



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 01:43 PM GMT

PDB ID : 3ULA  
Title : Crystal structure of the TV3 mutant F63W-MD-2-Eritoran complex  
Authors : Kim, H.J.; Cheong, H.K.; Jeon, Y.H.  
Deposited on : 2011-11-10  
Resolution : 3.60 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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.

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

MolProbity : 4.02b-467  
Mogul : 1.7 (RC4), CSD as536be (2015)  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026688  
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)  
Refmac : 5.8.0135  
CCP4 : 6.5.0  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : trunk26865

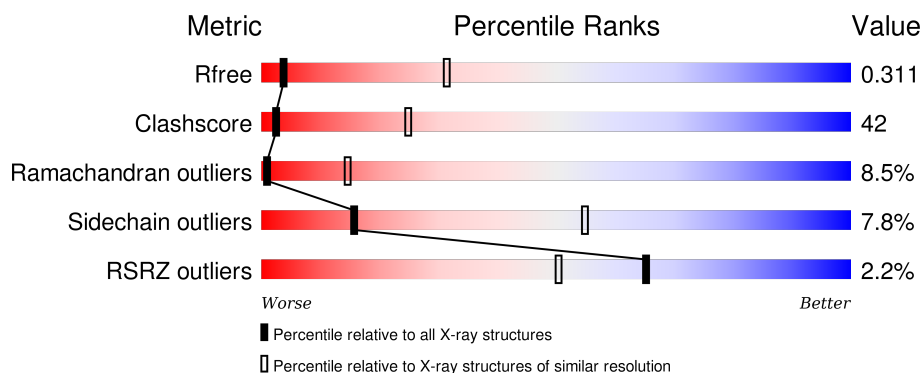
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.60 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))
$R_{free}$	91344	1408 (3.80-3.40)
Clashscore	102246	1010 (3.74-3.46)
Ramachandran outliers	100387	1007 (3.76-3.44)
Sidechain outliers	100360	1007 (3.76-3.44)
RSRZ outliers	91569	1003 (3.78-3.42)

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 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.

Mol	Chain	Length	Quality of chain
1	A	279	 34% 56% 8% .
1	C	279	 37% 54% 8% .
2	B	142	 35% 49% 14% 4% .
2	D	142	 35% 49% 14% 6% .

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
5	E55	A	1206	-	-	-	X
5	E55	C	401	-	-	-	X

## 2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6962 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 Toll-like receptor 4, Variable lymphocyte receptor B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	276	Total	C	N	O	S	0	0	0
			2191	1402	367	411	11			
1	C	276	Total	C	N	O	S	0	0	0
			2191	1402	367	411	11			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	25	GLY	-	EXPRESSION TAG	UNP O00206
A	26	SER	-	EXPRESSION TAG	UNP O00206
A	63	TRP	PHE	ENGINEERED MUTATION	UNP O00206
A	303	THR	-	EXPRESSION TAG	UNP Q4G1L2
C	25	GLY	-	EXPRESSION TAG	UNP O00206
C	26	SER	-	EXPRESSION TAG	UNP O00206
C	63	TRP	PHE	ENGINEERED MUTATION	UNP O00206
C	303	THR	-	EXPRESSION TAG	UNP Q4G1L2

- Molecule 2 is a protein called Lymphocyte antigen 96.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	140	Total	C	N	O	S	0	0	0
			1134	730	186	208	10			
2	D	140	Total	C	N	O	S	0	0	0
			1134	730	186	208	10			

There are 6 discrepancies between the modelled and reference sequences:

