



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 1, 2026 – 12:38 PM UTC

PDB ID : 1EB8 / pdb_00001eb8
Title : Structure Determinants of Substrate Specificity of Hydroxynitrile Lyase from *Manihot esculenta*
Authors : Lauble, H.; Miehlisch, B.; Foerster, S.; Kobler, C.; Wajant, H.; Effenberger, F.
Deposited on : 2001-07-24
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)	:	NOT EXECUTED
EDS	:	NOT EXECUTED
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

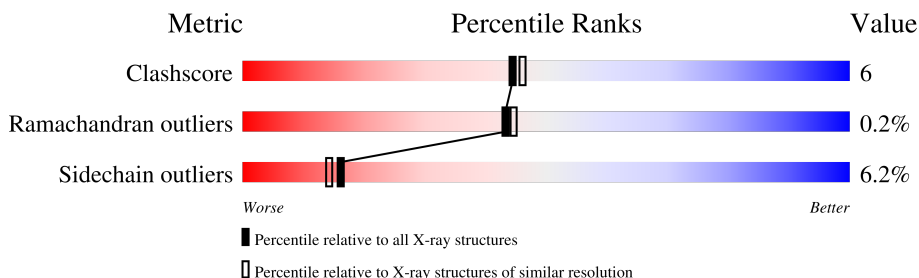
1 Overall quality at a glance

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))
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (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 $\leq 5\%$.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	A	262	 70% 23% 5% •
1	B	262	 77% 15% 5% ••

2 Entry composition [i](#)

There are 3 unique types of molecules in this entry. The entry contains 4426 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 (S)-ACETONE-CYANOHYDRIN LYASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	262	Total	C	N	O	S	0	0	0
			2095	1351	348	388	8			
1	B	258	Total	C	N	O	S	0	0	0
			2065	1331	343	383	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	128	ALA	TRP	engineered mutation	UNP P52705
B	128	ALA	TRP	engineered mutation	UNP P52705

- Molecule 2 is (4S)-2-METHYL-2,4-PENTANEDIOL (CCD ID: MPD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			8	6	2		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	B	1	Total	C	O	0	0
			8	6	2		

- Molecule 3 is water.

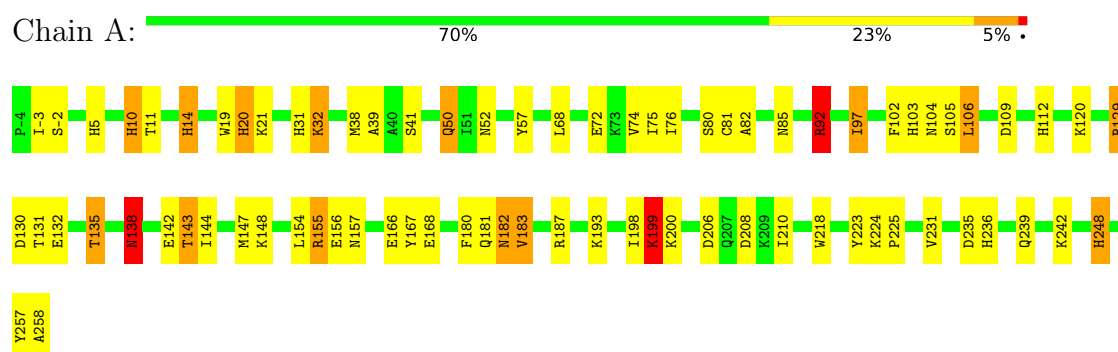
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	116	Total	O	0	0
			116	116		
3	B	134	Total	O	0	0
			134	134		

