



# wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2026 – 07:32 AM UTC

PDB ID : 3LB6 / pdb\_00003lb6  
Title : The structure of IL-13 in complex with IL-13Ralpha2  
Authors : Lupardus, P.J.; Garcia, K.C.; Birnbaum, M.E.  
Deposited on : 2010-01-07  
Resolution : 3.05 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

<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>.

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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) : 2.0  
EDS : 3.0  
Percentile statistics : 20250101.v01 (using entries in the PDB archive January 1st 2025)  
CCP4 : 9.0.010 (Gargrove)  
Density-Fitness : 1.0.12  
Ideal geometry (proteins) : Engh & Huber (2001)  
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)  
Validation Pipeline (wwPDB-VP) : 2.49

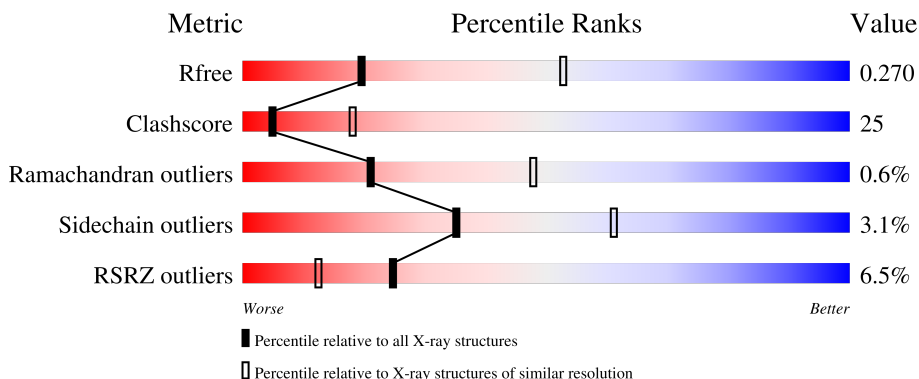
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 3.05 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))
$R_{free}$	180053	2469 (3.10-3.02)
Clashscore	190562	2569 (3.10-3.02)
Ramachandran outliers	187476	2424 (3.10-3.02)
Sidechain outliers	187428	2423 (3.10-3.02)
RSRZ outliers	180081	2469 (3.10-3.02)

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  $\geq 3$ , 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	132	 5% 49% 30% 17%
2	C	380	 6% 35% 28% 34%
3	B	132	 5% 59% 17% 6% 17%
4	D	380	 3% 43% 30% 25%

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6088 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 Interleukin-13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	109	830	526	145	152	7	0	0	0

- Molecule 2 is a protein called Interleukin-13 receptor subunit alpha-2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	C	252	2047	1343	315	379	10	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	151	GLN	ARG	engineered mutation	UNP A8K7E2

- Molecule 3 is a protein called Interleukin-13.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	B	109	840	533	147	153	7	0	0	0

- Molecule 4 is a protein called Interleukin-13 receptor subunit alpha-2.

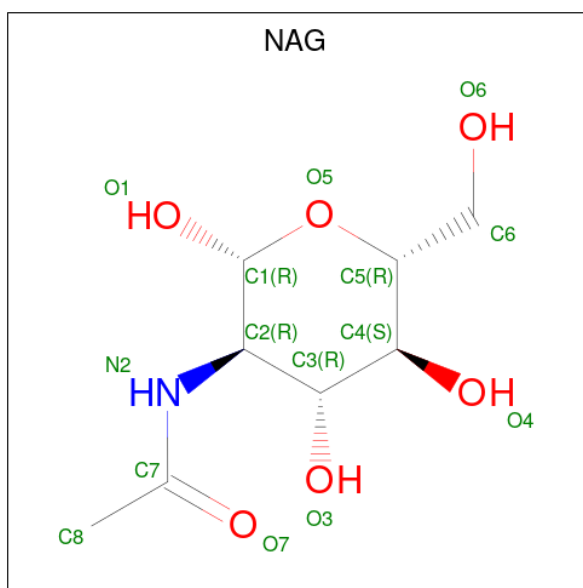
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
4	D	286	2310	1501	362	435	12	5	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	151	GLN	ARG	engineered mutation	UNP A8K7E2

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula:

C<sub>8</sub>H<sub>15</sub>NO<sub>6</sub>).



