



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 05:59 AM GMT

PDB ID : 2VIX
Title : METHYLATED SHIGELLA FLEXNERI MXIC
Authors : Deane, J.E.; Roversi, P.; King, C.; Johnson, S.; Lea, S.M.
Deposited on : 2007-12-05
Resolution : 2.85 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 ⓘ](#)) 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

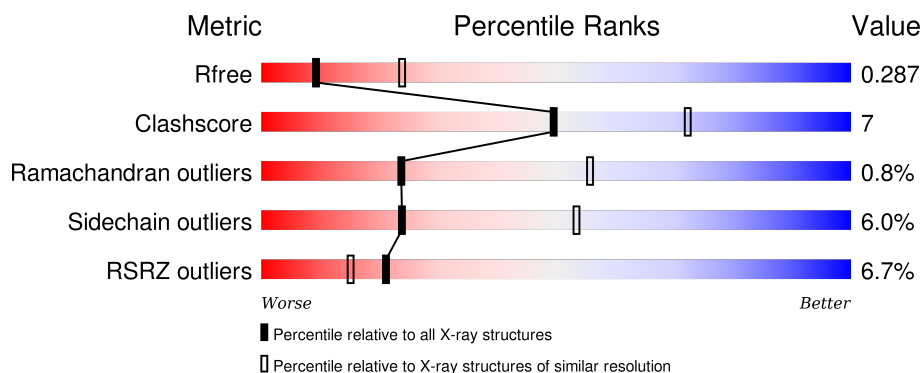
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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	2228 (2.90-2.82)
Clashscore	102246	2499 (2.90-2.82)
Ramachandran outliers	100387	2439 (2.90-2.82)
Sidechain outliers	100360	2442 (2.90-2.82)
RSRZ outliers	91569	2236 (2.90-2.82)

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 $\leq 5\%$. 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	294	<div> <div>6%</div> <div>83%</div> <div>12%</div> <div>• •</div> </div>
1	B	294	<div> <div>3%</div> <div>76%</div> <div>18%</div> <div>• •</div> </div>
1	C	294	<div> <div>9%</div> <div>72%</div> <div>21%</div> <div>• •</div> </div>

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
3	GOL	B	1356	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 7117 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 PROTEIN MXIC.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	283	Total	C	N	O	S	0	0	0
			2325	1489	381	447	8			
1	B	283	Total	C	N	O	S	0	0	0
			2325	1489	381	447	8			
1	C	281	Total	C	N	O	S	0	1	0
			2317	1487	378	444	8			

There are 36 discrepancies between the modelled and reference sequences:

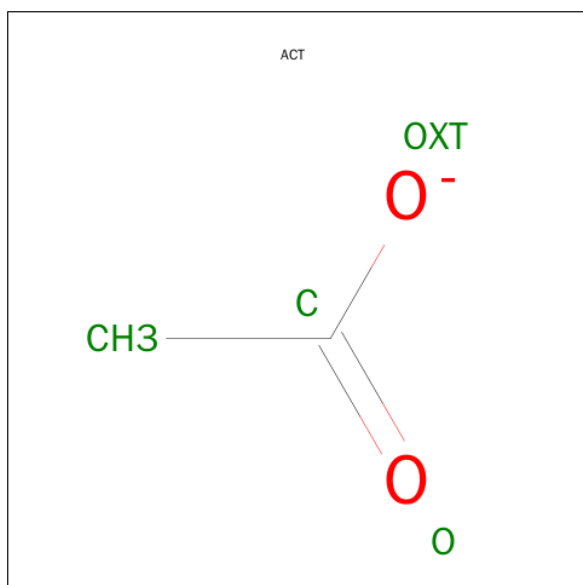
Chain	Residue	Modelled	Actual	Comment	Reference
A	62	HIS	-	EXPRESSION TAG	UNP Q04640
A	63	SER	-	EXPRESSION TAG	UNP Q04640
A	64	SER	-	EXPRESSION TAG	UNP Q04640
A	65	GLY	-	EXPRESSION TAG	UNP Q04640
A	66	LEU	-	EXPRESSION TAG	UNP Q04640
A	67	VAL	-	EXPRESSION TAG	UNP Q04640
A	68	PRO	-	EXPRESSION TAG	UNP Q04640
A	69	ARG	-	EXPRESSION TAG	UNP Q04640
A	70	GLY	-	EXPRESSION TAG	UNP Q04640
A	71	SER	-	EXPRESSION TAG	UNP Q04640
A	72	HIS	-	EXPRESSION TAG	UNP Q04640
A	73	MET	-	EXPRESSION TAG	UNP Q04640
B	62	HIS	-	EXPRESSION TAG	UNP Q04640
B	63	SER	-	EXPRESSION TAG	UNP Q04640
B	64	SER	-	EXPRESSION TAG	UNP Q04640
B	65	GLY	-	EXPRESSION TAG	UNP Q04640
B	66	LEU	-	EXPRESSION TAG	UNP Q04640
B	67	VAL	-	EXPRESSION TAG	UNP Q04640
B	68	PRO	-	EXPRESSION TAG	UNP Q04640
B	69	ARG	-	EXPRESSION TAG	UNP Q04640
B	70	GLY	-	EXPRESSION TAG	UNP Q04640
B	71	SER	-	EXPRESSION TAG	UNP Q04640
B	72	HIS	-	EXPRESSION TAG	UNP Q04640

