



# wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 09:09 AM GMT

PDB ID : 3HFH  
Title : Crystal structure of tandem FF domains  
Authors : Lu, M.; Yang, J.; Ren, Z.; Subir, S.; Bedford, M.T.; Jacobson, R.H.; McMurray, J.S.; Chen, X.  
Deposited on : 2009-05-11  
Resolution : 2.70 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

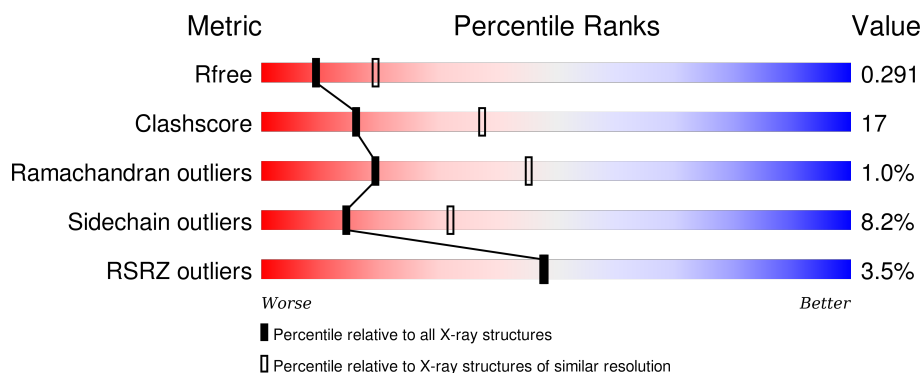
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.70 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	2103 (2.70-2.70)
Clashscore	102246	2422 (2.70-2.70)
Ramachandran outliers	100387	2382 (2.70-2.70)
Sidechain outliers	100360	2382 (2.70-2.70)
RSRZ outliers	91569	2107 (2.70-2.70)

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	190	 4% 56% 29% • 12%
1	B	190	 2% 67% 28% •

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 3178 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 Transcription elongation regulator 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	168	Total	C	N	O	Se	0	0	0
			1475	951	255	262	7			
1	B	190	Total	C	N	O	Se	0	0	0
			1648	1061	285	295	7			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	656	GLY	-	EXPRESSION TAG	UNP O14776
A	657	PRO	-	EXPRESSION TAG	UNP O14776
A	658	LEU	-	EXPRESSION TAG	UNP O14776
A	659	GLY	-	EXPRESSION TAG	UNP O14776
A	660	SER	-	EXPRESSION TAG	UNP O14776
B	656	GLY	-	EXPRESSION TAG	UNP O14776
B	657	PRO	-	EXPRESSION TAG	UNP O14776
B	658	LEU	-	EXPRESSION TAG	UNP O14776
B	659	GLY	-	EXPRESSION TAG	UNP O14776
B	660	SER	-	EXPRESSION TAG	UNP O14776

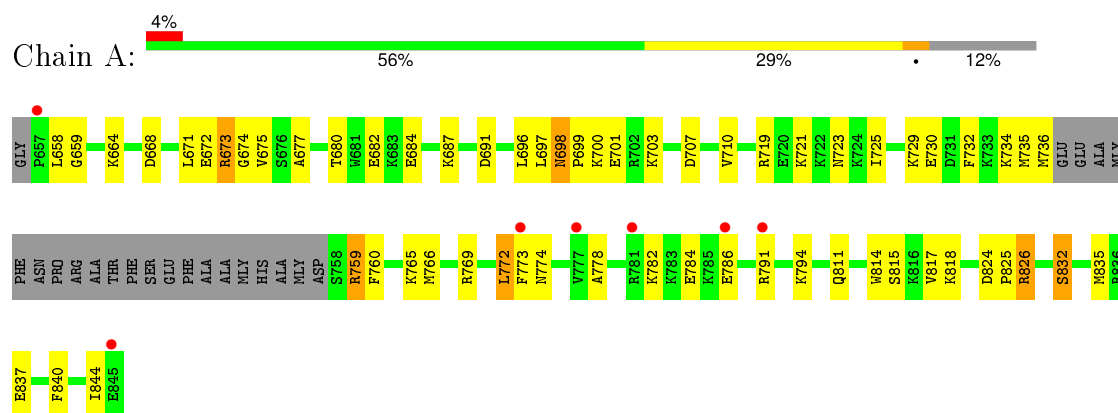
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	15	Total	O	0	0
			15	15		
2	B	40	Total	O	0	0
			40	40		

