Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 10:18 PM GMT

PDB ID	:	5CJ4
Title	:	Crystal Structure of Amino Acids 1562-1622 of MYH7
Authors	:	Korkmaz, N.E.; Taylor, K.C.; Andreas, M.P.; Ajay, G.; Heinze, N.T.; Cui, Q.; Rayment, I.
Deposited on	:	2015-07-13
Resolution	:	3.10 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
http://wwpdb.org/validation/2016/XrayValidationReportHelp
with specific help available everywhere you see the ⓘ symbol.

The following versions of software and data (see references ①) were used in the production of this report:

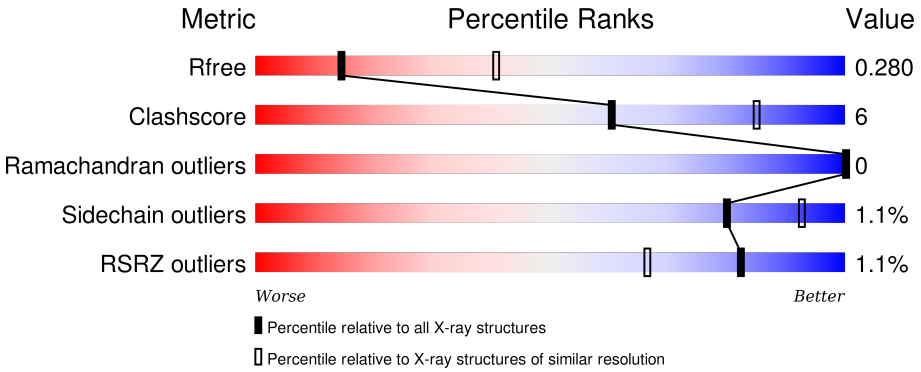
MolProbity	:	4.02b-467
Mogul	:	1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026982
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	rb-20026982

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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))
R_{free}	91344	1114 (3.14-3.06)
Clashscore	102246	1222 (3.14-3.06)
Ramachandran outliers	100387	1174 (3.14-3.06)
Sidechain outliers	100360	1174 (3.14-3.06)
RSRZ outliers	91569	1119 (3.14-3.06)

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 >=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 <=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	208	79% 14% 7%
1	B	208	75% 17% 9%
1	C	208	82% 13% 5%
1	D	208	2% 75% 16% 9%

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6343 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 Xrcc4-MYH7-(1562-1622) chimera protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	194	Total	C	N	O	S	0	0	0
			1598	1010	270	312	6			
1	B	190	Total	C	N	O	S	0	0	0
			1553	981	261	305	6			
1	C	197	Total	C	N	O	S	0	0	0
			1633	1034	275	317	7			
1	D	189	Total	C	N	O	S	0	0	0
			1557	985	261	305	6			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-2	GLY	-	expression tag	UNP Q13426
A	-1	GLY	-	expression tag	UNP Q13426
A	0	SER	-	expression tag	UNP Q13426
A	1	GLY	-	expression tag	UNP Q13426
A	134	THR	ILE	engineered mutation	UNP Q13426
B	-2	GLY	-	expression tag	UNP Q13426
B	-1	GLY	-	expression tag	UNP Q13426
B	0	SER	-	expression tag	UNP Q13426
B	1	GLY	-	expression tag	UNP Q13426
B	134	THR	ILE	engineered mutation	UNP Q13426
C	-2	GLY	-	expression tag	UNP Q13426
C	-1	GLY	-	expression tag	UNP Q13426
C	0	SER	-	expression tag	UNP Q13426
C	1	GLY	-	expression tag	UNP Q13426
C	134	THR	ILE	engineered mutation	UNP Q13426
D	-2	GLY	-	expression tag	UNP Q13426
D	-1	GLY	-	expression tag	UNP Q13426
D	0	SER	-	expression tag	UNP Q13426
D	1	GLY	-	expression tag	UNP Q13426
D	134	THR	ILE	engineered mutation	UNP Q13426

- Molecule 2 is water.