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Chain	Residue	Modelled	Actual	Comment	Reference
B	73	MET	-	EXPRESSION TAG	UNP Q04640
C	62	HIS	-	EXPRESSION TAG	UNP Q04640
C	63	SER	-	EXPRESSION TAG	UNP Q04640
C	64	SER	-	EXPRESSION TAG	UNP Q04640
C	65	GLY	-	EXPRESSION TAG	UNP Q04640
C	66	LEU	-	EXPRESSION TAG	UNP Q04640
C	67	VAL	-	EXPRESSION TAG	UNP Q04640
C	68	PRO	-	EXPRESSION TAG	UNP Q04640
C	69	ARG	-	EXPRESSION TAG	UNP Q04640
C	70	GLY	-	EXPRESSION TAG	UNP Q04640
C	71	SER	-	EXPRESSION TAG	UNP Q04640
C	72	HIS	-	EXPRESSION TAG	UNP Q04640
C	73	MET	-	EXPRESSION TAG	UNP Q04640

- Molecule 2 is ACETATE ION (three-letter code: ACT) (formula: $C_2H_3O_2$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	C	O	0	0
			4	2	2		

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			6	3	3		
3	B	1	Total	C	O	0	0
			6	3	3		

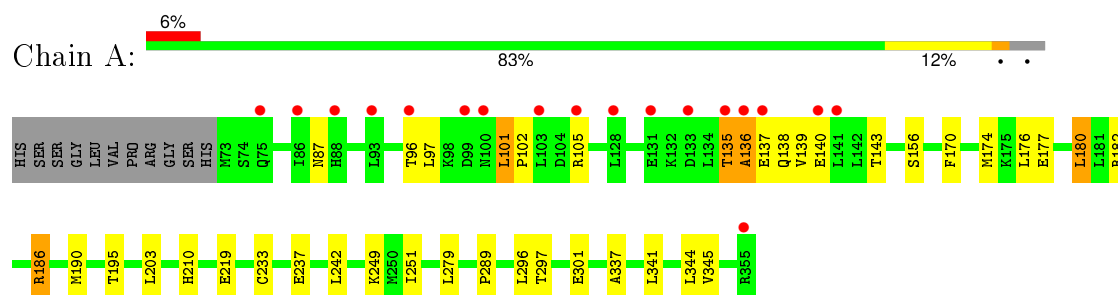
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	46	Total	O	0	0
			46	46		
4	B	46	Total	O	0	0
			46	46		
4	C	42	Total	O	0	0
			42	42		

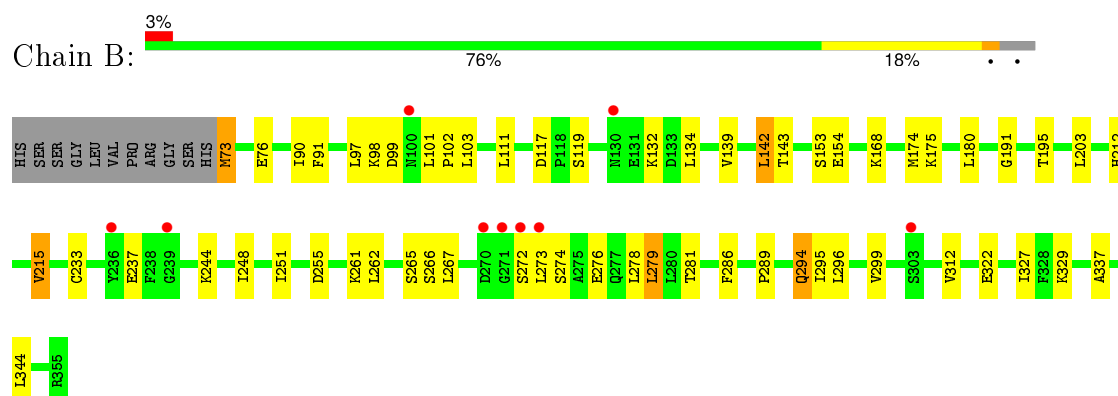
3 Residue-property plots [i](#)

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.