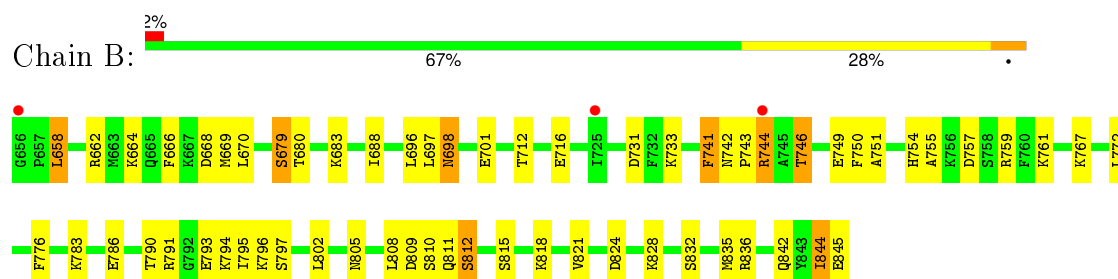
### 3 Residue-property plots [i](#)

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 ( $\text{RSRZ} > 2$ ). 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: Transcription elongation regulator 1



#### • Molecule 1: Transcription elongation regulator 1



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 6 2 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	141.30Å 141.30Å 155.42Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.02 – 2.70 20.02 – 2.70	Depositor EDS
% Data completeness (in resolution range)	93.2 (20.02-2.70) 96.2 (20.02-2.70)	Depositor EDS
$R_{merge}$	0.11	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.78 (at 2.71Å)	Xtriage
Refinement program	PHENIX	Depositor
R, $R_{free}$	0.230 , 0.283 0.242 , 0.291	Depositor DCC
$R_{free}$ test set	2363 reflections (9.80%)	DCC
Wilson B-factor (Å <sup>2</sup> )	54.9	Xtriage
Anisotropy	0.354	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.27 , 53.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.50$ , $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	1 of 47398 reflections (0.002%)	Xtriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	3178	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	91.0	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 68.92 % 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 4.0327e-06. 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: MLY

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	0.38	0/1195	0.55	0/1595
1	B	0.47	0/1347	0.61	1/1804 (0.1%)
All	All	0.43	0/2542	0.58	1/3399 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	679	SER	CB-CA-C	-7.45	95.94	110.10

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	1475	0	1519	59	0
1	B	1648	0	1673	48	0
2	A	15	0	0	0	0
2	B	40	0	0	2	0
All	All	3178	0	3192	107	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 17.

The worst 5 of 107 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:826:ARG:HG3	1:A:826:ARG:HH11	1.13	1.12
1:B:679:SER:O	2:B:9:HOH:O	1.77	1.02
1:A:765:MLY:HG2	1:A:766:MSE:H	1.38	0.87
1:A:826:ARG:HH11	1:A:826:ARG:CG	1.88	0.86
1:A:826:ARG:HG3	1:A:826:ARG:NH1	1.92	0.84

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	137/190 (72%)	127 (93%)	9 (7%)	1 (1%)	26	55
1	B	158/190 (83%)	147 (93%)	9 (6%)	2 (1%)	15	37
All	All	295/380 (78%)	274 (93%)	18 (6%)	3 (1%)	19	45

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	741	PHE
1	B	812	SER
1	A	659	GLY

### 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	128/134 (96%)	119 (93%)	9 (7%)	19	42
1	B	141/134 (105%)	128 (91%)	13 (9%)	11	25
All	All	269/268 (100%)	247 (92%)	22 (8%)	14	32

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	658	LEU
1	B	744	ARG
1	B	835	MSE
1	B	680	THR
1	B	698	ASN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 10 such sidechains are listed below:

Mol	Chain	Res	Type
1	A	805	ASN
1	B	698	ASN
1	B	708	GLN
1	A	727	GLN
1	B	704	GLN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

