



# Full wwPDB X-ray Structure Validation Report i

May 13, 2020 – 02:15 am BST

PDB ID : 4IYG  
Title : Structure of strictosidine synthase in complex with 2-(1H-INDOL-3-YL)-N-METHYLETHANAMINE  
Authors : Stoeckigt, J.; Fangrui, W.; Wang, M.; Rajendran, C.  
Deposited on : 2013-01-28  
Resolution : 2.70 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](mailto: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.

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The following versions of software and data (see [references](#) ①) 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 : 2.11  
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) : 2.11

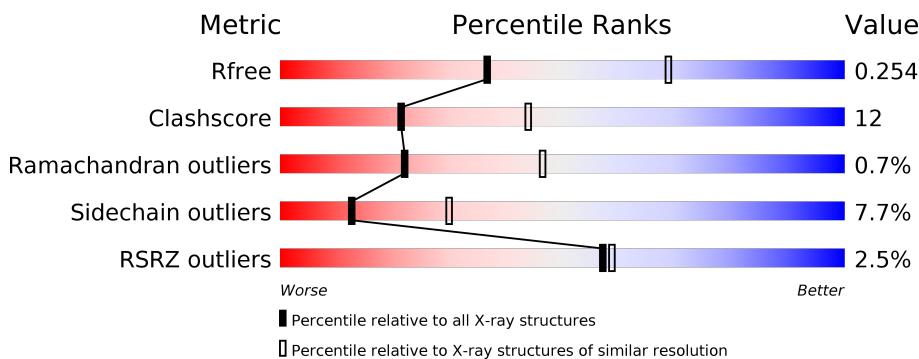
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## X-RAY DIFFRACTION

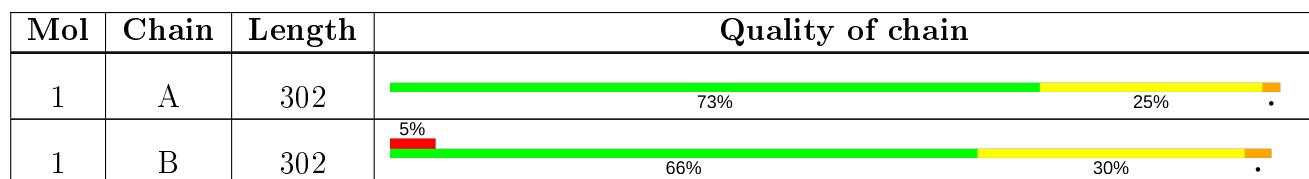
The reported resolution of this entry is 2.70 Å.

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	2808 (2.70-2.70)
Clashscore	141614	3122 (2.70-2.70)
Ramachandran outliers	138981	3069 (2.70-2.70)
Sidechain outliers	138945	3069 (2.70-2.70)
RSRZ outliers	127900	2737 (2.70-2.70)

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 on 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.



## 2 Entry composition (i)

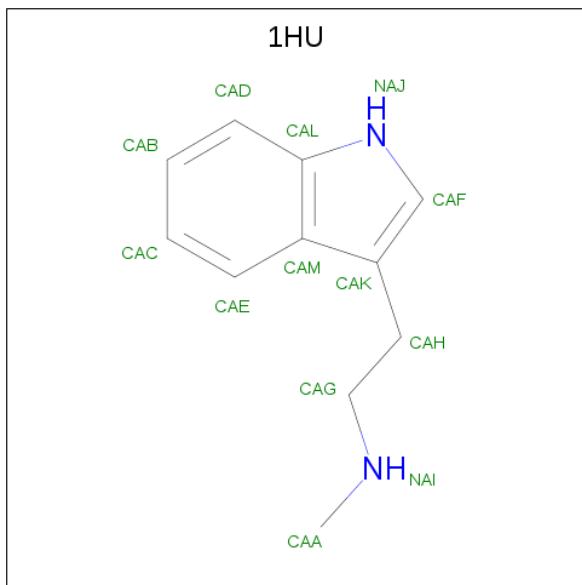
There are 3 unique types of molecules in this entry. The entry contains 4889 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Strictosidine synthase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	302	2380	1528	388	459	5	0	0	0
1	B	302	2379	1527	388	459	5	0	0	0

- Molecule 2 is 2-(1H-indol-3-yl)-N-methylethanamine (three-letter code: 1HU) (formula: C<sub>11</sub>H<sub>14</sub>N<sub>2</sub>).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	O		
2	A	1	13	11	2	0	0	0

- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
3	A	63	63	63	0	0

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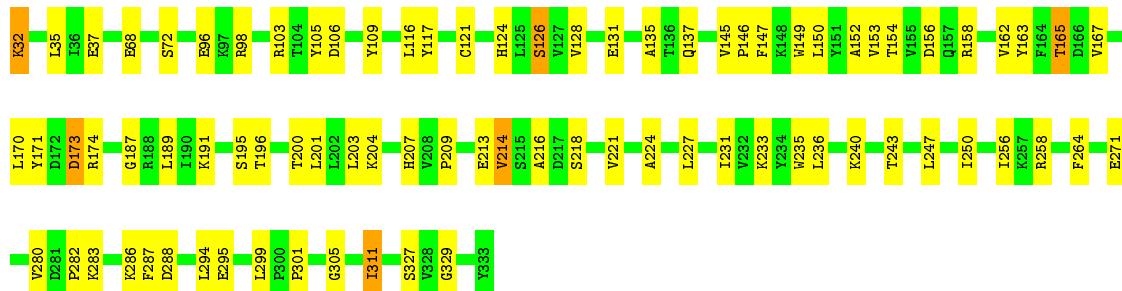
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	54	Total    O 54    54	0	0

### 3 Residue-property plots [\(i\)](#)

These plots are drawn for all protein, RNA and DNA 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.

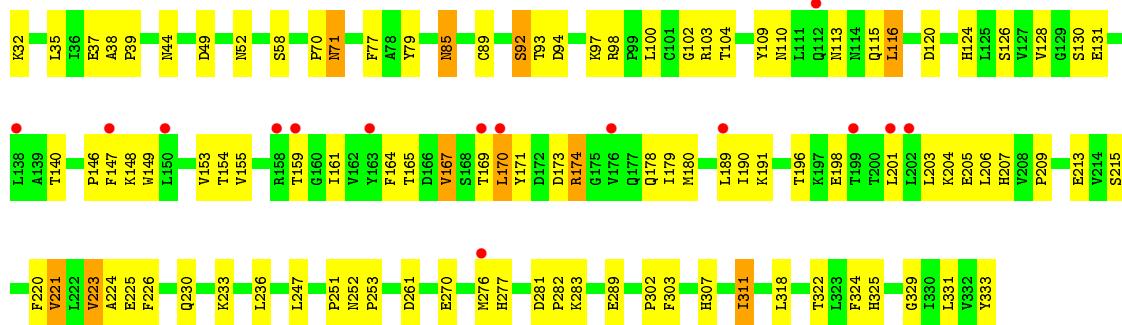
- Molecule 1: Strictosidine synthase

Chain A:



- Molecule 1: Strictosidine synthase

Chain B:



## 4 Data and refinement statistics (i)

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	150.23 Å    150.23 Å    122.10 Å 90.00°        90.00°        120.00°	Depositor
Resolution (Å)	38.30 – 2.70 45.61 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.2 (38.30-2.70) 98.3 (45.61-2.70)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle^1$	1.43 (at 2.69 Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
$R$ , $R_{free}$	0.212 , 0.252 0.213 , 0.254	Depositor DCC
$R_{free}$ test set	1383 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	41.9	Xtriage
Anisotropy	0.120	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.35 , 43.0	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.47$ , $\langle L^2 \rangle = 0.29$	Xtriage
Estimated twinning fraction	0.046 for h,-h-k,-l	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	4889	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.03% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>Theoretical values of  $\langle |L| \rangle$ ,  $\langle L^2 \rangle$  for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

## 5 Model quality [\(i\)](#)

### 5.1 Standard geometry [\(i\)](#)

Bond lengths and bond angles in the following residue types are not validated in this section:  
1HU

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	0.49	0/2445	0.66	1/3326 (0.0%)
1	B	0.43	0/2444	0.59	0/3325
All	All	0.46	0/4889	0.62	1/6651 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed( $^{\circ}$ )	Ideal( $^{\circ}$ )
1	A	311	ILE	CB-CA-C	-5.11	101.39	111.60

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	2380	0	2286	51	0
1	B	2379	0	2281	61	0
2	A	13	0	14	1	0
3	A	63	0	0	4	0
3	B	54	0	0	14	0
All	All	4889	0	4581	112	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 12.