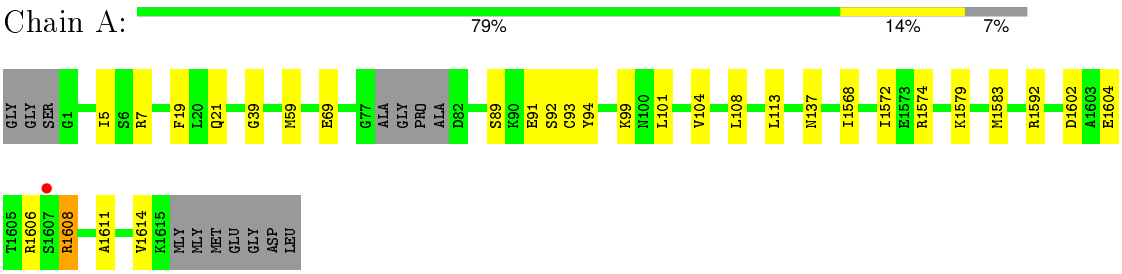
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	1	Total O 1 1	0	0
2	C	1	Total O 1 1	0	0

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 (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.

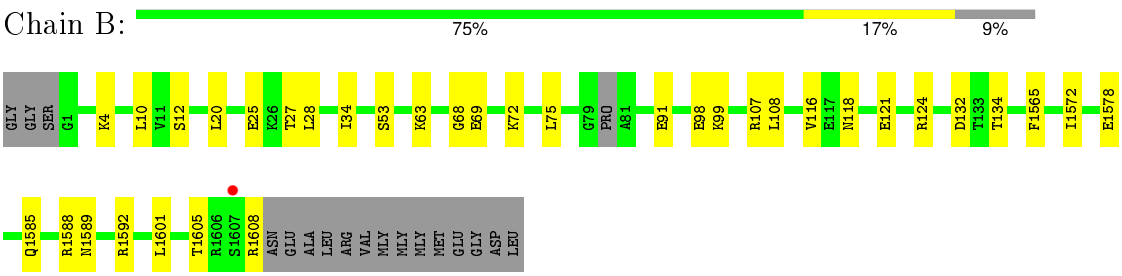
- Molecule 1: Xrcc4-MYH7-(1562-1622) chimera protein

Chain A:



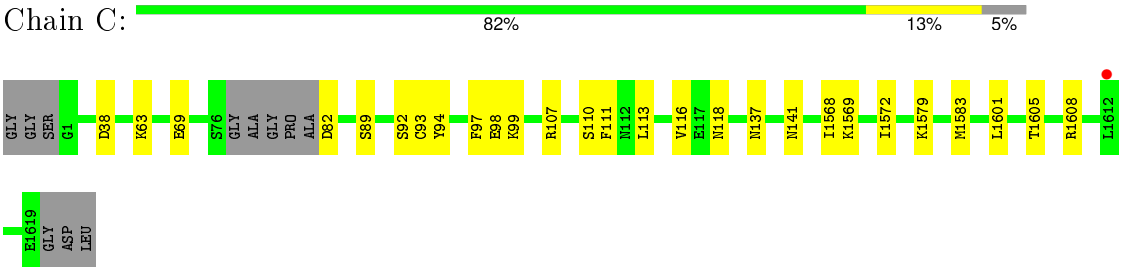
- Molecule 1: Xrcc4-MYH7-(1562-1622) chimera protein

Chain B:



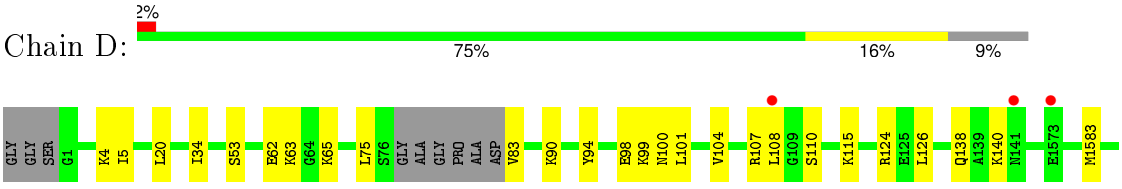
- Molecule 1: Xrcc4-MYH7-(1562-1622) chimera protein

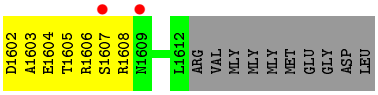
Chain C:



- Molecule 1: Xrcc4-MYH7-(1562-1622) chimera protein

Chain D:




