



Full wwPDB X-ray Structure Validation Report ⓘ

Nov 1, 2021 – 03:47 PM EDT

PDB ID : 2FPB
Title : Structure of Strictosidine Synthase, the Biosynthetic Entry to the Monoterpenoid Indole Alkaloid Family
Authors : Panjikar, S.
Deposited on : 2006-01-16
Resolution : 2.80 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

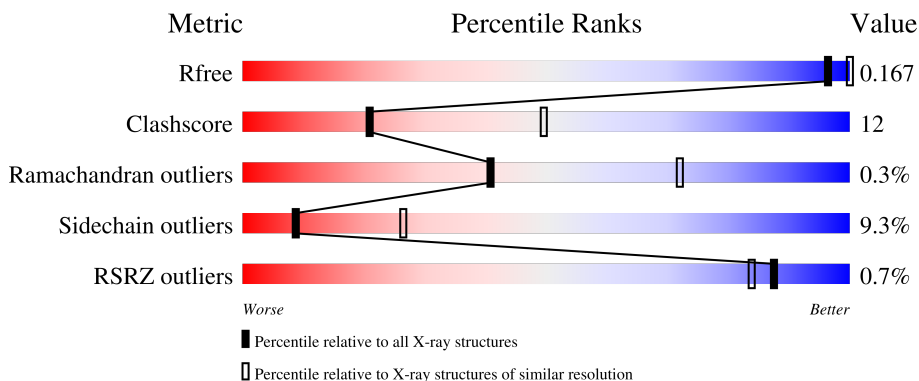
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	322	
1	B	322	

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
2	TSS	A	1001	-	-	X	-

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5007 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.

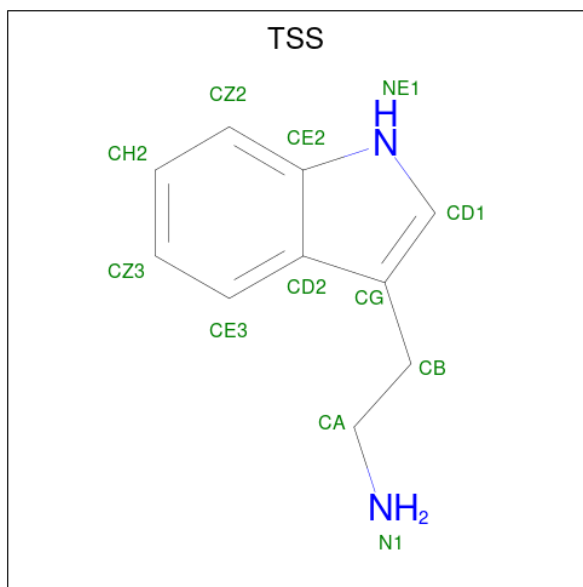
- Molecule 1 is a protein called Strictosidine Synthase.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	C	N	O	S	Se			
1	A	305	2405	1542	391	463	3	6	0	0	0
1	B	305	2405	1542	391	463	3	6	0	0	0

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	65	MSE	ILE	engineered mutation	UNP P68175
A	116	MSE	LEU	engineered mutation	UNP P68175
A	180	MSE	MET	modified residue	UNP P68175
A	190	MSE	ILE	engineered mutation	UNP P68175
A	203	MSE	LEU	engineered mutation	UNP P68175
A	276	MSE	MET	modified residue	UNP P68175
B	65	MSE	ILE	engineered mutation	UNP P68175
B	116	MSE	LEU	engineered mutation	UNP P68175
B	180	MSE	MET	modified residue	UNP P68175
B	190	MSE	ILE	engineered mutation	UNP P68175
B	203	MSE	LEU	engineered mutation	UNP P68175
B	276	MSE	MET	modified residue	UNP P68175

- Molecule 2 is 2-(1H-INDOL-3-YL)ETHANAMINE (three-letter code: TSS) (formula: C₁₀H₁₂N₂).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf	
2	A	1	Total	C	N	0	0
			12	10	2		
2	B	1	Total	C	N	0	0
			12	10	2		