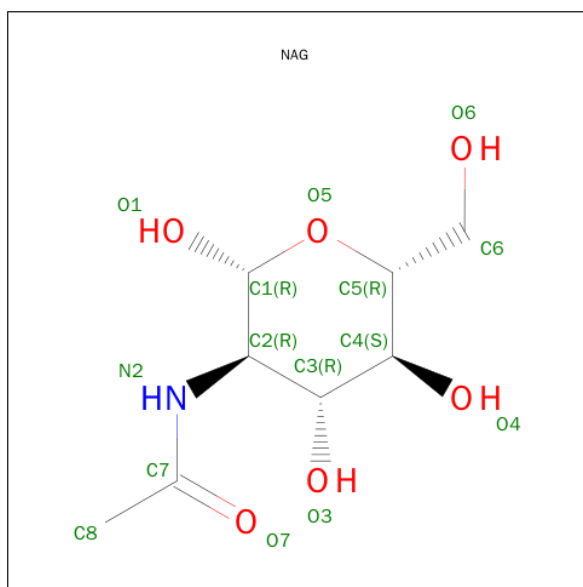
Chain	Residue	Modelled	Actual	Comment	Reference
B	17	GLY	-	EXPRESSION TAG	UNP Q9Y6Y9
B	18	SER	-	EXPRESSION TAG	UNP Q9Y6Y9
B	56	GLY	ARG	SEE REMARK 999	UNP Q9Y6Y9
D	17	GLY	-	EXPRESSION TAG	UNP Q9Y6Y9

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Chain	Residue	Modelled	Actual	Comment	Reference
D	18	SER	-	EXPRESSION TAG	UNP Q9Y6Y9
D	56	GLY	ARG	SEE REMARK 999	UNP Q9Y6Y9

- Molecule 3 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula:  $C_8H_{15}NO_6$ ).



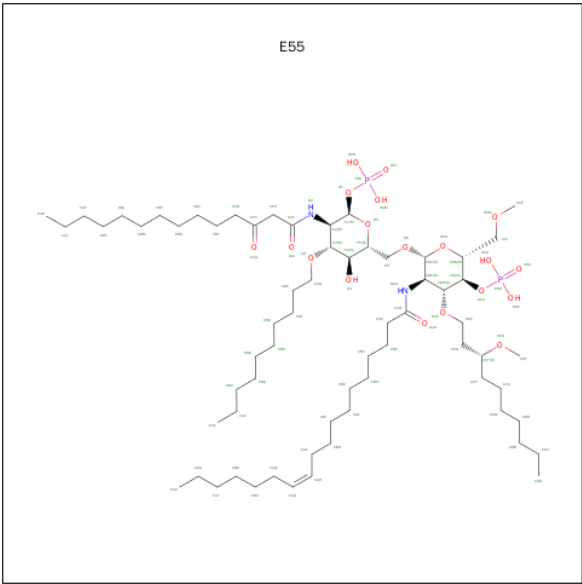
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		
3	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	3	Total	C	N	O	0	0
			39	22	2	15		
4	C	3	Total	C	N	O	0	0
			39	22	2	15		

- Molecule 5 is 3-O-DECYL-2-DEOXY-6-O-{2-DEOXY-3-O-[(3R)-3-METHOXYDECYL]-6-O-METHYL-2-[(11Z)-OCTADEC-11-ENOYLAMINO]-4-O-PHOSPHONO-BETA-D-GLU

COPYRANOSYL}-2-[(3-OXOTETRADECANOYL)AMINO]-1-O-PHOSPHONO-ALPHA-D-GLUCOPYRANOSE (three-letter code: E55) (formula: C<sub>66</sub>H<sub>126</sub>N<sub>2</sub>O<sub>19</sub>P<sub>2</sub>).