57 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
1	MLY	A	664	1	9,10,11	0.49	0	9,11,13	2.09	4 (44%)
1	MLY	A	667	1	9,10,11	0.61	0	9,11,13	2.07	4 (44%)
1	MLY	A	683	1	9,10,11	0.63	0	9,11,13	2.30	4 (44%)
1	MLY	A	687	1	9,10,11	0.59	0	9,11,13	2.22	4 (44%)
1	MLY	A	700	1	9,10,11	0.50	0	9,11,13	2.01	4 (44%)
1	MLY	A	703	1	9,10,11	0.40	0	9,11,13	2.00	5 (55%)
1	MLY	A	711	1	9,10,11	0.38	0	9,11,13	2.12	4 (44%)
1	MLY	A	721	1	9,10,11	0.58	0	9,11,13	2.17	4 (44%)
1	MLY	A	722	1	9,10,11	0.48	0	9,11,13	2.01	4 (44%)
1	MLY	A	724	1	9,10,11	0.45	0	9,11,13	2.15	4 (44%)
1	MLY	A	729	1	9,10,11	0.45	0	9,11,13	1.90	4 (44%)
1	MLY	A	733	1	9,10,11	0.42	0	9,11,13	1.97	4 (44%)
1	MLY	A	734	1	9,10,11	0.44	0	9,11,13	1.97	4 (44%)
1	MLY	A	761	1	9,10,11	0.45	0	9,11,13	2.10	4 (44%)
1	MLY	A	765	1	9,10,11	0.46	0	9,11,13	2.16	4 (44%)
1	MLY	A	767	1	9,10,11	0.45	0	9,11,13	2.14	5 (55%)
1	MLY	A	782	1	9,10,11	0.49	0	9,11,13	2.02	4 (44%)
1	MLY	A	783	1	9,10,11	0.49	0	9,11,13	2.14	4 (44%)
1	MLY	A	785	1	9,10,11	0.42	0	9,11,13	1.88	4 (44%)
1	MLY	A	789	1	9,10,11	0.41	0	9,11,13	2.02	5 (55%)
1	MLY	A	794	1	9,10,11	0.45	0	9,11,13	1.84	3 (33%)
1	MLY	A	796	1	9,10,11	0.43	0	9,11,13	1.87	3 (33%)
1	MLY	A	816	1	9,10,11	0.56	0	9,11,13	1.95	5 (55%)
1	MLY	A	818	1	9,10,11	0.44	0	9,11,13	2.13	4 (44%)
1	MLY	A	820	1	9,10,11	0.38	0	9,11,13	2.21	4 (44%)
1	MLY	A	828	1	9,10,11	0.45	0	9,11,13	2.01	4 (44%)
1	MLY	A	841	1	9,10,11	0.36	0	9,11,13	2.15	5 (55%)
1	MLY	B	664	1	9,10,11	0.83	1 (11%)	9,11,13	2.12	3 (33%)
1	MLY	B	667	1	9,10,11	0.96	1 (11%)	9,11,13	2.34	5 (55%)
1	MLY	B	683	1	9,10,11	0.37	0	9,11,13	2.47	4 (44%)
1	MLY	B	687	1	9,10,11	0.79	1 (11%)	9,11,13	2.24	5 (55%)
1	MLY	B	700	1	9,10,11	0.54	0	9,11,13	2.08	4 (44%)
1	MLY	B	703	1	9,10,11	0.49	0	9,11,13	2.06	5 (55%)
1	MLY	B	711	1	9,10,11	0.57	0	9,11,13	2.10	5 (55%)
1	MLY	B	721	1	9,10,11	0.55	0	9,11,13	2.06	4 (44%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z  > 2	Counts	RMSZ	# Z  > 2
1	MLY	B	722	1	9,10,11	0.55	0	9,11,13	2.03	4 (44%)
1	MLY	B	724	1	9,10,11	0.43	0	9,11,13	2.15	4 (44%)
1	MLY	B	729	1	9,10,11	0.40	0	9,11,13	1.92	4 (44%)
1	MLY	B	733	1	9,10,11	0.48	0	9,11,13	2.14	4 (44%)
1	MLY	B	734	1	9,10,11	0.48	0	9,11,13	2.13	4 (44%)
1	MLY	B	740	1	3,4,11	0.75	0	0,4,13	0.00	-
1	MLY	B	753	1	9,10,11	0.39	0	9,11,13	1.98	4 (44%)
1	MLY	B	756	1	9,10,11	0.51	0	9,11,13	1.81	3 (33%)
1	MLY	B	761	1	9,10,11	0.37	0	9,11,13	2.10	4 (44%)
1	MLY	B	765	1	9,10,11	0.54	0	9,11,13	1.92	4 (44%)
1	MLY	B	767	1	9,10,11	0.50	0	9,11,13	2.13	4 (44%)
1	MLY	B	782	1	9,10,11	0.54	0	9,11,13	2.06	4 (44%)
1	MLY	B	783	1	9,10,11	0.37	0	9,11,13	2.10	5 (55%)
1	MLY	B	785	1	9,10,11	0.50	0	9,11,13	2.03	4 (44%)
1	MLY	B	789	1	9,10,11	0.37	0	9,11,13	2.00	4 (44%)
1	MLY	B	794	1	9,10,11	0.54	0	9,11,13	2.21	3 (33%)
1	MLY	B	796	1	9,10,11	0.45	0	9,11,13	2.01	4 (44%)
1	MLY	B	816	1	9,10,11	0.39	0	9,11,13	2.18	4 (44%)
1	MLY	B	818	1	9,10,11	0.43	0	9,11,13	2.07	4 (44%)
1	MLY	B	820	1	9,10,11	0.36	0	9,11,13	2.05	4 (44%)
1	MLY	B	828	1	9,10,11	0.43	0	9,11,13	2.12	4 (44%)
1	MLY	B	841	1	9,10,11	0.41	0	9,11,13	2.04	4 (44%)

