



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 13, 2017 – 11:24 pm GMT

PDB ID : 1MDP  
Title : REFINED STRUCTURES OF TWO INSERTION(SLASH)DELETION MUTANTS PROBE FUNCTION OF THE MALTODEXTRIN BINDING PROTEIN  
Authors : Sharff, A.J.; Quiococho, F.A.  
Deposited on : 1994-08-10  
Resolution : 2.30 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

<http://wwpdb.org/validation/2016/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 : 1.7.2 (RC1), CSD as538be (2017)  
Xtriage (Phenix) : **NOT EXECUTED**  
EDS : **NOT EXECUTED**  
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : recalc28949

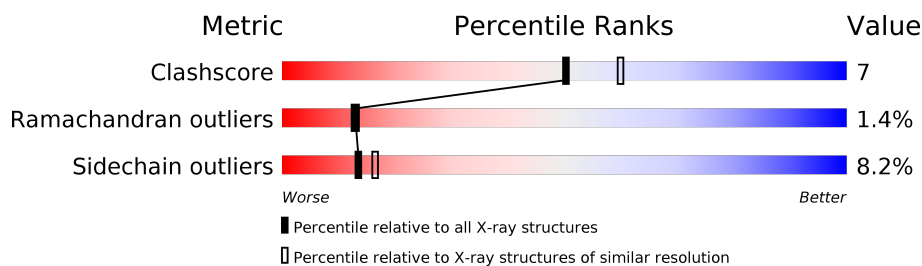
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.30 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	112137	4751 (2.30-2.30)
Ramachandran outliers	110173	4705 (2.30-2.30)
Sidechain outliers	110143	4704 (2.30-2.30)

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  $\geq 3$ , 2, 1 and 0 types of geometric quality criteria. 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.

Note EDS was not executed.

Mol	Chain	Length	Quality of chain
1	1	363	
1	2	363	

## 2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 5851 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.

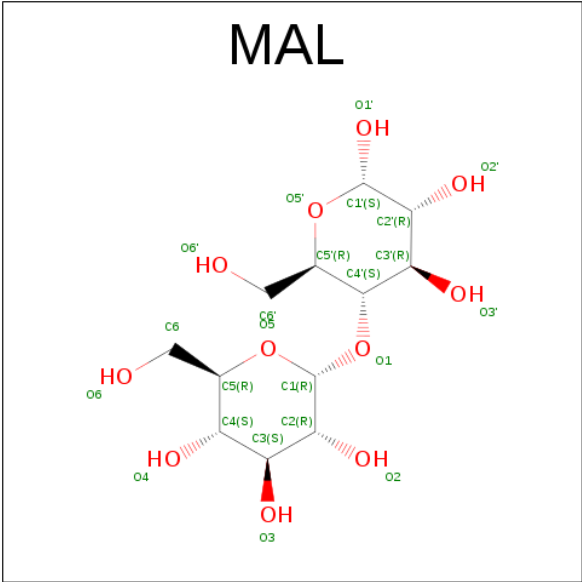
- Molecule 1 is a protein called MALTODEXTRIN BINDING PROTEIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	1	363	Total	C	N	O	S	0	0	0
			2822	1817	459	540	6			
1	2	363	Total	C	N	O	S	0	0	0
			2822	1817	459	540	6			

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
1	134	ASP	LYS	ENGINEERED	UNP P02928
1	135	PRO	LYS	ENGINEERED	UNP P02928
1	?	-	ALA	DELETION	UNP P02928
1	?	-	LEU	DELETION	UNP P02928
1	?	-	LYS	DELETION	UNP P02928
1	?	-	GLU	DELETION	UNP P02928
1	?	-	LEU	DELETION	UNP P02928
1	?	-	LYS	DELETION	UNP P02928
1	?	-	ALA	DELETION	UNP P02928
2	134	ASP	LYS	ENGINEERED	UNP P02928
2	135	PRO	LYS	ENGINEERED	UNP P02928
2	?	-	ALA	DELETION	UNP P02928
2	?	-	LEU	DELETION	UNP P02928
2	?	-	LYS	DELETION	UNP P02928
2	?	-	GLU	DELETION	UNP P02928
2	?	-	LEU	DELETION	UNP P02928
2	?	-	LYS	DELETION	UNP P02928
2	?	-	ALA	DELETION	UNP P02928

- Molecule 2 is SUGAR (MALTOSE) (three-letter code: MAL) (formula: C<sub>12</sub>H<sub>22</sub>O<sub>11</sub>).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	1	1	Total	C	O	0	0
			23	12	11		
2	2	1	Total	C	O	0	0
			23	12	11		

- Molecule 3 is water.