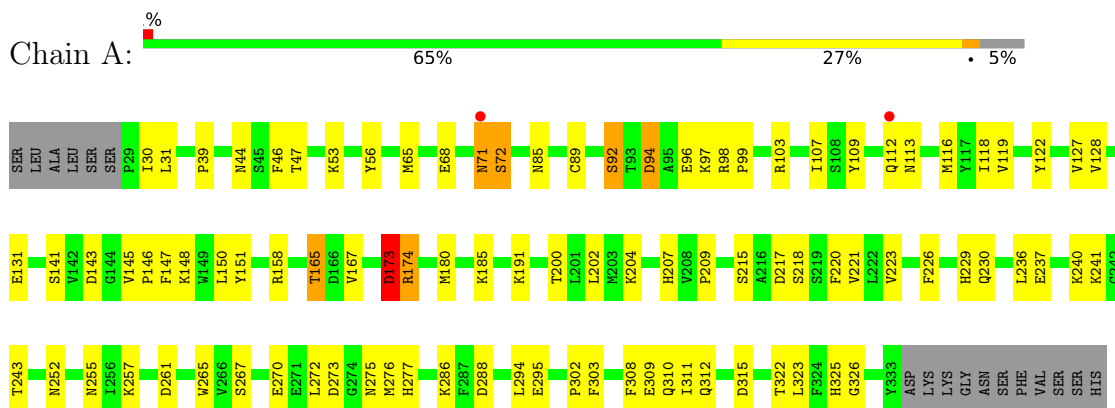
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	93	Total	O	0	0
			93	93		
3	B	80	Total	O	0	0
			80	80		

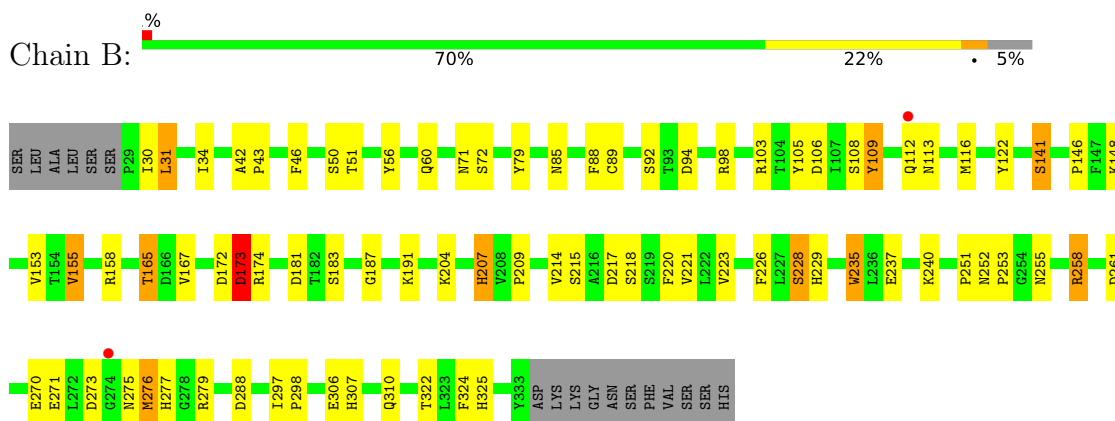
3 Residue-property plots [i](#)

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: Strictosidine Synthase



• Molecule 1: Strictosidine Synthase



4 Data and refinement statistics

Property	Value	Source
Space group	H 3	Depositor
Cell constants a, b, c, α , β , γ	148.94Å 148.94Å 121.34Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.80 19.65 – 2.80	Depositor EDS
% Data completeness (in resolution range)	99.9 (20.00-2.80) 99.9 (19.65-2.80)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.01 (at 2.79Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.164 , 0.217 0.165 , 0.167	Depositor DCC
R_{free} test set	1234 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	49.7	Xtrriage
Anisotropy	0.742	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 35.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtrriage
Estimated twinning fraction	0.028 for h,-h-k,-l	Xtrriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	5007	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.12% 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 [i](#)

5.1 Standard geometry [i](#)

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

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	0.86	0/2465	0.95	5/3340 (0.1%)
1	B	0.77	0/2465	0.91	6/3340 (0.2%)
All	All	0.82	0/4930	0.93	11/6680 (0.2%)

There are no bond length outliers.