D1602
A1603
E1604
T1605
R1606
S1607
R1608
N1609
L1612
ARG
VAL
MLY
MLY
MLY
MET
GLU
GLY
ASP
LEU

4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	83.14Å 57.28Å 112.10Å 90.00° 99.86° 90.00°	Depositor
Resolution (Å)	49.92 – 3.10 49.92 – 3.10	Depositor EDS
% Data completeness (in resolution range)	98.6 (49.92-3.10) 94.8 (49.92-3.10)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.11 (at 3.12Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.243 , 0.280 0.241 , 0.280	Depositor DCC
R_{free} test set	901 reflections (4.96%)	DCC
Wilson B-factor (Å^2)	65.5	Xtriage
Anisotropy	0.969	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.28 , 30.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	3 of 19043 reflections (0.016%)	Xtriage
F_o,F_c correlation	0.91	EDS
Total number of atoms	6343	wwPDB-VP
Average B, all atoms (Å^2)	81.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.05% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality

5.1 Standard geometry

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	0.27	0/1456	0.45	0/1971
1	B	0.25	0/1422	0.45	0/1925
1	C	0.25	0/1469	0.42	0/1988
1	D	0.25	0/1426	0.42	0/1931
All	All	0.26	0/5773	0.44	0/7815

There are no bond length outliers.

There are no bond angle outliers.

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	1598	0	1580	21	1
1	B	1553	0	1529	24	1
1	C	1633	0	1626	19	0
1	D	1557	0	1537	21	1
2	B	1	0	0	0	0
2	C	1	0	0	0	0
All	All	6343	0	6272	70	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 6.