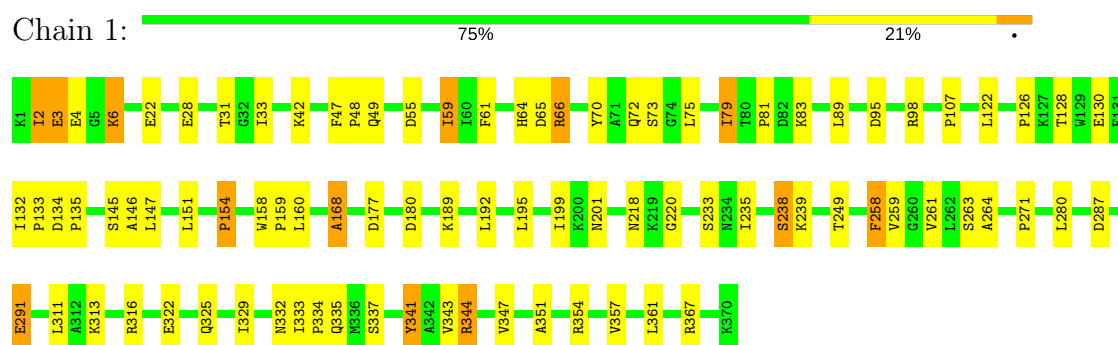
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	1	76	Total	O	0	0
			76	76		
3	2	85	Total	O	0	0
			85	85		

### 3 Residue-property plots

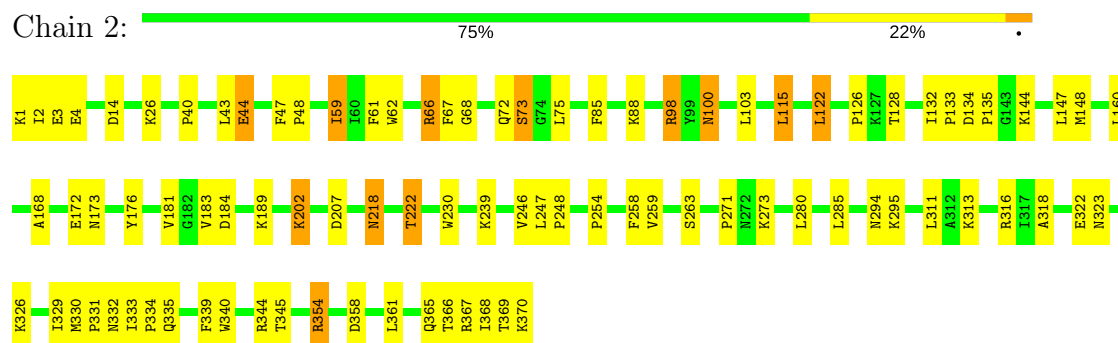
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are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

Note EDS was not executed.

#### • Molecule 1: MALTODEXTRIN BINDING PROTEIN



#### • Molecule 1: MALTODEXTRIN BINDING PROTEIN



## 4 Data and refinement statistics

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

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	55.51Å 88.33Å 75.79Å 90.00° 95.00° 90.00°	Depositor
Resolution (Å)	10.00 – 2.30	Depositor
% Data completeness (in resolution range)	(Not available) (10.00-2.30)	Depositor
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
Refinement program	PROLSQ, X-PLOR	Depositor
R, $R_{free}$	0.187 , (Not available)	Depositor
Estimated twinning fraction	No twinning to report.	Xtriage
Total number of atoms	5851	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	17.0	wwPDB-VP

## 5 Model quality

### 5.1 Standard geometry

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

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	1	0.74	0/2891	1.27	14/3925 (0.4%)
1	2	0.75	0/2891	1.33	14/3925 (0.4%)
All	All	0.75	0/5782	1.30	28/7850 (0.4%)

There are no bond length outliers.