3 Residue-property plots

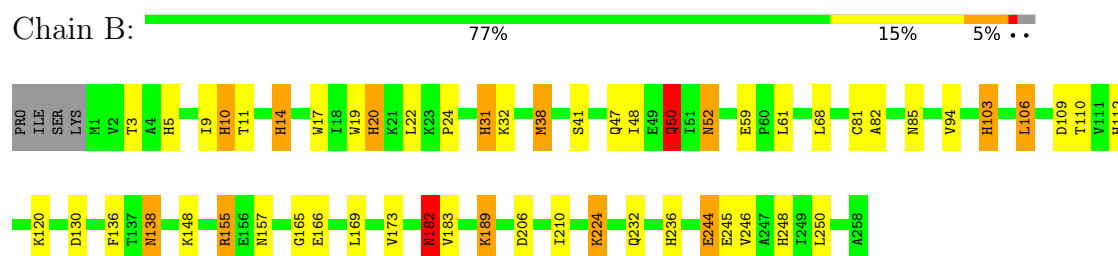
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry. Residues are color-coded 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. 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.

Note EDS was not executed.

• Molecule 1: (S)-ACETONE-CYANOHYDRIN LYASE



• Molecule 1: (S)-ACETONE-CYANOHYDRIN LYASE



4 Data and refinement statistics

Xtriage (Phenix) and EDS were not executed - this section is therefore incomplete.

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	106.40 Å 106.40 Å 188.43 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	8.00 – 2.10	Depositor
% Data completeness (in resolution range)	86.6 (8.00-2.10)	Depositor
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
Refinement program	X-PLOR 3.851	Depositor
R, R_{free}	0.192 , 0.234	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	4426	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

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: MPD

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	1.12	15/2145 (0.7%)	1.70	34/2905 (1.2%)
1	B	1.09	10/2114 (0.5%)	1.71	35/2864 (1.2%)
All	All	1.10	25/4259 (0.6%)	1.70	69/5769 (1.2%)

All (25) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	20	HIS	CD2-NE2	-7.98	1.29	1.37
1	A	10	HIS	CD2-NE2	-7.51	1.29	1.37
1	A	31	HIS	CD2-NE2	-7.31	1.29	1.37
1	B	10	HIS	CD2-NE2	-7.18	1.29	1.37
1	A	103	HIS	CD2-NE2	-6.90	1.30	1.37
1	A	14	HIS	CD2-NE2	-6.70	1.30	1.37
1	B	5	HIS	CD2-NE2	-6.36	1.30	1.37
1	A	5	HIS	CD2-NE2	-6.35	1.30	1.37
1	B	236	HIS	CD2-NE2	-6.32	1.30	1.37
1	B	248	HIS	CD2-NE2	-6.02	1.31	1.37
1	B	20	HIS	CD2-NE2	-5.96	1.31	1.37
1	A	198	ILE	CA-CB	5.95	1.60	1.54
1	A	143	THR	CA-CB	5.82	1.61	1.53
1	A	236	HIS	CD2-NE2	-5.70	1.31	1.37
1	A	248	HIS	CD2-NE2	-5.64	1.31	1.37
1	B	31	HIS	CD2-NE2	-5.54	1.31	1.37
1	B	173	VAL	CA-CB	5.52	1.61	1.54
1	A	112	HIS	CD2-NE2	-5.51	1.31	1.37
1	B	103	HIS	CD2-NE2	-5.45	1.31	1.37
1	A	97	ILE	CA-CB	5.26	1.60	1.54
1	B	112	HIS	CD2-NE2	-5.25	1.32	1.37
1	B	48	ILE	CA-CB	5.24	1.61	1.54
1	A	5	HIS	CG-ND1	-5.04	1.32	1.38
1	A	183	VAL	CA-CB	5.04	1.61	1.54

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	112	HIS	CG-ND1	-5.01	1.32	1.38