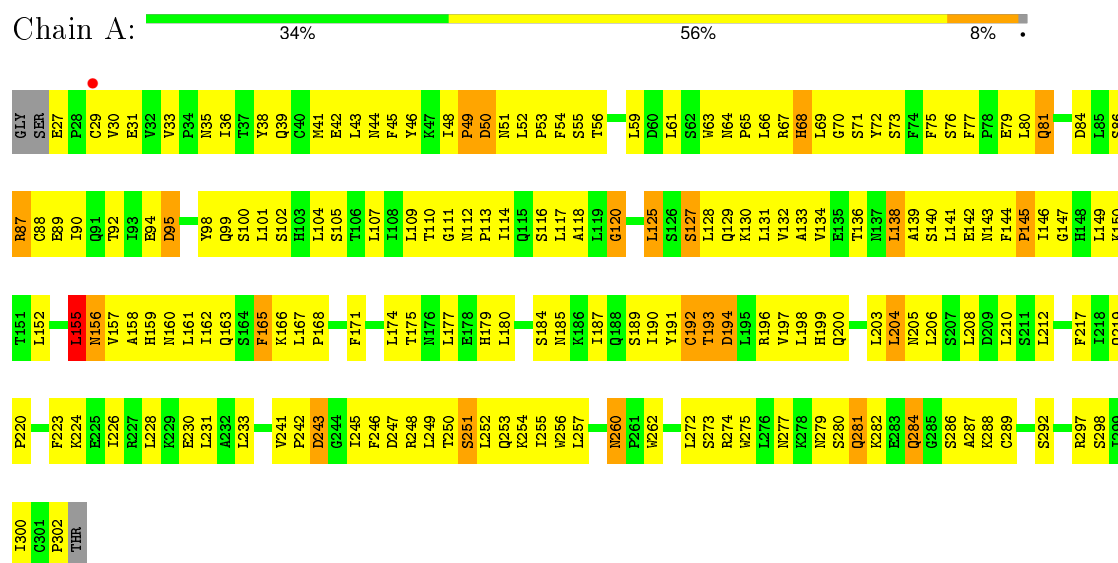


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			89	66	2	19	2		
5	C	1	Total	C	N	O	P	0	0
			89	66	2	19	2		

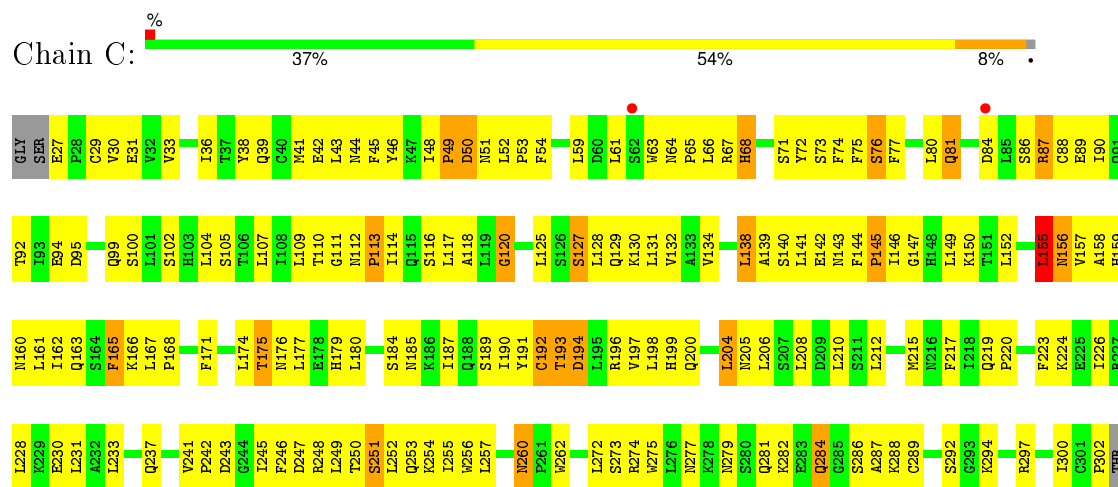
### 3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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: Toll-like receptor 4, Variable lymphocyte receptor B