All (28) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	2	316	ARG	CD-NE-CZ	15.50	145.30	123.60
1	2	316	ARG	NE-CZ-NH1	13.18	126.89	120.30
1	2	66	ARG	NE-CZ-NH1	8.06	124.33	120.30
1	1	341	TYR	CB-CG-CD1	7.63	125.58	121.00
1	2	98	ARG	NE-CZ-NH1	7.38	123.99	120.30
1	1	316	ARG	NE-CZ-NH1	7.16	123.88	120.30
1	1	341	TYR	CA-CB-CG	6.81	126.34	113.40
1	2	98	ARG	NE-CZ-NH2	-6.62	116.99	120.30
1	2	66	ARG	NE-CZ-NH2	-6.54	117.03	120.30
1	2	344	ARG	NE-CZ-NH1	6.40	123.50	120.30
1	2	44	GLU	CA-CB-CG	6.39	127.46	113.40
1	2	115	LEU	CA-CB-CG	6.36	129.93	115.30
1	1	344	ARG	NE-CZ-NH1	6.30	123.45	120.30
1	1	367	ARG	NE-CZ-NH1	6.22	123.41	120.30
1	1	98	ARG	NE-CZ-NH1	6.16	123.38	120.30
1	2	316	ARG	NE-CZ-NH2	-6.14	117.23	120.30
1	2	207	ASP	CB-CG-OD1	6.11	123.80	118.30
1	1	238	SER	C-N-CA	6.10	136.96	121.70
1	1	201	ASN	C-N-CA	5.88	136.40	121.70
1	1	95	ASP	CB-CG-OD1	5.74	123.46	118.30
1	1	367	ARG	NE-CZ-NH2	-5.62	117.49	120.30
1	2	285	LEU	C-N-CA	5.52	135.50	121.70

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	1	70	TYR	CB-CG-CD1	5.42	124.25	121.00
1	2	271	PRO	C-N-CA	5.40	135.19	121.70
1	1	154	PRO	C-N-CA	5.27	134.87	121.70
1	1	354	ARG	NE-CZ-NH1	5.25	122.93	120.30
1	1	66	ARG	NE-CZ-NH1	5.12	122.86	120.30
1	2	100	ASN	CA-CB-CG	5.08	124.59	113.40

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	1	2822	0	2785	37	0
1	2	2822	0	2785	39	0
2	1	23	0	22	0	0
2	2	23	0	21	1	0
3	1	76	0	0	1	0
3	2	85	0	0	0	0
All	All	5851	0	5613	75	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 7.

All (75) 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)
1:2:122:LEU:HD21	1:2:126:PRO:HD3	1.70	0.73
1:1:333:ILE:HD12	1:1:335:GLN:HE21	1.54	0.73
1:2:333:ILE:HD12	1:2:335:GLN:HE21	1.56	0.70
1:2:189:LYS:HG2	1:2:361:LEU:HD12	1.73	0.70
1:2:1:LYS:HE2	1:2:4:GLU:HG2	1.76	0.67
1:2:40:PRO:HG2	1:2:43:LEU:HB3	1.76	0.66
1:1:31:THR:HG22	1:1:33:ILE:HD13	1.78	0.64
1:1:42:LYS:HG3	1:2:354:ARG:HD2	1.80	0.64