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	143	ASP	CB-CG-OD2	7.49	125.04	118.30
1	A	273	ASP	CB-CG-OD2	7.12	124.71	118.30
1	B	94	ASP	CB-CG-OD2	6.50	124.15	118.30
1	B	273	ASP	CB-CG-OD2	5.80	123.52	118.30
1	A	261	ASP	CB-CG-OD2	5.66	123.39	118.30
1	B	288	ASP	CB-CG-OD2	5.48	123.24	118.30
1	B	261	ASP	CB-CG-OD2	5.46	123.21	118.30
1	B	172	ASP	CB-CG-OD2	5.41	123.17	118.30
1	A	315	ASP	CB-CG-OD2	5.37	123.13	118.30
1	B	181	ASP	CB-CG-OD2	5.09	122.88	118.30
1	A	173	ASP	CB-CA-C	-5.03	100.34	110.40

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	2405	0	2309	68	0
1	B	2405	0	2309	41	0
2	A	12	0	12	6	0
2	B	12	0	12	5	0
3	A	93	0	0	2	0
3	B	80	0	0	2	0
All	All	5007	0	4642	116	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 (116) 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:276:MSE:SE	1:B:276:MSE:CE	2.15	1.44
1:A:180:MSE:CE	1:A:180:MSE:SE	2.18	1.42
1:A:276:MSE:SE	1:A:276:MSE:CE	2.18	1.38
2:B:2001:TSS:HD1	2:B:2001:TSS:HN11	1.09	1.08
1:A:255:ASN:HD22	1:A:310:GLN:HB2	1.17	1.05
2:A:1001:TSS:HD1	2:A:1001:TSS:N1	1.71	1.03
2:A:1001:TSS:HN11	2:A:1001:TSS:CD1	1.70	0.96
2:A:1001:TSS:HD1	2:A:1001:TSS:HN11	1.28	0.95
1:B:229:HIS:HD2	1:B:252:ASN:H	1.00	0.93
1:A:229:HIS:HD2	1:A:252:ASN:H	1.03	0.91
2:A:1001:TSS:N1	2:A:1001:TSS:CD1	2.31	0.90
1:B:229:HIS:CD2	1:B:252:ASN:H	1.90	0.89
2:B:2001:TSS:HD1	2:B:2001:TSS:N1	1.87	0.87
1:A:68:GLU:HB2	1:A:72:SER:HB2	1.56	0.86
2:B:2001:TSS:HN11	2:B:2001:TSS:CD1	1.84	0.86
1:A:158:ARG:HB2	1:A:158:ARG:NH1	1.91	0.85
1:A:96:GLU:HB3	3:A:1046:HOH:O	1.78	0.83
1:A:39:PRO:HG3	1:A:65:MSE:HE2	1.64	0.80
1:A:229:HIS:CD2	1:A:252:ASN:H	1.95	0.79
1:A:158:ARG:HH11	1:A:158:ARG:CB	1.98	0.77
1:B:255:ASN:HD22	1:B:310:GLN:HB2	1.48	0.76
1:A:158:ARG:NH1	1:A:158:ARG:CB	2.48	0.76
1:A:221:VAL:CG2	1:A:236:LEU:HD11	2.18	0.73
1:B:167:VAL:HA	1:B:209:PRO:HD2	1.70	0.73
1:A:221:VAL:HG23	1:A:236:LEU:HD11	1.71	0.73
1:A:322:THR:OG1	1:A:325:HIS:HD2	1.73	0.72
1:B:60:GLN:HE22	1:B:98:ARG:HH21	1.35	0.71
1:A:275:ASN:ND2	1:A:277:HIS:H	1.90	0.69