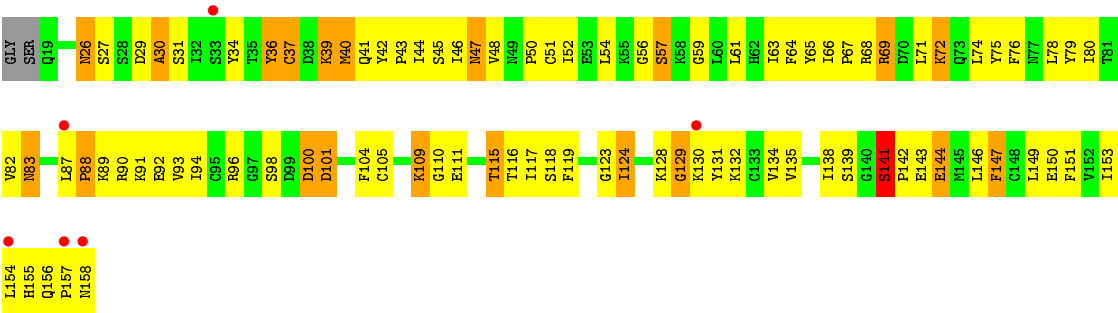


- Molecule 1: Toll-like receptor 4, Variable lymphocyte receptor B

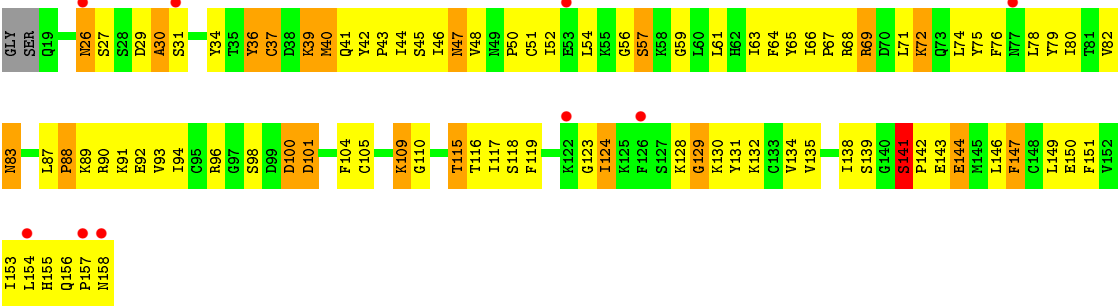


- Molecule 2: Lymphocyte antigen 96





• Molecule 2: Lymphocyte antigen 96





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	80.21Å 126.94Å 129.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.00 – 3.60 90.65 – 3.60	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.00-3.60) 99.3 (90.65-3.60)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.89 (at 3.58Å)	Xtriage
Refinement program	CNS	Depositor
R, $R_{free}$	0.306 , 0.341 0.307 , 0.311	Depositor DCC
$R_{free}$ test set	786 reflections (4.98%)	DCC
Wilson B-factor (Å <sup>2</sup> )	74.0	Xtriage
Anisotropy	0.681	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 21.3	EDS
Estimated twinning fraction	0.040 for -h,l,k	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.36$ , $\langle L^2 \rangle = 0.19$	Xtriage
Outliers	2 of 15822 reflections (0.013%)	Xtriage
$F_o, F_c$ correlation	0.87	EDS
Total number of atoms	6962	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	87.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 42.13 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 2.1344e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

<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, 0.375 respectively for untwinned datasets, and 0.333, 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: E55, BMA, NAG

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	0.51	0/2241	0.75	1/3046 (0.0%)
1	C	0.51	0/2241	0.75	1/3046 (0.0%)
2	B	0.54	0/1160	0.80	1/1562 (0.1%)
2	D	0.55	0/1160	0.81	1/1562 (0.1%)
All	All	0.52	0/6802	0.77	4/9216 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	141	SER	C-N-CD	6.67	142.40	128.40
2	B	141	SER	C-N-CD	6.42	141.89	128.40
1	A	155	LEU	CA-CB-CG	5.36	127.63	115.30
1	C	155	LEU	CA-CB-CG	5.32	127.53	115.30

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	2191	0	2194	183	0
1	C	2191	0	2194	172	0
2	B	1134	0	1130	111	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	1134	0	1130	119	0
3	A	28	0	26	3	0
3	C	28	0	26	2	0
4	A	39	0	34	7	0
4	C	39	0	34	3	0
5	A	89	0	122	18	0
5	C	89	0	122	14	0
All	All	6962	0	7012	586	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 42.