All (70) 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:C:89:SER:OG	1:C:92:SER:OG	2.05	0.73
1:D:83:VAL:HG13	1:D:100:ASN:HB2	1.72	0.70
1:C:94:TYR:HE1	1:C:110:SER:HB2	1.60	0.67
1:C:141:ASN:HD21	1:D:140:MLY:HD3	1.60	0.65
1:D:98:GLU:HG2	1:D:107:ARG:HA	1.79	0.64
1:A:1568:ILE:O	1:A:1572:ILE:HG13	1.98	0.63
1:A:39:GLY:H	1:B:124:ARG:HH11	1.49	0.60
1:A:69:GLU:HB3	1:A:108:LEU:HD21	1.84	0.59
1:B:68:GLY:O	1:B:72:MLY:HG3	2.03	0.58
1:A:101:LEU:N	1:A:104:VAL:O	2.32	0.56
1:B:20:LEU:HD11	1:B:34:ILE:HD11	1.87	0.56
1:C:1583:MET:HG2	1:D:1583:MET:HG2	1.89	0.55
1:A:1604:GLU:O	1:B:1608:ARG:NH2	2.39	0.55
1:A:89:SER:HG	1:A:92:SER:HG	1.58	0.52
1:C:116:VAL:HG12	1:C:118:ASN:H	1.75	0.51
1:C:38:ASP:O	1:D:124:ARG:NH1	2.38	0.51
1:A:69:GLU:OE2	1:A:99:MLY:HH22	2.11	0.50
1:B:1589:ASN:OD1	1:B:1592:ARG:NH2	2.44	0.49
1:C:1608:ARG:HG3	1:D:1607:SER:OG	2.13	0.49
1:C:98:GLU:HG2	1:C:107:ARG:HA	1.95	0.49
1:D:1603:ALA:O	1:D:1606:ARG:HB3	2.13	0.49
1:D:101:LEU:HB2	1:D:104:VAL:HG13	1.94	0.48
1:A:5:ILE:HG12	1:A:21:GLN:HG3	1.94	0.48
1:D:53:SER:HB2	1:D:63:MLY:HE2	1.95	0.48
1:A:93:CYS:HB3	1:A:113:LEU:O	2.13	0.48
1:A:1568:ILE:HD12	1:B:1565:PHE:HE2	1.77	0.48
1:B:53:SER:HB2	1:B:63:MLY:HH23	1.97	0.47
1:D:4:MLY:HB2	1:D:75:LEU:HD22	1.95	0.47
1:A:39:GLY:H	1:B:124:ARG:NH1	2.11	0.47
1:C:1579:MLY:O	1:C:1583:MET:HG3	2.14	0.47
1:C:93:CYS:HB3	1:C:113:LEU:O	2.13	0.47
1:B:91:GLU:OE2	1:B:91:GLU:N	2.45	0.47
1:B:1585:GLN:OE1	1:B:1588:ARG:NH1	2.48	0.46
1:C:1568:ILE:O	1:C:1572:ILE:HG13	2.15	0.46
1:C:137:ASN:ND2	1:D:138:GLN:OE1	2.48	0.46
1:A:137:ASN:ND2	1:B:134:THR:HG23	2.31	0.46
1:C:1569:MLY:HA	1:C:1572:ILE:HD12	1.97	0.46
1:A:1608:ARG:HD2	1:A:1608:ARG:HA	1.73	0.46
1:A:1568:ILE:HD12	1:B:1565:PHE:CE2	2.51	0.46
1:B:1601:LEU:O	1:B:1605:THR:HG23	2.15	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:28:LEU:HD11	1:B:75:LEU:HD11	1.98	0.46
1:C:1601:LEU:O	1:C:1605:THR:HG23	2.16	0.46
1:A:1611:ALA:HA	1:A:1614:VAL:HG22	1.99	0.45
1:D:20:LEU:HD11	1:D:34:ILE:HD11	1.97	0.45
1:A:1572:ILE:HG23	1:B:1572:ILE:HG12	1.98	0.45
1:B:116:VAL:HG12	1:B:118:ASN:H	1.82	0.45
1:A:7:ARG:NH2	1:B:132:ASP:OD1	2.36	0.44
1:D:1602:ASP:O	1:D:1605:THR:OG1	2.24	0.44
1:D:5:ILE:HD13	1:D:126:LEU:HG	1.99	0.44
1:B:99:MLY:HB3	1:B:108:LEU:HD22	1.98	0.44
1:D:115:MLY:HH22	1:D:115:MLY:HD2	1.69	0.44
1:D:53:SER:HB2	1:D:63:MLY:HH23	2.00	0.43
1:B:4:MLY:HB2	1:B:75:LEU:HD22	2.01	0.43
1:D:90:MLY:H	1:D:90:MLY:HG3	1.57	0.43
1:C:97:PHE:HE1	1:C:111:PHE:HE2	1.64	0.43
1:C:1608:ARG:HH21	1:D:1604:GLU:CD	2.22	0.43
1:B:98:GLU:HG2	1:B:107:ARG:HA	2.00	0.43
1:B:10:LEU:HB2	1:B:12:SER:O	2.19	0.43
1:C:69:GLU:OE2	1:C:99:MLY:HH22	2.19	0.43
1:D:99:MLY:HB3	1:D:108:LEU:HD22	2.02	0.42
1:D:62:GLU:HB3	1:D:65:MLY:HG3	2.01	0.42
1:B:69:GLU:OE1	1:B:99:MLY:HH22	2.20	0.42
1:A:19:PHE:HE2	1:B:124:ARG:HG2	1.85	0.42
1:D:94:TYR:CZ	1:D:110:SER:HB2	2.56	0.41
1:A:1602:ASP:O	1:A:1606:ARG:HG2	2.20	0.41
1:C:63:MLY:HH22	1:C:63:MLY:HD3	1.90	0.41
1:A:1579:MLY:O	1:A:1583:MET:HG3	2.21	0.41
1:B:121:GLU:CD	1:B:124:ARG:HH21	2.24	0.40
1:A:89:SER:HB2	1:A:91:GLU:OE2	2.21	0.40
1:C:1569:MLY:HD3	1:C:1569:MLY:HH12	1.90	0.40

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:B:1578:GLU:OE1	1:D:1606:ARG:NH1[2_646]	2.10	0.10
1:A:59:MET:O	1:A:1592:ARG:NH2[1_655]	2.18	0.02

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	A	176/208 (85%)	174 (99%)	2 (1%)	0	100	100
1	B	172/208 (83%)	172 (100%)	0	0	100	100
1	C	176/208 (85%)	174 (99%)	2 (1%)	0	100	100
1	D	171/208 (82%)	169 (99%)	2 (1%)	0	100	100
All	All	695/832 (84%)	689 (99%)	6 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	159/165 (96%)	156 (98%)	3 (2%)	65	87
1	B	154/165 (93%)	152 (99%)	2 (1%)	76	91
1	C	161/165 (98%)	160 (99%)	1 (1%)	90	95
1	D	156/165 (94%)	155 (99%)	1 (1%)	90	95
All	All	630/660 (96%)	623 (99%)	7 (1%)	80	93

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	94	TYR
1	A	1574	ARG

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Mol	Chain	Res	Type
1	A	1608	ARG
1	B	25	GLU
1	B	27	THR
1	C	82	ASP
1	D	1608	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	C	9	HIS
1	C	137	ASN
1	C	141	ASN

5.3.3 RNA

There are no RNA molecules in this entry.