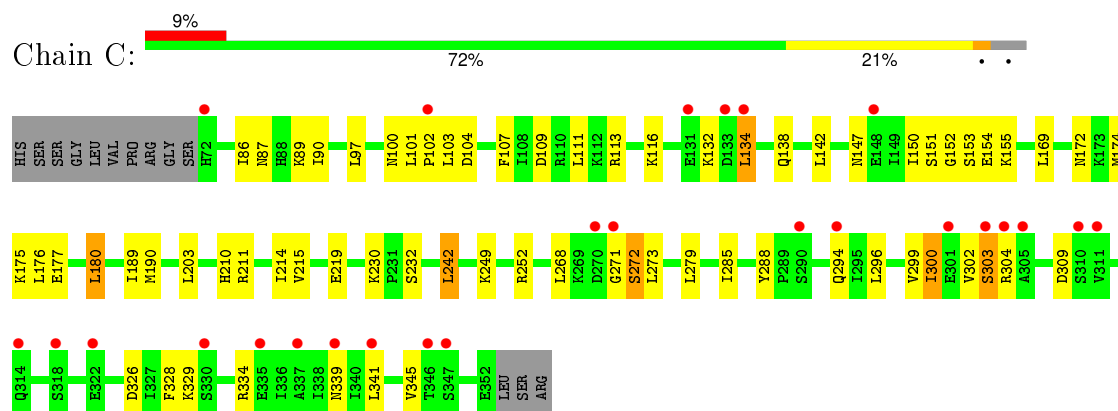
• Molecule 1: PROTEIN MXIC



• Molecule 1: PROTEIN MXIC



• Molecule 1: PROTEIN MXIC



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.79Å 102.57Å 122.64Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	50.40 – 2.85 47.32 – 2.85	Depositor EDS
% Data completeness (in resolution range)	(Not available) (50.40-2.85) 91.9 (47.32-2.85)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.30 (at 2.86Å)	Xtriage
Refinement program	TNT 5.13.1.0	Depositor
R, R_{free}	0.244 , 0.273 0.255 , 0.287	Depositor DCC
R_{free} test set	1216 reflections (5.20%)	DCC
Wilson B-factor (Å ²)	52.5	Xtriage
Anisotropy	0.019	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 51.5	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	1 of 24611 reflections (0.004%)	Xtriage
F_o, F_c correlation	0.89	EDS
Total number of atoms	7117	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.35% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical 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: GOL, MLY, ACT

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	0.25	0/2139	0.38	0/2901
1	B	0.26	0/2139	0.39	0/2901
1	C	0.25	0/2137	0.41	0/2901
All	All	0.25	0/6415	0.39	0/8703

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 [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	2325	0	2362	19	0
1	B	2325	0	2363	38	0
1	C	2317	0	2345	44	0
2	A	4	0	3	0	0
3	A	6	0	8	0	0
3	B	6	0	8	0	0
4	A	46	0	0	0	0
4	B	46	0	0	0	0
4	C	42	0	0	0	0
All	All	7117	0	7089	100	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 7.

