	2.03	0.41

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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	L	26/36~(72%)	25~(96%)	1 (4%)	0	100 100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	Н	262/259~(101%)	255~(97%)	7 (3%)	0	100	100
3	Ι	7/12~(58%)	7 (100%)	0	0	100	100
All	All	295/307~(96%)	287 (97%)	8 (3%)	0	100	100

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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	L	26/31~(84%)	25~(96%)	1 (4%)	33	4	
2	Н	230/225~(102%)	226~(98%)	4 (2%)	60	28	
3	Ι	7/10 (70%)	7 (100%)	0	100	100	
All	All	263/266~(99%)	258~(98%)	5 (2%)	55	22	

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

Mol	Chain	Res	Type
1	L	10	LYS
2	Н	50	ARG
2	Н	99	LEU
2	Н	182	CYS
2	Н	187	ARG

Sometimes side chains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such side chains are listed below:

Mol	Chain	Res	Type
2	Н	30	GLN
2	Н	244	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)

1 non-standard protein/DNA/RNA residue is 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).

Mal	Mol Type	Chain	Chain	Ros	Bos	Link	Bo	ond leng	ths	B	ond ang	les
Moi Type	Unam	nes		Counts	RMSZ	# Z >2	Counts	RMSZ	# Z >2			
3	TYS	Ι	563	3	15,16,17	1.52	2 (13%)	18,22,24	1.89	5 (27%)		

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
3	TYS	Ι	563	3	-	0/10/11/13	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	Ι	563	TYS	OH-CZ	-3.34	1.37	1.42
3	Ι	563	TYS	CE2-CZ	2.15	1.42	1.38

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Ζ	$\mathbf{Observed}(^{o})$	$Ideal(^{o})$
3	Ι	563	TYS	O3-S-O2	3.98	122.32	108.49
3	Ι	563	TYS	CE1-CD1-CG	-2.91	117.02	121.03
3	Ι	563	TYS	OH-S-O2	-2.90	99.26	107.71
3	Ι	563	TYS	CG-CB-CA	-2.86	108.32	114.10
3	Ι	563	TYS	CD1-CE1-CZ	2.41	122.69	119.73

There are no chirality outliers.



There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

5.5 Carbohydrates (i)

There are no monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 5 ligands modelled in this entry, 2 are monoatomic - leaving 3 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	Mol Type	Chain	Res	Link	Bond lengths			В	ond ang	les
Moi Type	Ullaili	Ites	LIIIK	Counts	RMSZ	# Z >2	Counts	RMSZ	# Z > 2	
4	NAG	Н	600	2	14,14,15	1.02	1 (7%)	$17,\!19,\!21$	2.55	<mark>6 (35%)</mark>
6	PO4	Н	1601	-	4,4,4	1.04	0	$6,\!6,\!6$	1.22	1 (16%)
5	99P	Н	1001	-	28,28,28	0.74	0	37,37,37	0.79	1 (2%)

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	NAG	Н	600	2	-	6/6/23/26	0/1/1/1
5	99P	Н	1001	-	-	0/21/31/31	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	Н	600	NAG	O5-C5	-2.10	1.39	1.43

All (8) bond angle outliers are listed below:



Mol	Chain	Res	Type	Atoms	Ζ	$Observed(^{o})$	$\mathbf{Ideal}(^{o})$
4	Н	600	NAG	C1-C2-N2	5.32	119.58	110.49
4	Н	600	NAG	C8-C7-N2	-4.08	109.19	116.10
4	Н	600	NAG	O5-C1-C2	-4.00	104.97	111.29
4	Н	600	NAG	O3-C3-C4	-3.79	101.59	110.35
4	Н	600	NAG	O7-C7-N2	2.82	127.13	121.95
4	Н	600	NAG	O5-C5-C4	-2.69	104.29	110.83
6	Н	1601	PO4	O2-P-O1	-2.26	102.63	110.89
5	Н	1001	99P	C14-C13-N6	-2.12	106.72	112.56

There are no chirality outliers.