The worst 5 of 586 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)
2:D:54:LEU:HD22	2:D:124:ILE:HD11	1.43	1.01
1:A:102:SER:O	1:A:127:SER:HB2	1.62	1.00
1:A:204:LEU:HD13	1:A:206:LEU:HB2	1.45	0.98
1:C:204:LEU:HD13	1:C:206:LEU:HB2	1.44	0.97
1:C:94:GLU:HA	1:C:118:ALA:HB2	1.45	0.97

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	274/279 (98%)	197 (72%)	55 (20%)	22 (8%)	1	16
1	C	274/279 (98%)	198 (72%)	54 (20%)	22 (8%)	1	16
2	B	138/142 (97%)	105 (76%)	20 (14%)	13 (9%)	1	12
2	D	138/142 (97%)	105 (76%)	20 (14%)	13 (9%)	1	12

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
All	All	824/842 (98%)	605 (73%)	149 (18%)	70 (8%)	1	14

5 of 70 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	67	ARG
1	A	89	GLU
1	A	99	GLN
1	A	175	THR
1	A	247	ASP

### 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	256/258 (99%)	235 (92%)	21 (8%)	14	53
1	C	256/258 (99%)	237 (93%)	19 (7%)	17	57
2	B	130/131 (99%)	120 (92%)	10 (8%)	16	56
2	D	130/131 (99%)	120 (92%)	10 (8%)	16	56
All	All	772/778 (99%)	712 (92%)	60 (8%)	16	55

5 of 60 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	100	ASP
1	C	76	SER
2	D	69	ARG
2	B	144	GLU
1	C	87	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 21 such sidechains are listed below:

Mol	Chain	Res	Type
2	B	155	HIS
1	C	44	ASN
1	C	200	GLN
1	A	260	ASN
1	C	237	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 ⓘ

6 carbohydrates 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	$\# Z  > 2$
4	NAG	A	1202	1,4	14,14,15	1.01	1 (7%)	15,19,21	0.77	0
4	NAG	A	1203	4	14,14,15	0.88	0	15,19,21	0.89	0
4	BMA	A	1204	4	11,11,12	1.08	0	14,15,17	0.86	1 (7%)
4	NAG	C	403	1,4	14,14,15	1.15	1 (7%)	15,19,21	0.62	0
4	NAG	C	404	4	14,14,15	0.97	0	15,19,21	0.65	0
4	BMA	C	405	4	11,11,12	1.07	0	14,15,17	0.87	1 (7%)

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	A	1202	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1203	4	-	0/6/23/26	0/1/1/1
4	BMA	A	1204	4	-	0/2/19/22	1/1/1/1
4	NAG	C	403	1,4	-	0/6/23/26	0/1/1/1
4	NAG	C	404	4	-	0/6/23/26	0/1/1/1
4	BMA	C	405	4	-	0/2/19/22	1/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1202	NAG	C1-C2	2.22	1.55	1.52
4	C	403	NAG	C1-C2	2.91	1.56	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1204	BMA	C1-O5-C5	2.12	114.94	112.25
4	C	405	BMA	C1-O5-C5	2.42	115.33	112.25

There are no chirality outliers.

There are no torsion outliers.