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
1	MLY	A	664	1	-	0/7/9/11	0/0/0/0
1	MLY	A	667	1	-	0/7/9/11	0/0/0/0
1	MLY	A	683	1	-	0/7/9/11	0/0/0/0
1	MLY	A	687	1	-	0/7/9/11	0/0/0/0
1	MLY	A	700	1	-	0/7/9/11	0/0/0/0
1	MLY	A	703	1	-	0/7/9/11	0/0/0/0
1	MLY	A	711	1	-	0/7/9/11	0/0/0/0
1	MLY	A	721	1	-	0/7/9/11	0/0/0/0
1	MLY	A	722	1	-	0/7/9/11	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	A	724	1	-	0/7/9/11	0/0/0/0
1	MLY	A	729	1	-	0/7/9/11	0/0/0/0
1	MLY	A	733	1	-	0/7/9/11	0/0/0/0
1	MLY	A	734	1	-	0/7/9/11	0/0/0/0
1	MLY	A	761	1	-	0/7/9/11	0/0/0/0
1	MLY	A	765	1	-	0/7/9/11	0/0/0/0
1	MLY	A	767	1	-	0/7/9/11	0/0/0/0
1	MLY	A	782	1	-	0/7/9/11	0/0/0/0
1	MLY	A	783	1	-	0/7/9/11	0/0/0/0
1	MLY	A	785	1	-	0/7/9/11	0/0/0/0
1	MLY	A	789	1	-	0/7/9/11	0/0/0/0
1	MLY	A	794	1	-	0/7/9/11	0/0/0/0
1	MLY	A	796	1	-	0/7/9/11	0/0/0/0
1	MLY	A	816	1	-	0/7/9/11	0/0/0/0
1	MLY	A	818	1	-	0/7/9/11	0/0/0/0
1	MLY	A	820	1	-	0/7/9/11	0/0/0/0
1	MLY	A	828	1	-	0/7/9/11	0/0/0/0
1	MLY	A	841	1	-	0/7/9/11	0/0/0/0
1	MLY	B	664	1	-	0/7/9/11	0/0/0/0
1	MLY	B	667	1	-	0/7/9/11	0/0/0/0
1	MLY	B	683	1	-	0/7/9/11	0/0/0/0
1	MLY	B	687	1	-	0/7/9/11	0/0/0/0
1	MLY	B	700	1	-	0/7/9/11	0/0/0/0
1	MLY	B	703	1	-	0/7/9/11	0/0/0/0
1	MLY	B	711	1	-	0/7/9/11	0/0/0/0
1	MLY	B	721	1	-	0/7/9/11	0/0/0/0
1	MLY	B	722	1	-	0/7/9/11	0/0/0/0
1	MLY	B	724	1	-	0/7/9/11	0/0/0/0
1	MLY	B	729	1	-	0/7/9/11	0/0/0/0
1	MLY	B	733	1	-	0/7/9/11	0/0/0/0
1	MLY	B	734	1	-	0/7/9/11	0/0/0/0
1	MLY	B	740	1	-	0/0/2/11	0/0/0/0
1	MLY	B	753	1	-	0/7/9/11	0/0/0/0
1	MLY	B	756	1	-	0/7/9/11	0/0/0/0
1	MLY	B	761	1	-	0/7/9/11	0/0/0/0
1	MLY	B	765	1	-	0/7/9/11	0/0/0/0
1	MLY	B	767	1	-	0/7/9/11	0/0/0/0
1	MLY	B	782	1	-	0/7/9/11	0/0/0/0
1	MLY	B	783	1	-	0/7/9/11	0/0/0/0
1	MLY	B	785	1	-	0/7/9/11	0/0/0/0
1	MLY	B	789	1	-	0/7/9/11	0/0/0/0
1	MLY	B	794	1	-	0/7/9/11	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	B	796	1	-	0/7/9/11	0/0/0/0
1	MLY	B	816	1	-	0/7/9/11	0/0/0/0
1	MLY	B	818	1	-	0/7/9/11	0/0/0/0
1	MLY	B	820	1	-	0/7/9/11	0/0/0/0
1	MLY	B	828	1	-	0/7/9/11	0/0/0/0
1	MLY	B	841	1	-	0/7/9/11	0/0/0/0