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

60 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	102	1	8,10,11	0.53	0	9,11,13	1.03	1 (11%)
1	MLY	A	115	1	8,10,11	0.47	0	9,11,13	0.94	0
1	MLY	A	140	1	8,10,11	0.50	0	9,11,13	0.94	0
1	MLY	A	1569	1	8,10,11	0.50	0	9,11,13	0.92	0
1	MLY	A	1575	1	8,10,11	0.48	0	9,11,13	1.00	0
1	MLY	A	1579	1	8,10,11	0.44	0	9,11,13	0.95	0
1	MLY	A	1587	1	8,10,11	0.53	0	9,11,13	0.97	0
1	MLY	A	1615	1	8,10,11	0.47	0	9,11,13	0.93	0
1	MLY	A	26	1	8,10,11	0.48	0	9,11,13	0.90	0
1	MLY	A	4	1	8,10,11	0.49	0	9,11,13	0.85	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	MLY	A	63	1	8,10,11	0.55	0	9,11,13	0.91	0
1	MLY	A	65	1	8,10,11	0.50	0	9,11,13	0.91	0
1	MLY	A	72	1	8,10,11	0.50	0	9,11,13	0.89	0
1	MLY	A	90	1	8,10,11	0.62	0	9,11,13	1.05	0
1	MLY	A	99	1	8,10,11	0.46	0	9,11,13	1.17	2 (22%)
1	MLY	B	102	1	8,10,11	0.47	0	9,11,13	0.97	0
1	MLY	B	115	1	8,10,11	0.56	0	9,11,13	0.81	0
1	MLY	B	140	1	8,10,11	0.51	0	9,11,13	0.94	0
1	MLY	B	1569	1	8,10,11	0.53	0	9,11,13	0.82	0
1	MLY	B	1575	1	8,10,11	0.50	0	9,11,13	0.98	0
1	MLY	B	1579	1	8,10,11	0.50	0	9,11,13	0.91	0
1	MLY	B	1587	1	8,10,11	0.45	0	9,11,13	0.99	0
1	MLY	B	26	1	8,10,11	0.55	0	9,11,13	0.86	0
1	MLY	B	4	1	8,10,11	0.50	0	9,11,13	0.95	0
1	MLY	B	63	1	8,10,11	0.51	0	9,11,13	0.95	0
1	MLY	B	65	1	8,10,11	0.51	0	9,11,13	0.94	0
1	MLY	B	72	1	8,10,11	0.48	0	9,11,13	0.94	0
1	MLY	B	90	1	8,10,11	0.64	0	9,11,13	0.81	0
1	MLY	B	99	1	8,10,11	0.41	0	9,11,13	0.99	0
1	MLY	C	102	1	8,10,11	0.52	0	9,11,13	0.93	0
1	MLY	C	115	1	8,10,11	0.48	0	9,11,13	0.86	0
1	MLY	C	140	1	8,10,11	0.51	0	9,11,13	0.92	0
1	MLY	C	1569	1	8,10,11	0.55	0	9,11,13	0.89	0
1	MLY	C	1575	1	8,10,11	0.46	0	9,11,13	0.98	0
1	MLY	C	1579	1	8,10,11	0.46	0	9,11,13	0.88	0
1	MLY	C	1587	1	8,10,11	0.42	0	9,11,13	1.03	1 (11%)
1	MLY	C	1615	1	8,10,11	0.46	0	9,11,13	0.94	0
1	MLY	C	1616	1	8,10,11	0.49	0	9,11,13	0.94	0
1	MLY	C	1617	1	8,10,11	0.47	0	9,11,13	0.93	0
1	MLY	C	26	1	8,10,11	0.50	0	9,11,13	0.86	0
1	MLY	C	4	1	8,10,11	0.48	0	9,11,13	0.86	0
1	MLY	C	63	1	8,10,11	0.46	0	9,11,13	0.94	0
1	MLY	C	65	1	8,10,11	0.47	0	9,11,13	0.92	0
1	MLY	C	72	1	8,10,11	0.50	0	9,11,13	0.95	0
1	MLY	C	90	1	8,10,11	0.63	0	9,11,13	0.92	0
1	MLY	C	99	1	8,10,11	0.46	0	9,11,13	1.04	0
1	MLY	D	102	1	8,10,11	0.49	0	9,11,13	0.91	0
1	MLY	D	115	1	8,10,11	0.48	0	9,11,13	0.98	0
1	MLY	D	140	1	8,10,11	0.52	0	9,11,13	0.97	0
1	MLY	D	1569	1	8,10,11	0.54	0	9,11,13	0.86	0
1	MLY	D	1575	1	8,10,11	0.49	0	9,11,13	0.92	0