All (100) 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:B:132:MLY:HA	1:B:134:LEU:H	1.10	1.11
1:B:102:PRO:HA	1:B:103:LEU:HB2	1.29	1.08
1:B:132:MLY:HA	1:B:134:LEU:N	1.83	0.93
1:B:102:PRO:HA	1:B:103:LEU:CB	2.07	0.85
1:C:328:PHE:N	1:C:329:MLY:HA	1.92	0.84
1:C:97:LEU:HD21	1:C:134:LEU:HD13	1.60	0.83
1:C:89:MLY:HH21	1:C:116:MLY:HH13	1.65	0.78
1:C:172:ASN:O	1:C:175:MLY:HE3	1.87	0.74
1:C:328:PHE:H	1:C:329:MLY:HA	1.53	0.72
1:C:300:ILE:HG23	1:C:303:SER:HB2	1.72	0.71
1:A:101:LEU:N	1:A:102:PRO:HD3	2.06	0.71
1:C:134:LEU:HD23	1:C:134:LEU:H	1.53	0.71
1:B:255:ASP:OD2	1:B:279:LEU:HD11	1.92	0.69
1:B:273:LEU:H	1:B:273:LEU:HD23	1.60	0.67
1:B:281:THR:HG23	1:B:295:ILE:HG22	1.76	0.67
1:A:101:LEU:HD21	1:A:135:THR:HG21	1.77	0.67
1:B:139:VAL:O	1:B:143:THR:HG23	1.94	0.67
1:C:272:SER:HB2	1:C:302:VAL:HG11	1.81	0.63
1:C:296:LEU:O	1:C:299:VAL:HG12	1.98	0.63
1:C:177:GLU:HB2	1:C:180:LEU:HD22	1.81	0.61
1:A:156:SER:HA	1:A:190:MET:HE1	1.83	0.60
1:B:132:MLY:CA	1:B:134:LEU:H	2.01	0.59
1:C:189:ILE:HG13	1:C:190:MET:HG3	1.85	0.58
1:C:299:VAL:HG13	1:C:300:ILE:CD1	2.33	0.58
1:A:219:GLU:OE2	1:A:249:MLY:HH22	2.06	0.56
1:C:268:LEU:HD23	1:C:268:LEU:O	2.07	0.54
1:C:150:ILE:HG23	1:C:151:SER:N	2.23	0.53
1:C:150:ILE:HG12	1:C:154:GLU:HG3	1.89	0.53
1:B:281:THR:CG2	1:B:295:ILE:HG22	2.39	0.51
1:B:195:THR:HG22	1:B:251:ILE:HD12	1.91	0.51
1:B:296:LEU:O	1:B:299:VAL:HG12	2.09	0.51
1:A:182:ARG:O	1:A:186:ARG:HB2	2.11	0.50
1:B:286:PHE:CZ	1:B:327:ILE:HD12	2.47	0.50
1:B:289:PRO:HB3	1:B:337:ALA:HB2	1.93	0.50
1:C:104:ASP:HA	1:C:107:PHE:HB3	1.92	0.50
1:A:289:PRO:HB3	1:A:337:ALA:HB2	1.94	0.50
1:A:96:THR:HG23	1:A:102:PRO:HG2	1.94	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:195:THR:HG23	1:B:248:ILE:HG13	1.95	0.49
1:A:170:PHE:HB3	1:A:174:MET:HE2	1.93	0.49
1:A:174:MET:HB3	1:A:210:HIS:CE1	2.48	0.48
1:C:219:GLU:OE2	1:C:249:MLY:HH13	2.14	0.48
1:C:299:VAL:HG13	1:C:300:ILE:HD11	1.95	0.48
1:C:328:PHE:N	1:C:329:MLY:CA	2.71	0.48
1:C:300:ILE:CG2	1:C:303:SER:HB2	2.42	0.48
1:B:265:SER:O	1:B:266:SER:HB2	2.15	0.47
1:B:265:SER:OG	1:B:267:LEU:HD12	2.15	0.47
1:B:101:LEU:HB2	1:B:102:PRO:HD2	1.96	0.47
1:B:174:MET:O	1:B:175:MLY:HB3	2.13	0.47
1:B:73:MET:N	1:B:76:GLU:OE1	2.47	0.47
1:C:100:ASN:O	1:C:102:PRO:HD3	2.14	0.47
1:C:299:VAL:C	1:C:300:ILE:HG12	2.32	0.47
1:C:299:VAL:HG13	1:C:300:ILE:HG12	1.97	0.46
1:C:242:LEU:HD22	1:C:242:LEU:O	2.15	0.46
1:C:111:LEU:O	1:C:111:LEU:HD23	2.14	0.46
1:B:99:ASP:HB2	1:B:101:LEU:HD22	1.97	0.46
1:A:101:LEU:N	1:A:102:PRO:CD	2.78	0.46
1:C:174:MET:O	1:C:175:MLY:HB3	2.16	0.45
1:C:138:GLN:O	1:C:142:LEU:HB2	2.16	0.45
1:B:168:MLY:HH13	1:B:168:MLY:HD2	1.75	0.45
1:C:174:MET:HB3	1:C:210:HIS:CE1	2.52	0.45
1:A:177:GLU:O	1:A:180:LEU:HB2	2.16	0.45
1:B:132:MLY:HH13	1:B:132:MLY:HD3	1.59	0.45
1:C:151:SER:HA	1:C:154:GLU:CD	2.37	0.45
1:B:97:LEU:HD11	1:B:142:LEU:HD21	1.99	0.45
1:A:136:ALA:O	1:A:138:GLN:N	2.49	0.45
1:A:233:CYS:HB3	1:A:237:GLU:HB2	1.99	0.44
1:B:154:GLU:HB3	1:C:152:GLY:HA2	1.98	0.44
1:B:98:MLY:HH22	1:B:98:MLY:HD3	1.80	0.44
1:C:155:MLY:HG2	1:C:232:SER:O	2.18	0.43
1:C:150:ILE:CG2	1:C:151:SER:N	2.82	0.43
1:B:91:PHE:CE2	1:B:98:MLY:HH21	2.54	0.43
1:B:273:LEU:O	1:B:274:SER:HB2	2.18	0.43
1:C:147:ASN:HA	1:C:150:ILE:HG22	2.00	0.43
1:B:191:GLY:O	1:B:244:MLY:HH11	2.19	0.43
1:B:117:ASP:OD1	1:B:119:SER:HB2	2.19	0.42
1:C:132:MLY:HD2	1:C:132:MLY:HH13	1.73	0.42
1:C:211:ARG:O	1:C:214:ILE:HG22	2.18	0.42
1:B:294:GLN:HG3	1:B:295:ILE:N	2.33	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:109:ASP:O	1:C:113:ARG:HG3	2.20	0.42
1:A:139:VAL:O	1:A:143:THR:HG23	2.20	0.42
1:A:297:THR:O	1:A:301:GLU:HG2	2.19	0.42
1:C:300:ILE:HG23	1:C:303:SER:CB	2.47	0.42
1:C:302:VAL:C	1:C:304:ARG:H	2.23	0.42
1:C:86:ILE:O	1:C:90:ILE:HD13	2.20	0.42
1:A:219:GLU:OE2	1:A:249:MLY:HH13	2.20	0.42
1:A:341:LEU:O	1:A:345:VAL:HG23	2.20	0.41
1:B:274:SER:O	1:B:276:GLU:N	2.47	0.41
1:B:262:LEU:HD21	1:B:278:LEU:HD23	2.01	0.41
1:B:279:LEU:HD23	1:B:279:LEU:O	2.20	0.41
1:C:215:VAL:HG11	1:C:252:ARG:HD3	2.01	0.41
1:B:212:HIS:O	1:B:215:VAL:HG13	2.20	0.41
1:C:230:MLY:HD3	1:C:230:MLY:HH22	1.86	0.41
1:C:285:ILE:HD11	1:C:296:LEU:HD21	2.03	0.41
1:A:195:THR:HG22	1:A:251:ILE:HD12	2.03	0.41
1:C:341:LEU:O	1:C:345:VAL:HG23	2.20	0.41
1:A:96:THR:CG2	1:A:102:PRO:HG2	2.50	0.41
1:B:329:MLY:HD2	1:B:329:MLY:HH13	1.80	0.40
1:B:233:CYS:HB3	1:B:237:GLU:HB2	2.03	0.40
1:B:261:MLY:HH22	1:B:322:GLU:OE2	2.21	0.40
1:C:101:LEU:CD2	1:C:103:LEU:HB2	2.51	0.40