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

- Molecule 6 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	C	1	Total	Ca	0	0
			1	1		
6	D	1	Total	Ca	0	0
			1	1		

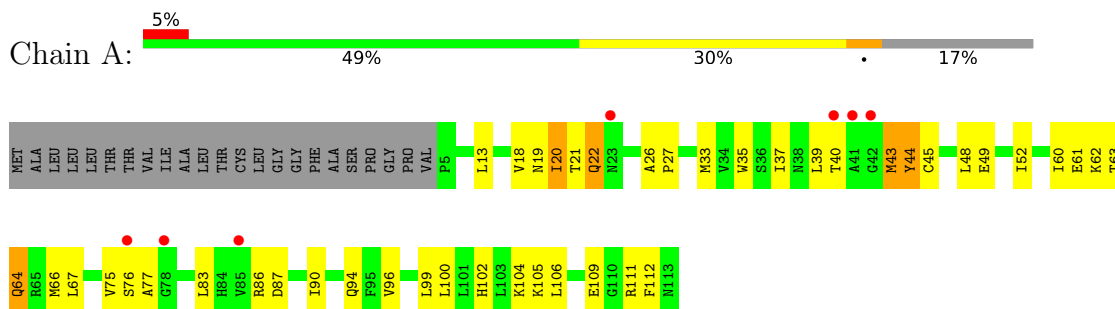
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	7	Total	O	0	0
			7	7		
7	C	4	Total	O	0	0
			4	4		
7	B	4	Total	O	0	0
			4	4		
7	D	16	Total	O	0	0
			16	16		

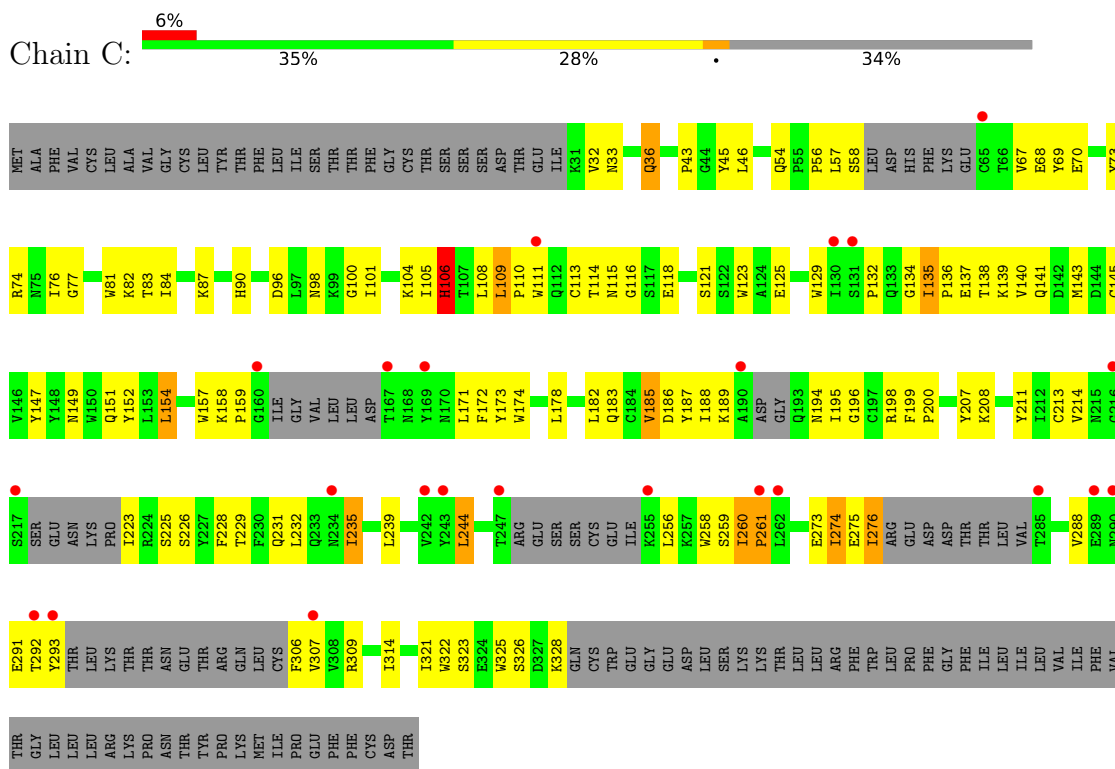
### 3 Residue-property plots [i](#)