1	MLY	D	1579	1	8,10,11	0.47	0	9,11,13	0.96	1 (11%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
1	MLY	D	1587	1	8,10,11	0.53	0	9,11,13	0.96	0
1	MLY	D	26	1	8,10,11	0.48	0	9,11,13	0.95	0
1	MLY	D	4	1	8,10,11	0.55	0	9,11,13	0.90	0
1	MLY	D	63	1	8,10,11	0.48	0	9,11,13	0.93	0
1	MLY	D	65	1	8,10,11	0.52	0	9,11,13	0.89	0
1	MLY	D	72	1	8,10,11	0.48	0	9,11,13	0.93	0
1	MLY	D	90	1	8,10,11	0.58	0	9,11,13	0.76	0
1	MLY	D	99	1	8,10,11	0.61	0	9,11,13	0.92	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
1	MLY	A	102	1	-	0/7/9/11	0/0/0/0
1	MLY	A	115	1	-	0/7/9/11	0/0/0/0
1	MLY	A	140	1	-	0/7/9/11	0/0/0/0
1	MLY	A	1569	1	-	0/7/9/11	0/0/0/0
1	MLY	A	1575	1	-	0/7/9/11	0/0/0/0
1	MLY	A	1579	1	-	0/7/9/11	0/0/0/0
1	MLY	A	1587	1	-	0/7/9/11	0/0/0/0
1	MLY	A	1615	1	-	0/7/9/11	0/0/0/0
1	MLY	A	26	1	-	0/7/9/11	0/0/0/0
1	MLY	A	4	1	-	0/7/9/11	0/0/0/0
1	MLY	A	63	1	-	0/7/9/11	0/0/0/0
1	MLY	A	65	1	-	0/7/9/11	0/0/0/0
1	MLY	A	72	1	-	0/7/9/11	0/0/0/0
1	MLY	A	90	1	-	0/7/9/11	0/0/0/0
1	MLY	A	99	1	-	0/7/9/11	0/0/0/0
1	MLY	B	102	1	-	0/7/9/11	0/0/0/0
1	MLY	B	115	1	-	0/7/9/11	0/0/0/0
1	MLY	B	140	1	-	0/7/9/11	0/0/0/0
1	MLY	B	1569	1	-	0/7/9/11	0/0/0/0
1	MLY	B	1575	1	-	0/7/9/11	0/0/0/0
1	MLY	B	1579	1	-	0/7/9/11	0/0/0/0
1	MLY	B	1587	1	-	0/7/9/11	0/0/0/0
1	MLY	B	26	1	-	0/7/9/11	0/0/0/0
1	MLY	B	4	1	-	0/7/9/11	0/0/0/0
1	MLY	B	63	1	-	0/7/9/11	0/0/0/0
1	MLY	B	65	1	-	0/7/9/11	0/0/0/0
1	MLY	B	72	1	-	0/7/9/11	0/0/0/0
1	MLY	B	90	1	-	0/7/9/11	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	B	99	1	-	0/7/9/11	0/0/0/0
1	MLY	C	102	1	-	0/7/9/11	0/0/0/0
1	MLY	C	115	1	-	0/7/9/11	0/0/0/0
1	MLY	C	140	1	-	0/7/9/11	0/0/0/0
1	MLY	C	1569	1	-	0/7/9/11	0/0/0/0
1	MLY	C	1575	1	-	0/7/9/11	0/0/0/0
1	MLY	C	1579	1	-	0/7/9/11	0/0/0/0
1	MLY	C	1587	1	-	0/7/9/11	0/0/0/0
1	MLY	C	1615	1	-	0/7/9/11	0/0/0/0
1	MLY	C	1616	1	-	0/7/9/11	0/0/0/0
1	MLY	C	1617	1	-	0/7/9/11	0/0/0/0
1	MLY	C	26	1	-	0/7/9/11	0/0/0/0
1	MLY	C	4	1	-	0/7/9/11	0/0/0/0
1	MLY	C	63	1	-	0/7/9/11	0/0/0/0
1	MLY	C	65	1	-	0/7/9/11	0/0/0/0
1	MLY	C	72	1	-	0/7/9/11	0/0/0/0
1	MLY	C	90	1	-	0/7/9/11	0/0/0/0
1	MLY	C	99	1	-	0/7/9/11	0/0/0/0
1	MLY	D	102	1	-	0/7/9/11	0/0/0/0
1	MLY	D	115	1	-	0/7/9/11	0/0/0/0
1	MLY	D	140	1	-	0/7/9/11	0/0/0/0
1	MLY	D	1569	1	-	0/7/9/11	0/0/0/0
1	MLY	D	1575	1	-	0/7/9/11	0/0/0/0
1	MLY	D	1579	1	-	0/7/9/11	0/0/0/0
1	MLY	D	1587	1	-	0/7/9/11	0/0/0/0
1	MLY	D	26	1	-	0/7/9/11	0/0/0/0
1	MLY	D	4	1	-	0/7/9/11	0/0/0/0
1	MLY	D	63	1	-	0/7/9/11	0/0/0/0
1	MLY	D	65	1	-	0/7/9/11	0/0/0/0
1	MLY	D	72	1	-	0/7/9/11	0/0/0/0
1	MLY	D	90	1	-	0/7/9/11	0/0/0/0
1	MLY	D	99	1	-	0/7/9/11	0/0/0/0