All (69) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	50	GLN	OE1-CD-NE2	-11.27	111.33	122.60
1	A	138	ASN	OD1-CG-ND2	-9.03	113.57	122.60
1	B	50	GLN	CG-CD-NE2	8.74	129.50	116.40
1	A	130	ASP	CA-CB-CG	8.22	120.82	112.60
1	B	50	GLN	CB-CG-CD	8.04	126.28	112.60
1	B	182	ASN	OD1-CG-ND2	-7.45	115.15	122.60
1	A	182	ASN	CA-CB-CG	7.36	119.96	112.60
1	A	31	HIS	CB-CG-CD2	-7.11	121.96	131.20
1	B	206	ASP	CA-CB-CG	7.06	119.66	112.60
1	B	244	GLU	CB-CG-CD	6.91	124.34	112.60
1	A	109	ASP	CA-CB-CG	6.71	119.31	112.60
1	B	32	LYS	CA-CB-CG	-6.70	100.71	114.10
1	A	50	GLN	OE1-CD-NE2	-6.60	116.00	122.60
1	B	182	ASN	CA-CB-CG	6.59	119.19	112.60
1	A	-3	ILE	N-CA-C	-6.57	98.57	108.17
1	A	235	ASP	CA-CB-CG	6.47	119.07	112.60
1	B	103	HIS	CB-CG-CD2	-6.43	122.84	131.20
1	A	138	ASN	CA-CB-CG	6.41	119.00	112.60
1	B	232	GLN	OE1-CD-NE2	-6.40	116.20	122.60
1	A	19	TRP	CG-CD2-CE3	6.36	140.26	133.90
1	B	157	ASN	CA-CB-CG	-6.36	106.25	112.60
1	B	155	ARG	NE-CZ-NH2	-6.29	113.54	119.20
1	A	236	HIS	CB-CG-CD2	-6.28	123.04	131.20
1	A	199	LYS	CA-CB-CG	-6.05	101.99	114.10
1	A	206	ASP	CA-CB-CG	6.04	118.64	112.60
1	A	157	ASN	OD1-CG-ND2	-6.03	116.57	122.60
1	B	109	ASP	CA-CB-CG	6.03	118.63	112.60
1	A	248	HIS	CB-CG-CD2	-6.02	123.37	131.20
1	A	183	VAL	N-CA-C	-5.98	103.43	111.44
1	A	103	HIS	CA-CB-CG	5.96	119.75	113.80
1	B	19	TRP	CG-CD2-CE3	5.94	139.84	133.90
1	B	183	VAL	N-CA-C	-5.92	104.55	111.00
1	B	52	ASN	OD1-CG-ND2	-5.92	116.69	122.60
1	A	19	TRP	CB-CG-CD1	-5.87	118.10	126.90
1	A	167	TYR	O-C-N	-5.74	116.16	122.07
1	A	104	ASN	OD1-CG-ND2	-5.70	116.90	122.60
1	B	248	HIS	CB-CG-CD2	-5.69	123.81	131.20

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	189	LYS	CB-CG-CD	-5.66	98.28	111.30
1	A	181	GLN	OE1-CD-NE2	-5.61	116.99	122.60
1	A	239	GLN	OE1-CD-NE2	-5.57	117.03	122.60
1	B	224	LYS	CA-C-N	5.54	125.84	119.92
1	B	224	LYS	C-N-CA	5.54	125.84	119.92
1	A	14	HIS	CB-CG-CD2	-5.53	124.01	131.20
1	B	236	HIS	CB-CG-CD2	-5.53	124.01	131.20
1	A	50	GLN	CB-CG-CD	5.48	121.92	112.60
1	B	136	PHE	CA-CB-CG	5.45	119.25	113.80
1	B	14	HIS	CB-CG-CD2	-5.44	124.12	131.20
1	B	14	HIS	CB-CG-ND1	5.38	130.78	122.70
1	A	236	HIS	CB-CG-ND1	5.36	130.73	122.70
1	B	130	ASP	CA-CB-CG	5.32	117.92	112.60
1	B	148	LYS	CA-CB-CG	5.29	124.67	114.10
1	A	131	THR	CA-CB-OG1	-5.24	101.74	109.60
1	A	32	LYS	N-CA-C	-5.24	101.16	109.96
1	B	31	HIS	CB-CG-CD2	-5.22	124.41	131.20
1	A	19	TRP	CE2-CD2-CG	-5.22	100.94	107.20
1	A	182	ASN	N-CA-C	5.21	117.70	111.71
1	B	94	VAL	N-CA-C	5.20	116.55	110.62
1	B	38	MET	N-CA-C	-5.20	103.83	110.53
1	A	31	HIS	CB-CG-ND1	5.17	130.46	122.70
1	B	10	HIS	CB-CG-CD2	-5.17	124.48	131.20
1	A	208	ASP	CA-CB-CG	5.16	117.76	112.60
1	A	20	HIS	CB-CG-CD2	-5.13	124.53	131.20
1	A	248	HIS	CB-CG-ND1	5.12	130.38	122.70
1	B	19	TRP	CE2-CD2-CG	-5.09	101.09	107.20
1	A	92	ARG	NE-CZ-NH2	-5.08	114.62	119.20
1	B	59	GLU	CA-C-O	-5.05	113.98	118.63
1	B	138	ASN	CA-CB-CG	5.05	117.65	112.60
1	B	245	GLU	CB-CG-CD	5.01	121.12	112.60
1	B	10	HIS	CB-CG-ND1	5.01	130.21	122.70