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: Interleukin-13

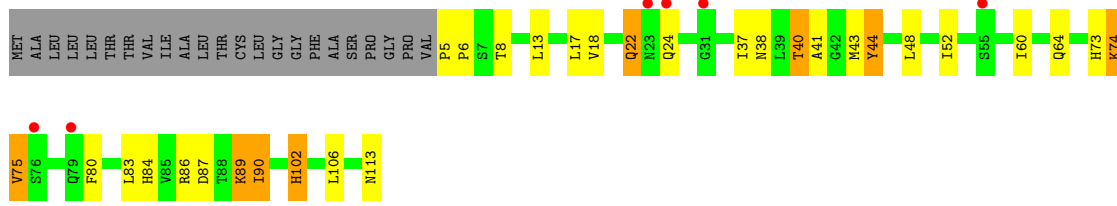


- Molecule 2: Interleukin-13 receptor subunit alpha-2

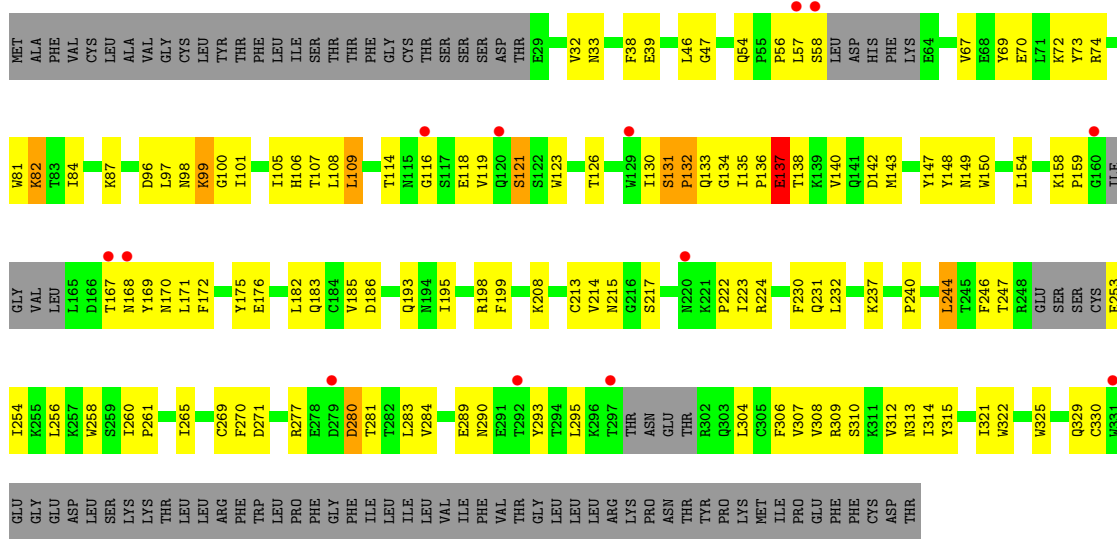


- Molecule 3: Interleukin-13





• Molecule 4: Interleukin-13 receptor subunit alpha-2



## 4 Data and refinement statistics i

Property	Value	Source
Space group	I 1 2 1	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	73.37Å 86.57Å 166.79Å 90.00° 96.77° 90.00°	Depositor
Resolution (Å)	82.80 – 3.05 82.80 – 3.05	Depositor EDS
% Data completeness (in resolution range)	94.2 (82.80-3.05) 100.0 (82.80-3.05)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$	-	Xtrriage
Refinement program	PHENIX (phenix.refine: 1.5_2)	Depositor
R, $R_{free}$	0.219 , 0.269 0.221 , 0.270	Depositor DCC
$R_{free}$ test set	1020 reflections (5.11%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	(Not available)	Xtrriage
Anisotropy	(Not available)	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 72.5	EDS
L-test for twinning <sup>1</sup>	$\langle  L  \rangle =$ (Not available), $\langle L^2 \rangle =$ (Not available)	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.91	EDS
Total number of atoms	6088	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	55.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *(Not available)*