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	261/294 (89%)	249 (95%)	9 (3%)	3 (1%)	17	47
1	B	261/294 (89%)	252 (97%)	9 (3%)	0	100	100
1	C	260/294 (88%)	242 (93%)	15 (6%)	3 (1%)	16	44

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
All	All	782/882 (89%)	743 (95%)	33 (4%)	6 (1%)	24 56

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	137	GLU
1	A	97	LEU
1	C	271	GLY
1	A	136	ALA
1	C	303	SER
1	C	153	SER

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	241/250 (96%)	228 (95%)	13 (5%)	27 59
1	B	241/250 (96%)	228 (95%)	13 (5%)	27 59
1	C	240/250 (96%)	223 (93%)	17 (7%)	18 44
All	All	722/750 (96%)	679 (94%)	43 (6%)	24 53

All (43) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	87	ASN
1	A	101	LEU
1	A	105	ARG
1	A	135	THR
1	A	140	GLU
1	A	176	LEU
1	A	180	LEU
1	A	186	ARG
1	A	203	LEU
1	A	242	LEU

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Mol	Chain	Res	Type
1	A	279	LEU
1	A	296	LEU
1	A	344	LEU
1	B	73	MET
1	B	90	ILE
1	B	111	LEU
1	B	142	LEU
1	B	153	SER
1	B	180	LEU
1	B	203	LEU
1	B	215	VAL
1	B	272	SER
1	B	279	LEU
1	B	294	GLN
1	B	312	VAL
1	B	344	LEU
1	C	87	ASN
1	C	134	LEU
1	C	169	LEU
1	C	176	LEU
1	C	180	LEU
1	C	203	LEU
1	C	242	LEU
1	C	272	SER
1	C	273	LEU
1	C	279	LEU
1	C	288	TYR
1	C	294	GLN
1	C	300	ILE
1	C	309	ASP
1	C	326	ASP
1	C	334	ARG
1	C	339	ASN