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts

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	2095	0	2096	33	0
1	B	2065	0	2060	18	0
2	A	8	0	14	0	0
2	B	8	0	14	1	0
3	A	116	0	0	2	0
3	B	134	0	0	2	0
All	All	4426	0	4184	50	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 (50) 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:10:HIS:HE1	1:A:38:MET:H	1.18	0.89
1:B:10:HIS:HE1	1:B:38:MET:H	1.21	0.85
1:B:52:ASN:HD22	1:B:138:ASN:HB2	1.52	0.75
1:A:52:ASN:HD22	1:A:138:ASN:HB2	1.53	0.74
1:A:10:HIS:HD2	1:A:11:THR:O	1.73	0.71
1:B:81:CYS:HA	1:B:106:LEU:HD22	1.75	0.67
1:A:50:GLN:HG2	3:A:2027:HOH:O	1.97	0.65
1:B:10:HIS:HD2	1:B:11:THR:O	1.81	0.63
1:A:199:LYS:HG2	1:A:257:TYR:CE1	2.34	0.63
1:A:168:GLU:HG3	1:B:24:PRO:HD3	1.79	0.63
1:B:82:ALA:HA	1:B:85:ASN:HD22	1.69	0.58
1:A:68:LEU:HD11	1:A:74:VAL:HG13	1.86	0.58
1:A:155:ARG:HD3	1:A:155:ARG:O	2.05	0.57
1:A:81:CYS:HA	1:A:106:LEU:HD22	1.88	0.55
1:A:155:ARG:HD3	1:A:155:ARG:C	2.33	0.54
1:A:138:ASN:ND2	1:A:142:GLU:H	2.05	0.54
1:A:248:HIS:HB3	3:A:2113:HOH:O	2.07	0.53
1:A:129:ARG:NH2	1:A:156:GLU:HB2	2.23	0.53
1:B:50:GLN:HG3	3:B:2041:HOH:O	2.08	0.52
1:A:10:HIS:HE1	1:A:38:MET:N	1.99	0.51
1:A:120:LYS:HG3	1:A:218:TRP:CH2	2.46	0.51
1:A:82:ALA:HA	1:A:85:ASN:HD22	1.76	0.51
1:A:135:THR:HA	1:A:144:ILE:O	2.12	0.50
1:B:182:ASN:H	1:B:182:ASN:HD22	1.58	0.49
1:A:20:HIS:HE1	1:A:166:GLU:OE1	1.95	0.48
1:A:92:ARG:HH22	1:A:187:ARG:NH2	2.11	0.48
1:A:180:PHE:HB3	1:A:183:VAL:HG22	1.96	0.48
1:B:20:HIS:HE1	1:B:166:GLU:OE1	1.98	0.47