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	102	MLY	O-C-CA	-2.21	119.78	125.72
1	A	99	MLY	CH2-NZ-CH1	-2.21	103.89	109.71
1	C	1587	MLY	O-C-CA	-2.08	120.15	125.72
1	A	99	MLY	O-C-CA	-2.06	120.19	125.72
1	D	1579	MLY	O-C-CA	-2.06	120.19	125.72

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

17 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	1579	MLY	1	0
1	A	99	MLY	1	0
1	B	4	MLY	1	0
1	B	63	MLY	1	0
1	B	72	MLY	1	0
1	B	99	MLY	2	0
1	C	1569	MLY	2	0
1	C	1579	MLY	1	0
1	C	63	MLY	1	0
1	C	99	MLY	1	0
1	D	115	MLY	1	0
1	D	140	MLY	1	0
1	D	4	MLY	1	0
1	D	63	MLY	2	0
1	D	65	MLY	1	0
1	D	90	MLY	1	0
1	D	99	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

6.1 Protein, DNA and RNA chains

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^{th} 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^2)	Q<0.9
1	A	179/208 (86%)	0.05	1 (0%)	90	80	41, 76, 134, 165	0
1	B	176/208 (84%)	0.07	1 (0%)	90	80	45, 76, 122, 146	0
1	C	180/208 (86%)	0.03	1 (0%)	90	80	41, 68, 103, 130	0
1	D	175/208 (84%)	0.19	5 (2%)	55	31	48, 86, 133, 153	0
All	All	710/832 (85%)	0.08	8 (1%)	82	66	41, 75, 126, 165	0

All (8) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	1612	LEU	2.5
1	D	1573	GLU	2.4
1	A	1607	SER	2.4
1	D	1609	ASN	2.3
1	D	1607	SER	2.1
1	D	141	ASN	2.0
1	B	1607	SER	2.0
1	D	108	LEU	2.0