<sup>1</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: MLY, NAG, CA

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	0.75	3/844 (0.4%)	1.09	7/1140 (0.6%)
2	C	0.61	5/2090 (0.2%)	0.99	14/2858 (0.5%)
3	B	0.79	4/843 (0.5%)	1.08	7/1138 (0.6%)
4	D	0.76	1/2357 (0.0%)	1.03	9/3225 (0.3%)
All	All	0.71	13/6134 (0.2%)	1.03	37/8361 (0.4%)

The worst 5 of 13 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	C	261	PRO	N-CD	6.28	1.56	1.47
1	A	102	HIS	ND1-CE1	5.63	1.38	1.32
3	B	102	HIS	ND1-CE1	5.43	1.38	1.32
3	B	84	HIS	ND1-CE1	5.42	1.38	1.32
2	C	90	HIS	ND1-CE1	5.32	1.37	1.32

The worst 5 of 37 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	75	VAL	N-CA-C	9.55	121.48	108.11
2	C	260	ILE	N-CA-C	7.97	116.43	109.02
1	A	22	GLN	N-CA-C	-7.67	104.45	113.88
3	B	44	TYR	N-CA-C	-7.12	102.72	111.33
1	A	102	HIS	CB-CG-CD2	-6.79	122.38	131.20

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	830	0	832	31	1
2	C	2047	0	1874	128	1
3	B	840	0	851	23	0
4	D	2310	0	2140	123	1
5	C	14	0	13	0	0
5	D	14	0	13	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
7	A	7	0	0	2	0
7	B	4	0	0	0	0
7	C	4	0	0	0	0
7	D	16	0	0	2	0
All	All	6088	0	5723	297	2

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 25.

The worst 5 of 297 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)
4:D:167:THR:HG23	4:D:217:SER:O	1.21	1.30
2:C:140:VAL:HG21	2:C:157:TRP:CD1	1.77	1.19
2:C:292:THR:HG22	2:C:293:TYR:H	1.26	1.00
4:D:134:GLY:O	4:D:224:ARG:NH2	1.94	1.00
4:D:167:THR:CG2	4:D:217:SER:O	2.08	0.99

All (2) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:76:SER:OG	4:D:118:GLU:OE1[4_555]	1.96	0.24
2:C:198:ARG:NH2	2:C:260:ILE:CD1[2_655]	2.11	0.09

## 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	107/132 (81%)	94 (88%)	12 (11%)	1 (1%)	14	39
2	C	234/380 (62%)	204 (87%)	30 (13%)	0	100	100
3	B	106/132 (80%)	94 (89%)	11 (10%)	1 (1%)	14	39
4	D	274/380 (72%)	240 (88%)	32 (12%)	2 (1%)	18	45
All	All	721/1024 (70%)	632 (88%)	85 (12%)	4 (1%)	21	48

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	131	SER
4	D	132	PRO
1	A	20	ILE
3	B	6	PRO

### 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	91/112 (81%)	89 (98%)	2 (2%)	45	67
2	C	215/349 (62%)	205 (95%)	10 (5%)	23	51
3	B	92/111 (83%)	89 (97%)	3 (3%)	33	60
4	D	246/349 (70%)	241 (98%)	5 (2%)	48	69
All	All	644/921 (70%)	624 (97%)	20 (3%)	35	61

5 of 20 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	B	113	ASN
4	D	137	GLU
4	D	321	ILE
4	D	244	LEU
2	C	154	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	79	GLN
2	C	115	ASN
3	B	79	GLN
4	D	183	GLN
4	D	329	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](#)

5 non-standard protein/DNA/RNA residues 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	MLY	D	99	4	9,10,11	0.65	0	6,11,13	1.43	1 (16%)
3	MLY	B	89	3	9,10,11	0.53	0	6,11,13	1.54	1 (16%)
2	MLY	C	139	2	9,10,11	0.59	0	6,11,13	0.77	0
2	MLY	C	104	2	9,10,11	0.54	0	6,11,13	1.11	1 (16%)
4	MLY	D	82	4	9,10,11	0.58	0	6,11,13	1.50	1 (16%)