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:71:ASN:HD22	1:A:72:SER:H	1.40	0.69
1:B:165:THR:HG21	1:B:209:PRO:O	1.93	0.68
1:B:306:GLU:HG2	1:B:324:PHE:CZ	2.29	0.68
1:B:141:SER:HB2	1:B:146:PRO:HA	1.75	0.67
1:A:158:ARG:HH11	1:A:158:ARG:HB3	1.61	0.65
1:A:255:ASN:ND2	1:A:310:GLN:HB2	2.01	0.64
1:B:106:ASP:HB3	1:B:153:VAL:HG12	1.78	0.64
1:A:94:ASP:N	1:A:94:ASP:OD1	2.32	0.61
1:A:122:TYR:OH	1:A:173:ASP:HB2	2.02	0.60
1:B:207:HIS:HD2	1:B:228:SER:OG	1.85	0.59
1:A:98:ARG:HD2	1:A:173:ASP:OD1	2.03	0.58
1:B:217:ASP:O	1:B:218:SER:HB2	2.02	0.58
1:A:229:HIS:HD2	1:A:252:ASN:N	1.88	0.58
1:B:103:ARG:HD2	1:B:105:TYR:CZ	2.37	0.58
1:A:180:MSE:HE3	3:A:1052:HOH:O	2.04	0.57
1:A:275:ASN:HD22	1:A:277:HIS:H	1.52	0.57
1:B:215:SER:HB3	1:B:220:PHE:CZ	2.40	0.56
1:A:191:LYS:HD3	1:A:202:LEU:HD21	1.87	0.56
1:A:267:SER:HB2	1:A:308:PHE:CZ	2.41	0.55
1:B:324:PHE:C	1:B:324:PHE:CD2	2.79	0.55
1:B:235:TRP:CZ3	1:B:240:LYS:HD2	2.42	0.55
1:A:226:PHE:CE1	2:A:1001:TSS:HB1	2.43	0.54
1:B:103:ARG:HD2	1:B:105:TYR:CE2	2.43	0.54
1:B:322:THR:HG21	1:B:325:HIS:HB3	1.89	0.52
1:B:252:ASN:ND2	1:B:271:GLU:H	2.07	0.52
1:B:226:PHE:HA	1:B:253:PRO:HD2	1.92	0.51
1:B:324:PHE:CD2	1:B:324:PHE:O	2.63	0.51
1:B:271:GLU:OE1	1:B:307:HIS:HE1	1.94	0.51
1:A:141:SER:CB	1:A:146:PRO:HA	2.41	0.50
1:B:306:GLU:HG2	1:B:324:PHE:CE1	2.46	0.50
1:B:214:VAL:O	1:B:258:ARG:NH1	2.45	0.50
1:B:85:ASN:HD22	1:B:88:PHE:H	1.58	0.49
1:A:309:GLU:OE2	2:A:1001:TSS:N1	2.45	0.49
1:A:158:ARG:HB2	1:A:158:ARG:CZ	2.43	0.49
1:A:174:ARG:HH11	1:A:174:ARG:HG3	1.78	0.49
1:A:46:PHE:HA	1:A:56:TYR:O	2.14	0.48
1:A:257:LYS:CB	1:A:312:GLN:HG3	2.44	0.48
1:B:60:GLN:NE2	1:B:98:ARG:HH21	2.08	0.48
1:A:151:TYR:HB2	1:A:167:VAL:HG13	1.96	0.48
1:A:119:VAL:HG23	1:A:119:VAL:O	2.15	0.47
1:A:302:PRO:HD2	1:A:303:PHE:CE2	2.49	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:165:THR:HG21	1:A:209:PRO:O	2.15	0.47
1:B:42:ALA:N	1:B:43:PRO:HD3	2.30	0.47
1:A:85:ASN:O	1:A:89:CYS:HB2	2.15	0.46
2:B:2001:TSS:N1	2:B:2001:TSS:CD1	2.54	0.46
2:B:2001:TSS:HA1	3:B:2064:HOH:O	2.16	0.46