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	100	ASN
1	C	294	GLN
1	C	339	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	112	1	9,10,11	0.53	0	9,11,13	0.87	0
1	MLY	A	116	1	9,10,11	0.50	0	9,11,13	0.88	0
1	MLY	A	132	1	9,10,11	0.45	0	9,11,13	0.96	0
1	MLY	A	144	1	9,10,11	0.46	0	9,11,13	0.89	0
1	MLY	A	155	1	9,10,11	0.48	0	9,11,13	0.95	0
1	MLY	A	168	1	9,10,11	0.51	0	9,11,13	0.87	0
1	MLY	A	173	1	9,10,11	0.48	0	9,11,13	0.87	0
1	MLY	A	175	1	9,10,11	0.53	0	9,11,13	0.81	0
1	MLY	A	230	1	9,10,11	0.51	0	9,11,13	0.87	0
1	MLY	A	244	1	9,10,11	0.50	0	9,11,13	0.97	0
1	MLY	A	249	1	9,10,11	0.58	0	9,11,13	0.88	0
1	MLY	A	260	1	9,10,11	0.43	0	9,11,13	0.90	0
1	MLY	A	261	1	9,10,11	0.48	0	9,11,13	1.01	0
1	MLY	A	269	1	9,10,11	0.46	0	9,11,13	0.85	0
1	MLY	A	329	1	9,10,11	0.51	0	9,11,13	0.84	0
1	MLY	A	350	1	9,10,11	0.53	0	9,11,13	0.84	0
1	MLY	A	351	1	9,10,11	0.54	0	9,11,13	0.87	0
1	MLY	A	89	1	9,10,11	0.55	0	9,11,13	0.84	0
1	MLY	A	94	1	9,10,11	0.51	0	9,11,13	0.83	0
1	MLY	A	98	1	9,10,11	0.49	0	9,11,13	0.90	0
1	MLY	B	112	1	9,10,11	0.49	0	9,11,13	0.98	1 (11%)
1	MLY	B	116	1	9,10,11	0.51	0	9,11,13	0.92	1 (11%)
1	MLY	B	132	1	9,10,11	0.48	0	9,11,13	1.00	1 (11%)
1	MLY	B	144	1	9,10,11	0.45	0	9,11,13	0.84	0
1	MLY	B	155	1	9,10,11	0.49	0	9,11,13	0.86	0
1	MLY	B	168	1	9,10,11	0.48	0	9,11,13	0.91	0
1	MLY	B	173	1	9,10,11	0.49	0	9,11,13	0.91	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
1	MLY	B	175	1	9,10,11	0.50	0	9,11,13	0.86	0
1	MLY	B	230	1	9,10,11	0.52	0	9,11,13	0.84	0
1	MLY	B	244	1	9,10,11	0.52	0	9,11,13	0.85	0
1	MLY	B	249	1	9,10,11	0.57	0	9,11,13	0.90	0
1	MLY	B	260	1	9,10,11	0.50	0	9,11,13	0.86	0
1	MLY	B	261	1	9,10,11	0.58	0	9,11,13	0.88	0
1	MLY	B	269	1	9,10,11	0.51	0	9,11,13	0.87	0
1	MLY	B	329	1	9,10,11	0.48	0	9,11,13	0.90	0
1	MLY	B	350	1	9,10,11	0.43	0	9,11,13	0.92	0
1	MLY	B	351	1	9,10,11	0.48	0	9,11,13	0.88	0
1	MLY	B	89	1	9,10,11	0.54	0	9,11,13	0.84	0
1	MLY	B	94	1	9,10,11	0.50	0	9,11,13	0.89	0
1	MLY	B	98	1	9,10,11	0.49	0	9,11,13	1.00	0
1	MLY	C	112	1	9,10,11	0.54	0	9,11,13	0.86	0
1	MLY	C	116	1	9,10,11	0.51	0	9,11,13	0.86	0
1	MLY	C	132	1	9,10,11	0.44	0	9,11,13	0.96	0
1	MLY	C	144	1	9,10,11	0.47	0	9,11,13	0.89	0
1	MLY	C	155	1	9,10,11	0.45	0	9,11,13	0.88	0
1	MLY	C	168	1	9,10,11	0.48	0	9,11,13	0.86	0
1	MLY	C	173	1	9,10,11	0.54	0	9,11,13	0.84	0
1	MLY	C	175	1	9,10,11	0.50	0	9,11,13	0.88	0
1	MLY	C	230	1	9,10,11	0.49	0	9,11,13	0.85	0
1	MLY	C	244	1	9,10,11	0.56	0	9,11,13	0.86	0
1	MLY	C	249	1	9,10,11	0.53	0	9,11,13	0.90	0
1	MLY	C	260	1	9,10,11	0.51	0	9,11,13	0.88	0