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

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^{th} 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^2)	Q<0.9
1	MLY	C	140	11/12	0.92	0.46	-	78,92,103,104	0
1	MLY	A	72	11/12	0.96	0.29	-	48,60,78,78	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	MLY	B	65	11/12	0.85	0.22	-	92,101,122,126	0
1	MLY	C	72	11/12	0.93	0.22	-	51,57,79,92	0
1	MLY	D	4	11/12	0.90	0.28	-	56,63,69,75	0
1	MLY	A	90	11/12	0.78	0.49	-	81,94,104,107	0
1	MLY	D	1587	11/12	0.89	0.33	-	52,61,88,110	0
1	MLY	D	90	11/12	0.71	0.45	-	79,88,90,105	0
1	MLY	D	102	11/12	0.65	0.56	-	140,153,162,172	0
1	MLY	D	63	11/12	0.90	0.36	-	102,115,133,135	0
1	MLY	B	63	11/12	0.91	0.47	-	99,110,121,122	0
1	MLY	D	1569	11/12	0.87	0.38	-	130,140,151,156	0
1	MLY	B	99	11/12	0.94	0.34	-	72,81,90,92	0
1	MLY	C	1575	11/12	0.92	0.33	-	87,98,108,111	0
1	MLY	B	140	11/12	0.94	0.24	-	71,77,88,102	0
1	MLY	C	1579	11/12	0.92	0.32	-	77,85,93,99	0
1	MLY	A	4	11/12	0.94	0.25	-	40,49,58,59	0
1	MLY	A	1575	11/12	0.91	0.36	-	110,123,132,138	0
1	MLY	C	4	11/12	0.97	0.21	-	46,51,57,58	0
1	MLY	D	65	11/12	0.83	0.38	-	102,114,134,145	0
1	MLY	C	1615	11/12	0.88	0.50	-	94,111,123,123	0
1	MLY	C	99	11/12	0.94	0.31	-	52,58,67,71	0
1	MLY	C	90	11/12	0.82	0.35	-	66,72,80,82	0
1	MLY	A	99	11/12	0.95	0.26	-	58,66,76,81	0
1	MLY	A	63	11/12	0.89	0.48	-	75,82,92,96	0
1	MLY	B	26	11/12	0.82	0.31	-	98,115,135,139	0
1	MLY	A	1579	11/12	0.93	0.31	-	93,103,109,122	0
1	MLY	C	1617	11/12	0.89	0.24	-	82,97,131,131	0
1	MLY	A	1587	11/12	0.94	0.30	-	62,70,112,112	0
1	MLY	B	1569	11/12	0.88	0.57	-	119,129,134,144	0
1	MLY	D	26	11/12	0.80	0.35	-	105,118,134,140	0
1	MLY	C	1569	11/12	0.89	0.31	-	94,101,109,121	0
1	MLY	A	65	11/12	0.85	0.25	-	60,69,75,75	0
1	MLY	B	72	11/12	0.89	0.22	-	66,75,92,98	0
1	MLY	C	65	11/12	0.91	0.36	-	57,65,75,78	0
1	MLY	A	26	11/12	0.88	0.31	-	72,97,114,114	0
1	MLY	A	1615	11/12	0.58	0.43	-	146,153,162,163	0
1	MLY	A	140	11/12	0.87	0.27	-	86,98,117,120	0
1	MLY	D	1579	11/12	0.91	0.29	-	78,90,102,103	0
1	MLY	C	26	11/12	0.86	0.45	-	87,99,137,139	0
1	MLY	C	102	11/12	0.87	0.30	-	73,78,91,98	0
1	MLY	A	102	11/12	0.86	0.20	-	95,112,116,117	0
1	MLY	B	90	11/12	0.69	0.39	-	66,81,88,96	0
1	MLY	D	140	11/12	0.88	0.40	-	85,91,116,118	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å^2)	Q<0.9
1	MLY	D	99	11/12	0.79	0.53	-	104,109,116,125	0
1	MLY	B	115	11/12	0.94	0.20	-	63,66,71,81	0
1	MLY	C	1616	11/12	0.84	0.44	-	90,103,109,110	0
1	MLY	D	1575	11/12	0.84	0.35	-	94,115,129,133	0
1	MLY	B	1575	11/12	0.93	0.28	-	94,100,107,112	0
1	MLY	B	4	11/12	0.93	0.21	-	47,48,53,56	0
1	MLY	D	72	11/12	0.91	0.25	-	85,95,111,113	0
1	MLY	B	1579	11/12	0.92	0.44	-	75,87,107,117	0
1	MLY	C	115	11/12	0.93	0.21	-	60,62,64,67	0
1	MLY	B	1587	11/12	0.94	0.33	-	51,56,84,88	0
1	MLY	A	115	11/12	0.96	0.19	-	54,57,64,65	0
1	MLY	C	63	11/12	0.94	0.26	-	66,72,95,99	0
1	MLY	B	102	11/12	0.75	0.18	-	112,126,138,139	0
1	MLY	D	115	11/12	0.90	0.20	-	59,63,75,76	0
1	MLY	C	1587	11/12	0.95	0.20	-	59,61,79,80	0
1	MLY	A	1569	11/12	0.93	0.28	-	103,108,122,124	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.