1:A:215:SER:HB3	1:A:220:PHE:CZ	2.51	0.46
1:A:217:ASP:O	1:A:218:SER:HB2	2.17	0.45
1:B:122:TYR:OH	1:B:173:ASP:HB2	2.17	0.45
1:A:148:LYS:HD2	1:A:148:LYS:HA	1.90	0.44
1:A:98:ARG:NH1	1:A:173:ASP:HB3	2.32	0.44
1:A:96:GLU:H	1:A:96:GLU:CD	2.20	0.44
1:A:322:THR:HG21	1:A:325:HIS:HB2	1.99	0.44
1:A:323:LEU:HA	1:A:323:LEU:HD23	1.72	0.44
1:A:286:LYS:HB3	1:A:295:GLU:HB3	2.00	0.44
1:A:98:ARG:N	1:A:99:PRO:CD	2.80	0.44
1:A:288:ASP:HB3	1:A:294:LEU:HD11	1.99	0.44
1:A:167:VAL:HA	1:A:209:PRO:HD2	2.00	0.43
1:A:191:LYS:HG2	1:A:200:THR:HB	2.00	0.43
1:A:236:LEU:O	1:A:241:LYS:HG3	2.18	0.43
1:A:44:ASN:OD1	1:A:103:ARG:NH1	2.52	0.43
1:A:141:SER:HB3	1:A:146:PRO:HA	2.00	0.43
1:A:221:VAL:HG22	1:A:236:LEU:HD11	1.95	0.43
1:B:229:HIS:HD2	1:B:252:ASN:N	1.86	0.43
1:A:92:SER:HB2	1:A:97:LYS:HD2	2.01	0.43
1:A:240:LYS:O	1:A:243:THR:HB	2.18	0.43
1:B:297:ILE:HA	1:B:298:PRO:HD2	1.91	0.43
1:A:147:PHE:CG	1:A:150:LEU:HD21	2.55	0.42
1:A:145:VAL:HA	1:A:146:PRO:HD3	1.78	0.42
1:A:265:TRP:HB3	1:A:311:ILE:HG23	2.02	0.42
1:B:85:ASN:O	1:B:89:CYS:HB2	2.20	0.42
1:A:116:MSE:HE3	1:A:118:ILE:HG12	2.02	0.42
1:A:71:ASN:HD22	1:A:72:SER:N	2.11	0.41
1:B:240:LYS:HB2	3:B:2043:HOH:O	2.20	0.41
1:A:85:ASN:HD22	1:A:85:ASN:HA	1.74	0.41
1:B:46:PHE:HA	1:B:56:TYR:O	2.21	0.41
1:A:47:THR:HG22	1:A:107:ILE:HD12	2.03	0.41
1:A:326:GLY:H	1:B:71:ASN:HA	1.85	0.41
1:B:108:SER:OG	1:B:155:VAL:HG23	2.21	0.41
1:A:270:GLU:HG2	1:A:272:LEU:HD23	2.03	0.41
1:B:275:ASN:ND2	1:B:277:HIS:H	2.18	0.41
1:B:187:GLY:HA3	1:B:209:PRO:HD3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:71:ASN:N	1:B:71:ASN:ND2	2.69	0.41
1:A:31:LEU:HB3	1:B:31:LEU:HD23	2.02	0.40
1:A:71:ASN:ND2	1:A:71:ASN:N	2.68	0.40
1:A:127:VAL:HG22	1:A:128:VAL:N	2.37	0.40
1:B:109:TYR:CE1	1:B:116:MSE:CE	3.05	0.40
1:B:251:PRO:HB2	1:B:270:GLU:HG3	2.02	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	303/322 (94%)	289 (95%)	13 (4%)	1 (0%)	41	72
1	B	303/322 (94%)	289 (95%)	13 (4%)	1 (0%)	41	72
All	All	606/644 (94%)	578 (95%)	26 (4%)	2 (0%)	41	72