1	MLY	C	261	1	9,10,11	0.60	0	9,11,13	0.86	0
1	MLY	C	269	1	9,10,11	0.55	0	9,11,13	0.80	0
1	MLY	C	329	1	9,10,11	0.51	0	9,11,13	0.83	0
1	MLY	C	350	1	9,10,11	0.44	0	9,11,13	0.88	0
1	MLY	C	351	1	9,10,11	0.53	0	9,11,13	0.81	0
1	MLY	C	89	1	9,10,11	0.51	0	9,11,13	0.82	0
1	MLY	C	94	1	9,10,11	0.49	0	9,11,13	0.85	0
1	MLY	C	98	1	9,10,11	0.50	0	9,11,13	0.88	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	112	1	-	0/7/9/11	0/0/0/0
1	MLY	A	116	1	-	0/7/9/11	0/0/0/0
1	MLY	A	132	1	-	0/7/9/11	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	A	144	1	-	0/7/9/11	0/0/0/0
1	MLY	A	155	1	-	0/7/9/11	0/0/0/0
1	MLY	A	168	1	-	0/7/9/11	0/0/0/0
1	MLY	A	173	1	-	0/7/9/11	0/0/0/0
1	MLY	A	175	1	-	0/7/9/11	0/0/0/0
1	MLY	A	230	1	-	0/7/9/11	0/0/0/0
1	MLY	A	244	1	-	0/7/9/11	0/0/0/0
1	MLY	A	249	1	-	0/7/9/11	0/0/0/0
1	MLY	A	260	1	-	0/7/9/11	0/0/0/0
1	MLY	A	261	1	-	0/7/9/11	0/0/0/0
1	MLY	A	269	1	-	0/7/9/11	0/0/0/0
1	MLY	A	329	1	-	0/7/9/11	0/0/0/0
1	MLY	A	350	1	-	0/7/9/11	0/0/0/0
1	MLY	A	351	1	-	0/7/9/11	0/0/0/0
1	MLY	A	89	1	-	0/7/9/11	0/0/0/0
1	MLY	A	94	1	-	0/7/9/11	0/0/0/0
1	MLY	A	98	1	-	0/7/9/11	0/0/0/0
1	MLY	B	112	1	-	0/7/9/11	0/0/0/0
1	MLY	B	116	1	-	0/7/9/11	0/0/0/0
1	MLY	B	132	1	-	0/7/9/11	0/0/0/0
1	MLY	B	144	1	-	0/7/9/11	0/0/0/0
1	MLY	B	155	1	-	0/7/9/11	0/0/0/0
1	MLY	B	168	1	-	0/7/9/11	0/0/0/0
1	MLY	B	173	1	-	0/7/9/11	0/0/0/0
1	MLY	B	175	1	-	0/7/9/11	0/0/0/0
1	MLY	B	230	1	-	0/7/9/11	0/0/0/0
1	MLY	B	244	1	-	0/7/9/11	0/0/0/0
1	MLY	B	249	1	-	0/7/9/11	0/0/0/0
1	MLY	B	260	1	-	0/7/9/11	0/0/0/0
1	MLY	B	261	1	-	0/7/9/11	0/0/0/0
1	MLY	B	269	1	-	0/7/9/11	0/0/0/0
1	MLY	B	329	1	-	0/7/9/11	0/0/0/0
1	MLY	B	350	1	-	0/7/9/11	0/0/0/0
1	MLY	B	351	1	-	0/7/9/11	0/0/0/0
1	MLY	B	89	1	-	0/7/9/11	0/0/0/0
1	MLY	B	94	1	-	0/7/9/11	0/0/0/0
1	MLY	B	98	1	-	0/7/9/11	0/0/0/0
1	MLY	C	112	1	-	0/7/9/11	0/0/0/0
1	MLY	C	116	1	-	0/7/9/11	0/0/0/0
1	MLY	C	132	1	-	0/7/9/11	0/0/0/0
1	MLY	C	144	1	-	0/7/9/11	0/0/0/0
1	MLY	C	155	1	-	0/7/9/11	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
1	MLY	C	168	1	-	0/7/9/11	0/0/0/0
1	MLY	C	173	1	-	0/7/9/11	0/0/0/0
1	MLY	C	175	1	-	0/7/9/11	0/0/0/0
1	MLY	C	230	1	-	0/7/9/11	0/0/0/0
1	MLY	C	244	1	-	0/7/9/11	0/0/0/0
1	MLY	C	249	1	-	0/7/9/11	0/0/0/0
1	MLY	C	260	1	-	0/7/9/11	0/0/0/0
1	MLY	C	261	1	-	0/7/9/11	0/0/0/0
1	MLY	C	269	1	-	0/7/9/11	0/0/0/0
1	MLY	C	329	1	-	0/7/9/11	0/0/0/0
1	MLY	C	350	1	-	0/7/9/11	0/0/0/0
1	MLY	C	351	1	-	0/7/9/11	0/0/0/0
1	MLY	C	89	1	-	0/7/9/11	0/0/0/0
1	MLY	C	94	1	-	0/7/9/11	0/0/0/0
1	MLY	C	98	1	-	0/7/9/11	0/0/0/0