All (112) 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:B:130:SER:O	3:B:438:HOH:O	1.95	0.83
1:B:146:PRO:O	3:B:413:HOH:O	1.97	0.82
1:A:271:GLU:OE2	3:A:548:HOH:O	1.97	0.81
1:B:71:ASN:OD1	3:B:425:HOH:O	1.97	0.81
1:B:77:PHE:N	3:B:410:HOH:O	1.87	0.80
1:B:147:PHE:O	3:B:449:HOH:O	1.99	0.79
1:A:37:GLU:N	3:A:529:HOH:O	2.00	0.78
1:B:44:ASN:OD1	1:B:58:SER:OG	2.07	0.73
1:B:322:THR:HG21	1:B:325:HIS:HB2	1.71	0.73
1:B:261:ASP:OD2	3:B:418:HOH:O	2.09	0.70
1:A:221:VAL:HG23	1:A:236:LEU:HD11	1.77	0.67
1:A:167:VAL:HA	1:A:209:PRO:HD2	1.75	0.67
1:B:167:VAL:O	3:B:403:HOH:O	2.12	0.67
1:A:214:VAL:O	1:A:258:ARG:NH1	2.26	0.66
1:B:189:LEU:HB3	1:B:203:LEU:HB2	1.81	0.60
1:A:147:PHE:CD2	1:A:150:LEU:HD11	2.37	0.60
1:B:85:ASN:ND2	3:B:431:HOH:O	2.19	0.59
1:B:225:GLU:OE2	1:B:230:GLN:NE2	2.27	0.58
1:A:152:ALA:H	1:A:165:THR:HG22	1.69	0.57
1:B:203:LEU:HB3	1:B:206:LEU:HD21	1.86	0.56
1:B:148:LYS:HB3	1:B:171:TYR:O	2.04	0.56
1:B:171:TYR:HB2	1:B:179:ILE:HD11	1.87	0.56
1:A:126:SER:HB2	1:A:135:ALA:HB1	1.88	0.55
1:A:121:CYS:SG	1:A:173:ASP:HB2	2.46	0.54
1:A:231:ILE:HD12	1:A:250:ILE:HD12	1.88	0.54
1:B:109:TYR:HD1	1:B:116:LEU:HD12	1.71	0.54
1:B:226:PHE:HA	1:B:253:PRO:HD2	1.90	0.54
1:A:158:ARG:NH1	1:A:216:ALA:O	2.41	0.53
1:B:113:ASN:OD1	1:B:115:GLN:NE2	2.39	0.53
1:B:311:ILE:N	3:B:407:HOH:O	2.04	0.53
1:A:149:TRP:HB3	1:A:167:VAL:HG22	1.91	0.53
1:B:233:LYS:HD2	1:B:247:LEU:HD13	1.89	0.53
1:A:35:LEU:HD13	1:B:70:PRO:HB3	1.89	0.53
1:B:98:ARG:O	1:B:102:GLY:N	2.29	0.53
1:A:286:LYS:HG2	1:A:294:LEU:HB2	1.91	0.52
1:B:170:LEU:HB2	1:B:171:TYR:CD2	2.44	0.52
1:A:329:GLY:N	3:A:523:HOH:O	2.39	0.52
1:B:302:PRO:HG2	1:B:303:PHE:CD2	2.45	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:201:LEU:HD21	1:A:204:LYS:HD3	1.92	0.52
1:A:224:ALA:HB2	1:A:256:ILE:HD11	1.91	0.52
1:B:221:VAL:HG22	1:B:236:LEU:HD21	1.91	0.51
1:A:282:PRO:HB2	1:A:299:LEU:HD12	1.92	0.51
1:B:49:ASP:HA	1:B:109:TYR:CD2	2.45	0.51
1:B:209:PRO:HA	1:B:224:ALA:O	2.10	0.51
1:B:130:SER:HB2	3:B:438:HOH:O	2.11	0.51
1:B:154:THR:HG21	1:B:213:GLU:HA	1.93	0.51
1:B:307:HIS:HD2	3:B:436:HOH:O	1.92	0.50
1:A:106:ASP:HB3	1:A:153:VAL:HG12	1.94	0.50
1:B:113:ASN:O	1:B:115:GLN:HG3	2.12	0.50
1:B:35:LEU:HD23	1:B:329:GLY:HA2	1.93	0.50
1:A:68:GLU:HB2	1:A:72:SER:HB3	1.94	0.49
1:A:163:TYR:CD1	1:A:221:VAL:HG21	2.47	0.49
1:A:158:ARG:HD2	1:A:218:SER:OG	2.12	0.49
1:A:233:LYS:HE3	1:A:247:LEU:HD13	1.94	0.48
1:A:231:ILE:HD13	1:A:287:PHE:CZ	2.48	0.48
1:B:104:THR:N	3:B:402:HOH:O	2.33	0.48
1:A:105:TYR:OH	1:A:173:ASP:OD2	2.13	0.48
1:B:180:MET:HG3	1:B:276:MET:SD	2.54	0.48