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	667	MLY	CB-CA	-2.74	1.51	1.53
1	B	664	MLY	CB-CA	-2.36	1.51	1.53
1	B	687	MLY	CB-CA	-2.17	1.51	1.53

The worst 5 of 229 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	683	MLY	CD-CE-NZ	-4.72	101.76	113.92
1	B	667	MLY	CD-CE-NZ	-3.79	104.16	113.92
1	A	820	MLY	CD-CE-NZ	-3.56	104.76	113.92
1	B	816	MLY	CD-CE-NZ	-3.47	104.97	113.92
1	A	765	MLY	CD-CE-NZ	-3.47	104.98	113.92

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

21 monomers are involved in 31 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	664	MLY	1	0
1	A	687	MLY	1	0
1	A	700	MLY	1	0
1	A	703	MLY	1	0
1	A	721	MLY	1	0
1	A	729	MLY	1	0
1	A	734	MLY	3	0
1	A	765	MLY	5	0
1	A	782	MLY	1	0
1	A	794	MLY	2	0
1	A	818	MLY	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	B	664	MLY	1	0
1	B	683	MLY	1	0
1	B	733	MLY	1	0
1	B	761	MLY	1	0
1	B	767	MLY	1	0
1	B	783	MLY	2	0
1	B	794	MLY	1	0
1	B	796	MLY	2	0
1	B	818	MLY	1	0
1	B	828	MLY	1	0

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

There are no ligands in this entry.

## 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	134/190 (70%)	0.22	7 (5%) 31 30	51, 94, 161, 172	0
1	B	153/190 (80%)	-0.12	3 (1%) 68 69	44, 71, 123, 144	0
All	All	287/380 (75%)	0.04	10 (3%) 48 48	44, 79, 145, 172	0

The worst 5 of 10 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	656	GLY	5.6
1	A	773	PHE	4.1
1	A	791	ARG	3.9
1	A	657	PRO	3.7
1	A	777	VAL	2.9