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:1:189:LYS:HG2	1:1:361:LEU:HD12	1.81	0.63
1:1:47:PHE:HB3	1:1:48:PRO:HD3	1.83	0.61
1:1:122:LEU:HD21	1:1:126:PRO:HD3	1.85	0.59
1:2:47:PHE:HB3	1:2:48:PRO:HD3	1.86	0.58
1:2:73:SER:HB3	1:2:75:LEU:HG	1.89	0.55
1:2:259:VAL:HB	1:2:329:ILE:HA	1.89	0.55
1:1:177:ASP:HB3	1:1:180:ASP:HB3	1.88	0.54
1:1:73:SER:HB2	1:1:75:LEU:HG	1.89	0.54
1:2:1:LYS:HB2	1:2:4:GLU:HB3	1.89	0.54
1:2:366:THR:HG23	1:2:370:LYS:HD2	1.90	0.54
1:1:134:ASP:HB2	1:1:135:PRO:HD2	1.91	0.53
1:2:181:VAL:HG12	1:2:183:VAL:HG22	1.90	0.53
1:1:333:ILE:HB	1:1:334:PRO:HD2	1.91	0.51
1:1:259:VAL:HG12	1:1:329:ILE:HD12	1.93	0.50
1:2:345:THR:HG21	1:2:367:ARG:HH12	1.78	0.49
1:2:333:ILE:HD12	1:2:335:GLN:NE2	2.26	0.48
1:1:218:ASN:HD21	1:1:235:ILE:HG12	1.77	0.48
1:2:318:ALA:O	1:2:322:GLU:HG3	2.15	0.47
1:1:192:LEU:HD23	1:1:357:VAL:HG13	1.95	0.47
1:1:64:HIS:HD2	1:1:261:VAL:H	1.63	0.47
1:1:59:ILE:CD1	1:1:280:LEU:HD21	2.45	0.47
1:1:65:ASP:HA	1:1:332:ASN:HA	1.98	0.46
1:1:220:GLY:HA2	3:1:419:HOH:O	2.16	0.46
1:2:144:LYS:NZ	1:2:202:LYS:HD3	2.31	0.45
1:2:247:LEU:HA	1:2:248:PRO:HD3	1.82	0.45
1:1:61:PHE:HA	1:1:263:SER:O	2.16	0.45
1:1:6:LYS:HB2	1:1:6:LYS:HZ3	1.81	0.45
1:1:59:ILE:CD1	1:1:264:ALA:HB1	2.47	0.44
1:2:132:ILE:HB	1:2:133:PRO:HD3	1.98	0.44
1:1:168:ALA:HB2	1:1:258:PHE:HZ	1.81	0.44
1:2:62:TRP:HB3	1:2:67:PHE:HE1	1.82	0.44
1:2:59:ILE:HD11	1:2:61:PHE:CE1	2.53	0.44
1:2:148:MET:HB2	1:2:222:THR:HG21	2.00	0.43
1:2:72:GLN:HG3	1:2:334:PRO:HG3	2.00	0.43
1:2:254:PRO:HB3	1:2:326:LYS:NZ	2.34	0.43
1:2:176:TYR:CZ	1:2:331:PRO:HB3	2.54	0.43
1:2:134:ASP:HA	1:2:135:PRO:HD3	1.91	0.43
1:1:333:ILE:HD12	1:1:335:GLN:NE2	2.28	0.43
1:1:89:LEU:HD13	1:1:107:PRO:HG2	1.99	0.43
1:2:59:ILE:CD1	1:2:280:LEU:HD21	2.49	0.42
1:2:184:ASP:HB3	1:2:365:GLN:NE2	2.34	0.42

*Continued on next page...*

*Continued from previous page...*

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:2:246:VAL:HA	1:2:323:ASN:HD21	1.83	0.42
1:1:154:PRO:HG3	1:1:344:ARG:HB2	2.01	0.42
1:2:339:PHE:HA	1:2:368:ILE:HG12	2.02	0.42
1:1:132:ILE:N	1:1:133:PRO:HD2	2.34	0.42
1:1:132:ILE:N	1:1:133:PRO:CD	2.82	0.42
1:1:128:THR:HG22	1:1:249:THR:OG1	2.19	0.42
1:1:343:VAL:O	1:1:347:VAL:HG22	2.19	0.42
1:1:199:ILE:HD13	1:1:351:ALA:HB1	2.02	0.42
1:2:259:VAL:O	1:2:330:MET:HG3	2.19	0.42
1:2:68:GLY:HA3	1:2:332:ASN:O	2.19	0.42
1:2:132:ILE:N	1:2:133:PRO:CD	2.83	0.42
1:2:340:TRP:CD1	2:2:371:MAL:H4	2.55	0.41
1:2:1:LYS:HD2	1:2:4:GLU:OE2	2.20	0.41
1:1:79:ILE:HD12	1:1:81:PRO:HD3	2.01	0.41
1:2:85:PHE:HA	1:2:88:LYS:HD3	2.02	0.41
1:2:98:ARG:HH11	1:2:103:LEU:HD21	1.85	0.41
1:2:14:ASP:O	1:2:230:TRP:HB2	2.21	0.41
1:1:287:ASP:O	1:1:291:GLU:HB2	2.21	0.41
1:1:128:THR:HB	1:1:130:GLU:OE2	2.20	0.41
1:1:158:TRP:HB3	1:1:159:PRO:HD3	2.03	0.41
1:2:218:ASN:N	1:2:218:ASN:HD22	2.19	0.41
1:1:151:LEU:HD21	1:1:195:LEU:HD11	2.04	0.40
1:1:59:ILE:HD12	1:1:264:ALA:HB1	2.02	0.40
1:1:4:GLU:HG3	1:1:271:PRO:HB2	2.02	0.40
1:2:44:GLU:HB2	1:2:66:ARG:HD3	2.02	0.40
1:1:64:HIS:CD2	1:1:261:VAL:H	2.39	0.40