1:B:318:LEU:HB2	1:B:331:LEU:HB2	1.95	0.48
1:A:124:HIS:CD2	1:A:147:PHE:HB2	2.50	0.47
1:A:32:LYS:N	3:A:501:HOH:O	2.47	0.47
1:A:258:ARG:HG3	1:A:264:PHE:CE1	2.49	0.47
1:B:110:ASN:HD22	1:B:155:VAL:HG11	1.80	0.47
1:B:89:CYS:O	1:B:92:SER:HB3	2.15	0.47
1:A:288:ASP:HB3	1:A:294:LEU:HD11	1.96	0.46
1:A:96:GLU:OE1	1:A:96:GLU:N	2.39	0.46
1:A:264:PHE:O	1:A:286:LYS:HA	2.15	0.46
1:B:190:ILE:HG22	1:B:191:LYS:H	1.80	0.46
1:B:307:HIS:HB2	1:B:324:PHE:HE2	1.79	0.46
1:B:251:PRO:HB2	1:B:270:GLU:HB2	1.98	0.46
1:A:195:SER:OG	1:A:196:THR:N	2.49	0.46
1:A:240:LYS:O	1:A:243:THR:OG1	2.34	0.46
1:A:280:VAL:O	1:A:282:PRO:HD3	2.16	0.46
1:B:94:ASP:HB3	1:B:97:LYS:HG3	1.98	0.46
1:A:98:ARG:NH1	1:A:173:ASP:OD1	2.49	0.45
1:B:204:LYS:HG3	1:B:205:GLU:HG3	1.97	0.45
1:B:276:MET:HG3	1:B:277:HIS:CE1	2.51	0.45
1:B:198:GLU:HA	3:B:419:HOH:O	2.17	0.45
1:A:214:VAL:HG23	1:A:221:VAL:HG22	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:189:LEU:HB3	1:A:203:LEU:HB2	1.98	0.45
1:B:281:ASP:HA	1:B:282:PRO:HD3	1.86	0.45
1:A:283:LYS:NZ	1:A:283:LYS:HB2	2.31	0.44
1:B:167:VAL:HA	1:B:209:PRO:HD2	1.99	0.44
1:A:214:VAL:O	1:A:258:ARG:HD3	2.18	0.44
1:A:126:SER:HB3	1:A:137:GLN:HA	2.00	0.43
1:A:207:HIS:CD2	1:A:227:LEU:HB2	2.53	0.43
1:A:98:ARG:HH12	1:A:174:ARG:HG2	1.83	0.43
1:B:104:THR:HA	1:B:120:ASP:HA	1.99	0.43
1:B:159:THR:OG1	1:B:161:ILE:HG13	2.19	0.43
1:A:170:LEU:HB2	1:A:171:TYR:CD2	2.54	0.43
1:B:153:VAL:HG23	1:B:164:PHE:HB3	2.01	0.42
1:B:38:ALA:HB1	1:B:39:PRO:HD2	2.01	0.42
1:B:289:GLU:HB2	3:B:422:HOH:O	2.19	0.42
1:B:281:ASP:OD2	1:B:283:LYS:HE3	2.19	0.42
1:B:148:LYS:HD3	1:B:148:LYS:HA	1.81	0.42
1:A:154:THR:HG21	1:A:213:GLU:HA	2.02	0.42
1:A:37:GLU:HA	1:A:327:SER:OG	2.20	0.42
1:A:213:GLU:HG2	1:A:258:ARG:HB2	2.00	0.42
1:B:174:ARG:H	1:B:174:ARG:HG2	1.54	0.42
1:A:145:VAL:HA	1:A:146:PRO:HD3	1.88	0.41
1:B:201:LEU:HD21	1:B:204:LYS:HB3	2.02	0.41
1:B:226:PHE:CE1	1:B:252:ASN:HB3	2.55	0.41
2:A:401:1HU:H3	2:A:401:1HU:CAE	2.50	0.41
1:A:280:VAL:HB	1:A:305:GLY:O	2.21	0.41
1:B:189:LEU:HD22	1:B:223:VAL:HG11	2.03	0.41
1:A:116:LEU:HB3	1:A:128:VAL:HG12	2.01	0.41
1:B:190:ILE:HG22	1:B:191:LYS:N	2.36	0.41
1:A:187:GLY:HA3	1:A:209:PRO:HD3	2.01	0.41
1:B:149:TRP:HB3	1:B:167:VAL:HG13	2.03	0.41
1:A:117:TYR:CD1	1:A:162:VAL:HG21	2.56	0.41
1:B:215:SER:HB3	1:B:220:PHE:CE2	2.56	0.40
1:B:276:MET:H	1:B:276:MET:HG2	1.63	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	300/302 (99%)	277 (92%)	20 (7%)	3 (1%)	15 37
1	B	300/302 (99%)	268 (89%)	31 (10%)	1 (0%)	41 66
All	All	600/604 (99%)	545 (91%)	51 (8%)	4 (1%)	22 46