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	173	ASP
1	B	173	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	263/272 (97%)	244 (93%)	19 (7%)	14	38
1	B	263/272 (97%)	233 (89%)	30 (11%)	5	18
All	All	526/544 (97%)	477 (91%)	49 (9%)	9	26

All (49) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	30	ILE
1	A	53	LYS
1	A	71	ASN
1	A	72	SER
1	A	92	SER
1	A	94	ASP
1	A	109	TYR
1	A	112	GLN
1	A	113	ASN
1	A	131	GLU
1	A	165	THR
1	A	173	ASP
1	A	174	ARG
1	A	185	LYS
1	A	204	LYS
1	A	207	HIS
1	A	223	VAL
1	A	230	GLN
1	A	237	GLU
1	B	30	ILE
1	B	31	LEU
1	B	34	ILE
1	B	50	SER
1	B	51	THR
1	B	72	SER
1	B	79	TYR
1	B	92	SER
1	B	109	TYR
1	B	112	GLN
1	B	113	ASN
1	B	141	SER
1	B	148	LYS
1	B	155	VAL
1	B	158	ARG
1	B	165	THR

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Mol	Chain	Res	Type
1	B	173	ASP
1	B	174	ARG
1	B	183	SER
1	B	191	LYS
1	B	204	LYS
1	B	207	HIS
1	B	221	VAL
1	B	223	VAL
1	B	228	SER
1	B	235	TRP
1	B	237	GLU
1	B	258	ARG
1	B	276	MSE
1	B	279	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	71	ASN
1	A	85	ASN
1	A	113	ASN
1	A	115	GLN
1	A	207	HIS
1	A	229	HIS
1	A	230	GLN
1	A	252	ASN
1	A	255	ASN
1	A	275	ASN
1	A	292	ASN
1	A	310	GLN
1	A	312	GLN
1	A	325	HIS
1	B	60	GLN
1	B	71	ASN
1	B	85	ASN
1	B	91	ASN
1	B	113	ASN
1	B	207	HIS
1	B	229	HIS
1	B	230	GLN
1	B	252	ASN
1	B	255	ASN

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Mol	Chain	Res	Type
1	B	275	ASN
1	B	307	HIS
1	B	310	GLN
1	B	312	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](#)

2 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	TSS	A	1001	-	11,13,13	1.41	0	11,17,17	0.87	0
2	TSS	B	2001	-	11,13,13	1.16	0	11,17,17	1.22	2 (18%)

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	TSS	A	1001	-	-	1/3/3/3	0/2/2/2
2	TSS	B	2001	-	-	1/3/3/3	0/2/2/2

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	2001	TSS	CE3-CD2-CE2	2.37	121.31	118.17
2	B	2001	TSS	CZ3-CE3-CD2	-2.34	117.64	120.89

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	B	2001	TSS	N1-CA-CB-CG
2	A	1001	TSS	N1-CA-CB-CG

There are no ring outliers.

2 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1001	TSS	6	0
2	B	2001	TSS	5	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, 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	299/322 (92%)	-0.63	2 (0%) 87 84	15, 21, 29, 66	0
1	B	299/322 (92%)	-0.56	2 (0%) 87 84	15, 21, 28, 67	0
All	All	598/644 (92%)	-0.60	4 (0%) 87 84	15, 21, 28, 67	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	274	GLY	3.5
1	B	112	GLN	2.8
1	A	112	GLN	2.5
1	A	71	ASN	2.4

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
2	TSS	A	1001	12/12	0.87	0.20	55,65,74,74	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	TSS	B	2001	12/12	0.88	0.24	55,70,74,75	0

6.5 Other polymers [i](#)

There are no such residues in this entry.