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. '2' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MLY	D	99	4	-	0/8/9/11	-
3	MLY	B	89	3	-	1/8/9/11	-
2	MLY	C	139	2	-	4/8/9/11	-
2	MLY	C	104	2	-	1/8/9/11	-
4	MLY	D	82	4	-	0/8/9/11	-

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	99	MLY	CD-CE-NZ	-2.95	106.09	113.71
3	B	89	MLY	CD-CE-NZ	-2.80	106.47	113.71
4	D	82	MLY	CD-CE-NZ	-2.65	106.86	113.71
2	C	104	MLY	CD-CE-NZ	-2.17	108.09	113.71

There are no chirality outliers.

5 of 6 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	C	104	MLY	O-C-CA-CB
2	C	139	MLY	CE-CD-CG-CB
2	C	139	MLY	CG-CD-CE-NZ
2	C	139	MLY	N-CA-CB-CG
2	C	139	MLY	CD-CE-NZ-CH2

There are no ring outliers.

4 monomers are involved in 10 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	99	MLY	1	0
3	B	89	MLY	1	0
2	C	139	MLY	5	0
4	D	82	MLY	3	0

## 5.5 Carbohydrates [i](#)

There are no oligosaccharides in this entry.

## 5.6 Ligand geometry [i](#)

Of 4 ligands modelled in this entry, 2 are monoatomic - leaving 2 for Mogul analysis.

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
5	NAG	D	501	4	14,14,15	0.55	0	17,19,21	1.15	3 (17%)
5	NAG	C	501	2	14,14,15	0.58	0	17,19,21	1.21	3 (17%)

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
5	NAG	D	501	4	-	2/6/23/26	0/1/1/1
5	NAG	C	501	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

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

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	D	501	NAG	C2-N2-C7	-2.49	119.56	122.90
5	C	501	NAG	C1-C2-N2	-2.30	106.81	110.43
5	C	501	NAG	C4-C3-C2	2.14	114.15	111.02
5	D	501	NAG	C1-C2-N2	-2.08	107.16	110.43
5	D	501	NAG	O5-C1-C2	2.05	114.47	111.29

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	D	501	NAG	C8-C7-N2-C2
5	D	501	NAG	O7-C7-N2-C2

There are no ring outliers.

No monomer is involved in short contacts.

## 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 [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	109/132 (82%)	0.09	7 (6%) 25 13	17, 52, 107, 169	0
2	C	250/380 (65%)	0.46	23 (9%) 14 8	25, 59, 125, 204	0
3	B	108/132 (81%)	0.10	6 (5%) 30 15	20, 48, 93, 145	0
4	D	284/380 (74%)	0.05	13 (4%) 37 19	18, 44, 90, 143	1 (0%)
All	All	751/1024 (73%)	0.20	49 (6%) 25 12	17, 51, 111, 204	1 (0%)

The worst 5 of 49 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	C	262	LEU	5.6
2	C	217	SER	5.2
2	C	160	GLY	4.4
2	C	247	THR	4.2
4	D	279	ASP	3.6

### 6.2 Non-standard residues in protein, DNA, RNA chains [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	MLY	C	139	11/12	0.75	0.19	66,89,95,97	0
4	MLY	D	99	11/12	0.90	0.13	33,35,47,51	0
4	MLY	D	82	11/12	0.94	0.10	33,36,40,40	0
2	MLY	C	104	11/12	0.95	0.09	29,33,54,64	0
3	MLY	B	89	11/12	0.97	0.08	24,35,45,46	0

### 6.3 Carbohydrates [i](#)

There are no oligosaccharides 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
5	NAG	D	501	14/15	0.80	0.16	78,80,83,84	0
5	NAG	C	501	14/15	0.84	0.11	67,69,71,72	0
6	CA	D	381	1/1	0.87	0.19	70,70,70,70	0
6	CA	C	381	1/1	0.91	0.13	85,85,85,85	0

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

There are no such residues in this entry.