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	ASP
1	B	124	HIS
1	A	301	PRO
1	A	156	ASP

### 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	260/260 (100%)	248 (95%)	12 (5%)	27 54
1	B	259/260 (100%)	231 (89%)	28 (11%)	6 15
All	All	519/520 (100%)	479 (92%)	40 (8%)	13 30

All (40) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	32	LYS
1	A	103	ARG

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Mol	Chain	Res	Type
1	A	109	TYR
1	A	126	SER
1	A	131	GLU
1	A	165	THR
1	A	191	LYS
1	A	200	THR
1	A	214	VAL
1	A	235	TRP
1	A	295	GLU
1	A	311	ILE
1	B	32	LYS
1	B	37	GLU
1	B	52	ASN
1	B	71	ASN
1	B	79	TYR
1	B	85	ASN
1	B	92	SER
1	B	93	THR
1	B	100	LEU
1	B	103	ARG
1	B	116	LEU
1	B	126	SER
1	B	128	VAL
1	B	131	GLU
1	B	140	THR
1	B	165	THR
1	B	167	VAL
1	B	169	THR
1	B	170	LEU
1	B	173	ASP
1	B	174	ARG
1	B	178	GLN
1	B	196	THR
1	B	207	HIS
1	B	221	VAL
1	B	223	VAL
1	B	311	ILE
1	B	333	TYR

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

Mol	Chain	Res	Type
1	B	71	ASN
1	B	178	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 carbohydrates in this entry.

### 5.6 Ligand geometry [\(i\)](#)

1 ligand 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).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
2	1HU	A	401	-	13,14,14	1.43	2 (15%)	13,18,18	2.10	3 (23%)

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	1HU	A	401	-	-	3/4/4/4	0/2/2/2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	401	1HU	CAF-CAK	2.55	1.44	1.37
2	A	401	1HU	CAM-CAL	-2.41	1.36	1.42

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	401	1HU	CAG-CAH-CAK	4.67	120.30	111.28
2	A	401	1HU	CAH-CAG-NAI	4.66	122.16	111.83
2	A	401	1HU	CAM-CAL-NAJ	2.17	112.73	107.92

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	401	1HU	NAI-CAG-CAH-CAK
2	A	401	1HU	CAG-CAH-CAK-CAM
2	A	401	1HU	CAH-CAG-NAI-CAA

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	401	1HU	1	0

## 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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	302/302 (100%)	-0.14	0 [100] [100]	16, 29, 47, 58	0
1	B	302/302 (100%)	0.44	15 (4%) 28 27	25, 52, 76, 96	0
All	All	604/604 (100%)	0.15	15 (2%) 57 59	16, 38, 72, 96	0

All (15) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	276	MET	3.8
1	B	176	VAL	3.7
1	B	112	GLN	3.3
1	B	158	ARG	2.9
1	B	169	THR	2.9
1	B	150	LEU	2.6
1	B	189	LEU	2.5
1	B	138	LEU	2.4
1	B	202	LEU	2.3
1	B	170	LEU	2.3
1	B	163	TYR	2.3
1	B	201	LEU	2.2
1	B	159	THR	2.2
1	B	147	PHE	2.1
1	B	199	THR	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 carbohydrates 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<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
2	1HU	A	401	13/13	0.87	0.24	28,38,48,51	0

## 6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.