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:HIS:HD2	1:B:165:GLY:O	1.97	0.47
1:B:9:ILE:HD11	1:B:61:LEU:HD13	1.96	0.46
1:B:10:HIS:CE1	1:B:38:MET:H	2.13	0.45
1:A:224:LYS:HA	1:A:225:PRO:HD3	1.73	0.45
1:A:75:ILE:HD11	1:A:258:ALA:HB2	1.98	0.45
1:A:14:HIS:O	1:A:41:SER:HB3	2.17	0.45
1:B:22:LEU:HD13	1:B:246:VAL:HG23	2.00	0.44
1:A:231:VAL:HG11	1:A:242:LYS:HG3	1.99	0.43
1:B:47:GLN:O	1:B:50:GLN:HG2	2.18	0.43
1:B:3:THR:HA	1:B:31:HIS:ND1	2.34	0.43
1:B:50:GLN:HG3	3:B:2007:HOH:O	2.19	0.43
1:A:10:HIS:CE1	1:A:38:MET:H	2.11	0.42
1:A:11:THR:HB	1:A:80:SER:HB3	2.00	0.42
1:A:102:PHE:HB3	1:A:105:SER:HB3	2.01	0.42
1:A:39:ALA:HB3	1:A:57:TYR:HA	2.01	0.42
2:B:1301:MPD:O4	2:B:1301:MPD:O2	2.35	0.42
1:B:110:THR:O	1:B:189:LYS:HD3	2.21	0.41
1:A:200:LYS:HE2	1:A:223:TYR:HE2	1.85	0.41
1:B:14:HIS:O	1:B:41:SER:HB3	2.21	0.40
1:A:76:ILE:HD11	1:A:97:ILE:HD12	2.01	0.40
1:A:132:GLU:O	1:A:147:MET:HA	2.21	0.40
1:A:148:LYS:HD2	1:A:148:LYS:HA	1.94	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	260/262 (99%)	251 (96%)	9 (4%)	0	100	100
1	B	256/262 (98%)	244 (95%)	11 (4%)	1 (0%)	30	28
All	All	516/524 (98%)	495 (96%)	20 (4%)	1 (0%)	43	44

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	17	TRP

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	226/226 (100%)	210 (93%)	16 (7%)	13	11
1	B	222/226 (98%)	210 (95%)	12 (5%)	20	18
All	All	448/452 (99%)	420 (94%)	28 (6%)	16	14

All (28) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-2	SER
1	A	21	LYS
1	A	32	LYS
1	A	72	GLU
1	A	92	ARG
1	A	106	LEU
1	A	129	ARG
1	A	135	THR
1	A	138	ASN
1	A	143	THR
1	A	154	LEU
1	A	155	ARG
1	A	182	ASN
1	A	193	LYS
1	A	199	LYS
1	A	210	ILE
1	B	50	GLN
1	B	68	LEU
1	B	103	HIS
1	B	106	LEU
1	B	120	LYS
1	B	155	ARG

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	169	LEU
1	B	182	ASN
1	B	210	ILE
1	B	224	LYS
1	B	244	GLU
1	B	250	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (19) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	HIS
1	A	20	HIS
1	A	47	GLN
1	A	52	ASN
1	A	85	ASN
1	A	103	HIS
1	A	138	ASN
1	A	182	ASN
1	A	248	HIS
1	A	251	GLN
1	B	10	HIS
1	B	20	HIS
1	B	47	GLN
1	B	50	GLN
1	B	52	ASN
1	B	85	ASN
1	B	181	GLN
1	B	182	ASN
1	B	216	GLN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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](#)

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	MPD	B	1301	-	7,7,7	0.61	0	9,10,10	0.51	0
2	MPD	A	1301	-	7,7,7	0.56	0	9,10,10	0.53	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
2	MPD	B	1301	-	-	0/5/5/5	-
2	MPD	A	1301	-	-	0/5/5/5	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	1301	MPD	1	0

5.7 Other polymers

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

EDS was not executed - this section is therefore empty.

6.2 Non-standard residues in protein, DNA, RNA chains

EDS was not executed - this section is therefore empty.

6.3 Carbohydrates

EDS was not executed - this section is therefore empty.

6.4 Ligands

EDS was not executed - this section is therefore empty.

6.5 Other polymers

EDS was not executed - this section is therefore empty.