There are no symmetry-related clashes.

## 5.3 Torsion angles

### 5.3.1 Protein backbone

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	1	359/363 (99%)	338 (94%)	16 (4%)	5 (1%)	13	13
1	2	359/363 (99%)	335 (93%)	19 (5%)	5 (1%)	13	13
All	All	718/726 (99%)	673 (94%)	35 (5%)	10 (1%)	13	13

All (10) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	1	2	ILE
1	1	3	GLU
1	2	2	ILE
1	2	100	ASN
1	2	173	ASN
1	2	369	THR
1	1	145	SER
1	1	146	ALA
1	1	168	ALA
1	2	168	ALA

### 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	1	291/292 (100%)	266 (91%)	25 (9%)	12	14
1	2	291/292 (100%)	268 (92%)	23 (8%)	14	18
All	All	582/584 (100%)	534 (92%)	48 (8%)	13	16

All (48) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	1	2	ILE
1	1	3	GLU
1	1	6	LYS
1	1	22	GLU
1	1	28	GLU
1	1	49	GLN

*Continued on next page...*

*Continued from previous page...*

Mol	Chain	Res	Type
1	1	55	ASP
1	1	59	ILE
1	1	66	ARG
1	1	72	GLN
1	1	79	ILE
1	1	83	LYS
1	1	147	LEU
1	1	160	LEU
1	1	233	SER
1	1	238	SER
1	1	239	LYS
1	1	258	PHE
1	1	291	GLU
1	1	311	LEU
1	1	313	LYS
1	1	322	GLU
1	1	325	GLN
1	1	337	SER
1	1	341	TYR
1	2	3	GLU
1	2	26	LYS
1	2	59	ILE
1	2	73	SER
1	2	115	LEU
1	2	122	LEU
1	2	128	THR
1	2	147	LEU
1	2	160	LEU
1	2	172	GLU
1	2	202	LYS
1	2	218	ASN
1	2	222	THR
1	2	239	LYS
1	2	258	PHE
1	2	263	SER
1	2	273	LYS
1	2	294	ASN
1	2	295	LYS
1	2	311	LEU
1	2	313	LYS
1	2	354	ARG
1	2	358	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	1	64	HIS
1	1	205	ASN
1	1	218	ASN
1	1	335	GLN
1	2	218	ASN
1	2	335	GLN
1	2	365	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](#)

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	MAL	1	371	-	24,24,24	1.08	1 (4%)	35,35,35	1.51	3 (8%)
2	MAL	2	371	-	24,24,24	1.17	2 (8%)	35,35,35	2.12	3 (8%)

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	MAL	1	371	-	-	0/8/48/48	0/2/2/2
2	MAL	2	371	-	-	0/8/48/48	0/2/2/2

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	2	371	MAL	O5'-C1'	-4.97	1.34	1.43
2	1	371	MAL	O5'-C1'	-4.89	1.34	1.43
2	2	371	MAL	C1'-C2'	-2.05	1.48	1.52

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	2	371	MAL	O1'-C1'-O5'	-7.09	89.23	110.20
2	1	371	MAL	O1'-C1'-O5'	-4.27	97.57	110.20
2	1	371	MAL	O5'-C1'-C2'	4.01	116.69	110.04
2	1	371	MAL	C1'-O5'-C5'	5.56	123.42	113.39
2	2	371	MAL	O5'-C1'-C2'	6.23	120.37	110.04
2	2	371	MAL	C1'-O5'-C5'	6.67	125.41	113.39

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	2	371	MAL	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

### 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.