All (2) ring outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	C	405	BMA	C1-C2-C3-C4-C5-O5
4	A	1204	BMA	C1-C2-C3-C4-C5-O5

6 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	1202	NAG	4	0
4	A	1203	NAG	5	0
4	A	1204	BMA	3	0
4	C	403	NAG	1	0
4	C	404	NAG	2	0
4	C	405	BMA	2	0

## 5.6 Ligand geometry ⓘ

6 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	$\# Z  > 2$
3	NAG	A	1201	1	14,14,15	1.10	1 (7%)	15,19,21	1.09	1 (6%)
3	NAG	A	1205	-	14,14,15	1.10	1 (7%)	15,19,21	0.85	0
5	E55	A	1206	-	89,90,90	0.71	1 (1%)	103,111,111	0.90	5 (4%)
5	E55	C	401	-	89,90,90	0.68	1 (1%)	103,111,111	0.92	5 (4%)
3	NAG	C	402	1	14,14,15	1.10	1 (7%)	15,19,21	0.96	1 (6%)
3	NAG	C	406	-	14,14,15	1.01	1 (7%)	15,19,21	0.85	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
3	NAG	A	1201	1	-	0/6/23/26	0/1/1/1
3	NAG	A	1205	-	-	0/6/23/26	0/1/1/1
5	E55	A	1206	-	-	0/83/124/124	0/2/2/2
5	E55	C	401	-	-	0/83/124/124	0/2/2/2
3	NAG	C	402	1	-	0/6/23/26	0/1/1/1
3	NAG	C	406	-	-	0/6/23/26	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	C	401	E55	O6-CDC	2.22	1.44	1.40
5	A	1206	E55	O6-CDC	2.26	1.44	1.40
3	C	406	NAG	C1-C2	2.43	1.55	1.52
3	A	1205	NAG	C1-C2	2.47	1.55	1.52
3	A	1201	NAG	C1-C2	2.79	1.56	1.52

The worst 5 of 12 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	401	E55	C6-C5-C4	-2.99	105.26	112.03

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	C	401	E55	O3-C3-C4	-2.49	105.03	110.04
5	A	1206	E55	CBY-CCD-CCV	-2.44	109.18	115.12
5	A	1206	E55	C6-C5-C4	-2.41	106.57	112.03
3	A	1201	NAG	C2-N2-C7	-2.39	119.97	123.04

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

6 monomers are involved in 37 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1201	NAG	2	0
3	A	1205	NAG	1	0
5	A	1206	E55	18	0
5	C	401	E55	14	0
3	C	402	NAG	1	0
3	C	406	NAG	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	276/279 (98%)	0.24	1 (0%) 93 88	51, 87, 100, 100	0
1	C	276/279 (98%)	0.23	2 (0%) 89 81	49, 87, 100, 100	0
2	B	140/142 (98%)	0.48	6 (4%) 39 27	72, 94, 100, 100	0
2	D	140/142 (98%)	0.51	9 (6%) 23 15	71, 94, 100, 100	0
All	All	832/842 (98%)	0.32	18 (2%) 65 50	49, 89, 100, 100	0

The worst 5 of 18 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	D	158	ASN	7.0
2	D	31	SER	3.7
1	C	62	SER	3.5
2	B	154	LEU	3.3
2	B	157	PRO	3.3

### 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](#)

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
4	NAG	C	403	14/15	0.74	0.40	-	100,100,100,100	0
4	BMA	C	405	11/12	0.70	0.41	-	100,100,100,100	0
4	NAG	A	1203	14/15	0.82	0.51	-	100,100,100,100	0
4	BMA	A	1204	11/12	0.68	0.44	-	100,100,100,100	0
4	NAG	A	1202	14/15	0.68	0.71	-	100,100,100,100	0
4	NAG	C	404	14/15	0.79	0.39	-	100,100,100,100	0

## 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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
5	E55	C	401	89/89	0.91	0.51	1.00	66,100,100,100	0
5	E55	A	1206	89/89	0.92	0.48	0.84	44,94,100,100	0
3	NAG	C	402	14/15	0.68	0.26	-	98,100,100,100	0
3	NAG	C	406	14/15	0.66	0.35	-	100,100,100,100	0
3	NAG	A	1201	14/15	0.73	0.19	-	100,100,100,100	0
3	NAG	A	1205	14/15	0.52	0.33	-	100,100,100,100	0

## 6.5 Other polymers [i](#)

There are no such residues in this entry.