### 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. 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(Å <sup>2</sup> )	Q<0.9
1	MLY	B	687	11/12	0.98	0.16	-	47,52,71,73	0
1	MLY	A	664	11/12	0.92	0.20	-	54,58,78,81	0
1	MLY	A	820	11/12	0.86	0.16	-	113,120,127,129	0
1	MLY	B	721	11/12	0.91	0.22	-	74,86,124,128	0
1	MLY	A	721	11/12	0.93	0.21	-	109,116,121,122	0
1	MLY	A	683	11/12	0.92	0.17	-	65,73,85,90	0
1	MLY	A	667	11/12	0.92	0.23	-	53,63,100,100	0
1	MLY	A	687	11/12	0.98	0.19	-	51,58,80,84	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	MLY	A	722	11/12	0.91	0.34	-	113,149,155,157	0
1	MLY	B	828	11/12	0.85	0.36	-	91,102,126,128	0
1	MLY	A	761	11/12	0.86	0.24	-	133,143,155,158	0
1	MLY	B	818	11/12	0.91	0.23	-	91,98,133,133	0
1	MLY	A	767	11/12	0.87	0.41	-	114,125,148,148	0
1	MLY	B	783	11/12	0.92	0.36	-	103,106,131,134	0
1	MLY	A	711	11/12	0.89	0.33	-	67,83,120,120	0
1	MLY	A	794	11/12	0.87	0.29	-	105,111,116,116	0
1	MLY	B	711	11/12	0.93	0.27	-	55,71,115,116	0
1	MLY	A	828	11/12	0.83	0.41	-	103,119,136,141	0
1	MLY	A	796	11/12	0.89	0.35	-	100,105,120,121	0
1	MLY	A	733	11/12	0.86	0.34	-	146,157,169,171	0
1	MLY	B	664	11/12	0.94	0.20	-	52,60,74,75	0
1	MLY	B	733	11/12	0.94	0.20	-	72,86,114,117	0
1	MLY	B	785	11/12	0.91	0.30	-	103,109,132,133	0
1	MLY	B	683	11/12	0.96	0.16	-	51,54,65,68	0
1	MLY	A	729	11/12	0.89	0.26	-	119,126,148,150	0
1	MLY	B	756	11/12	0.83	0.21	-	70,86,102,107	0
1	MLY	B	740	5/12	0.86	0.28	-	120,134,137,138	0
1	MLY	A	789	11/12	0.80	0.40	-	147,154,170,171	0
1	MLY	A	783	11/12	0.83	0.36	-	158,166,170,170	0
1	MLY	B	782	11/12	0.94	0.32	-	93,113,142,143	0
1	MLY	B	722	11/12	0.91	0.34	-	63,82,122,126	0
1	MLY	B	789	11/12	0.86	0.36	-	113,134,169,169	0
1	MLY	A	785	11/12	0.75	0.45	-	153,163,167,167	0
1	MLY	A	700	11/12	0.94	0.42	-	56,68,111,111	0
1	MLY	B	700	11/12	0.84	0.40	-	53,66,98,101	0
1	MLY	A	816	11/12	0.73	0.26	-	100,113,131,132	0
1	MLY	B	703	11/12	0.97	0.15	-	55,61,100,103	0
1	MLY	A	841	11/12	0.95	0.23	-	69,82,120,121	0
1	MLY	B	765	11/12	0.84	0.28	-	64,74,107,107	0
1	MLY	B	734	11/12	0.90	0.32	-	84,96,136,138	0
1	MLY	A	818	11/12	0.84	0.29	-	98,115,159,162	0
1	MLY	B	794	11/12	0.90	0.28	-	86,96,115,115	0
1	MLY	A	734	11/12	0.80	0.42	-	144,157,170,170	0
1	MLY	B	729	11/12	0.94	0.29	-	70,86,125,128	0
1	MLY	B	841	11/12	0.94	0.27	-	64,84,111,111	0
1	MLY	B	767	11/12	0.92	0.24	-	60,75,102,109	0
1	MLY	A	782	11/12	0.76	0.33	-	164,175,190,191	0
1	MLY	A	724	11/12	0.96	0.16	-	110,118,122,122	0
1	MLY	B	724	11/12	0.96	0.29	-	60,79,105,107	0
1	MLY	B	667	11/12	0.94	0.22	-	52,64,84,89	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors( $\text{\AA}^2$ )	Q<0.9
1	MLY	B	796	11/12	0.85	0.30	-	77,82,110,111	0
1	MLY	B	816	11/12	0.88	0.21	-	103,117,148,149	0
1	MLY	B	820	11/12	0.94	0.17	-	95,106,121,123	0
1	MLY	B	761	11/12	0.93	0.18	-	64,69,95,100	0
1	MLY	B	753	11/12	0.94	0.22	-	69,72,108,109	0
1	MLY	A	765	11/12	0.72	0.44	-	123,133,139,139	0
1	MLY	A	703	11/12	0.93	0.28	-	54,75,122,122	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [i](#)

There are no ligands in this entry.

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

There are no such residues in this entry.