All	(6)	torsion	outliers	are	listed	below:	

Mol	Chain	Res	Type	Atoms
4	Н	600	NAG	O5-C5-C6-O6
4	Н	600	NAG	C8-C7-N2-C2
4	Н	600	NAG	O7-C7-N2-C2
4	Н	600	NAG	C4-C5-C6-O6
4	Н	600	NAG	C3-C2-N2-C7
4	Н	600	NAG	C1-C2-N2-C7

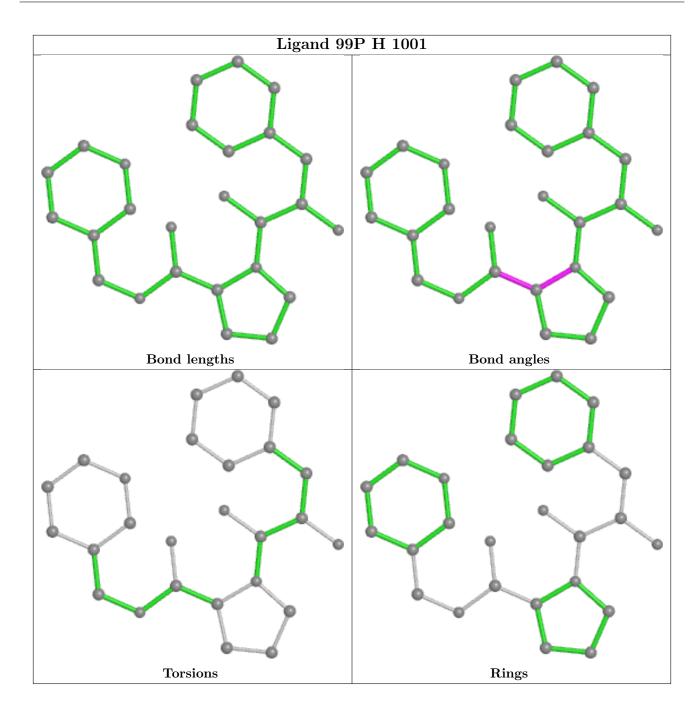
There are no ring outliers.

1 monomer is involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	Н	600	NAG	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 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.





5.7 Other polymers (i)

There are no such residues in this entry.

5.8 Polymer linkage issues (i)

The following chains have linkage breaks:

Mol	Chain	Number of breaks
2	Н	1



All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	60(F):LYS	С	60(G):ASN	N	1.19



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, 95^{th} 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	$\langle RSRZ \rangle$	#RSRZ>2	$\mathbf{OWAB}(\mathbf{A}^2)$	Q < 0.9
1	L	27/36~(75%)	-0.55	1 (3%) 41 42	10, 14, 31, 44	0
2	Н	251/259~(96%)	-0.28	6 (2%) 59 60	8, 16, 39, 55	0
3	Ι	9/12 (75%)	0.78	1 (11%) 5 5	28, 32, 50, 64	0
All	All	287/307~(93%)	-0.27	8 (2%) 53 53	8, 16, 41, 64	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	Н	245	PHE	4.8
1	L	1(B)	ALA	3.6
2	Н	246	GLY	3.5
2	Н	186(C)	GLY	3.2
2	Н	147	THR	3.2
3	Ι	564	LEU	2.6
2	Н	37	PRO	2.6
2	Н	244	GLN	2.4

6.2 Non-standard residues in protein, DNA, RNA chains (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, 95^{th} 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	TYS	Ι	563	16/17	0.98	0.08	$29,\!31,\!34,\!40$	0



6.3 Carbohydrates (i)

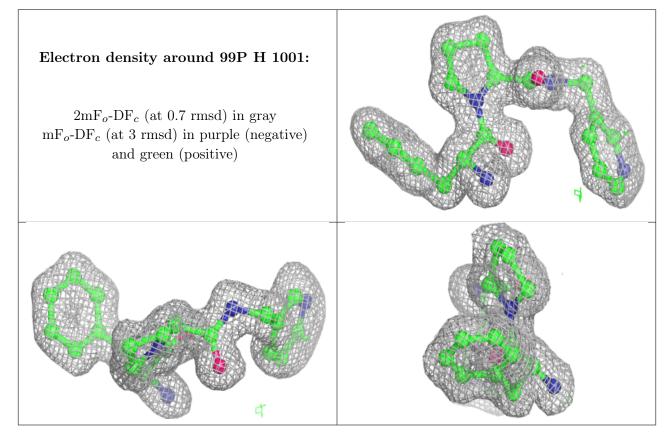
There are no monosaccharides in this entry.

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, 95^{th} 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	NAG	Н	600	14/15	0.82	0.18	43,55,65,71	0
5	99P	Н	1001	26/26	0.97	0.06	11,16,26,27	0
6	PO4	Н	1601	5/5	0.97	0.08	24,27,32,38	0
7	NA	Н	1701	1/1	1.00	0.04	13,13,13,13	0
7	NA	Н	1702	1/1	1.00	0.04	$17,\!17,\!17,\!17$	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 (i)

There are no such residues in this entry.