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	132	MLY	O-C-CA	-2.31	119.48	125.49
1	B	116	MLY	O-C-CA	-2.06	120.14	125.49
1	B	112	MLY	O-C-CA	-2.04	120.18	125.49

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

16 monomers are involved in 23 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	A	249	MLY	2	0
1	B	132	MLY	4	0
1	B	168	MLY	1	0
1	B	175	MLY	1	0
1	B	244	MLY	1	0
1	B	261	MLY	1	0
1	B	329	MLY	1	0
1	B	98	MLY	2	0
1	C	116	MLY	1	0
1	C	132	MLY	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
1	C	155	MLY	1	0
1	C	175	MLY	2	0
1	C	230	MLY	1	0
1	C	249	MLY	1	0
1	C	329	MLY	3	0
1	C	89	MLY	1	0

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

3 ligands are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the chemical component dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	ACT	A	1356	-	1,3,3	3.65	1 (100%)	0,3,3	0.00	-
3	GOL	A	1357	-	5,5,5	0.36	0	5,5,5	1.57	1 (20%)
3	GOL	B	1356	-	5,5,5	0.50	0	5,5,5	1.57	1 (20%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACT	A	1356	-	-	0/0/0/0	0/0/0/0
3	GOL	A	1357	-	-	0/4/4/4	0/0/0/0
3	GOL	B	1356	-	-	0/4/4/4	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	1356	ACT	CH3-C	3.65	1.53	1.48

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
3	B	1356	GOL	O1-C1-C2	-2.48	98.16	110.18
3	A	1357	GOL	O3-C3-C2	-2.15	99.76	110.18

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

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, 95th 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	263/294 (89%)	0.42	18 (6%) 20 14	32, 53, 96, 103	0
1	B	263/294 (89%)	0.24	9 (3%) 49 41	31, 50, 70, 83	0
1	C	261/294 (88%)	0.64	26 (9%) 9 5	32, 65, 121, 131	0
All	All	787/882 (89%)	0.43	53 (6%) 21 15	31, 53, 112, 131	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	339	ASN	5.3
1	C	346	THR	5.3
1	A	100	ASN	4.8
1	A	103	LEU	4.6
1	C	301	GLU	4.4
1	C	347	SER	4.4
1	A	137	GLU	4.3
1	A	355	ARG	4.1
1	C	270	ASP	4.1
1	A	141	LEU	4.0
1	A	135	THR	3.9
1	C	304	ARG	3.8
1	C	134	LEU	3.6
1	A	99	ASP	3.6
1	C	133	ASP	3.5
1	C	310	SER	3.4
1	C	322	GLU	3.4
1	C	271	GLY	3.3
1	C	294	GLN	3.3
1	C	305	ALA	3.3
1	C	314	GLN	3.2
1	B	273	LEU	3.2
1	C	341	LEU	3.0

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Mol	Chain	Res	Type	RSRZ
1	B	271	GLY	2.9
1	A	93	LEU	2.9
1	A	133	ASP	2.9
1	A	140	GLU	2.9
1	A	88	HIS	2.8
1	C	337	ALA	2.7
1	A	136	ALA	2.6
1	A	131	GLU	2.6
1	B	236	TYR	2.5
1	A	96	THR	2.5
1	A	75	GLN	2.5
1	B	272	SER	2.4
1	C	102	PRO	2.4
1	C	290	SER	2.3
1	B	270	ASP	2.3
1	C	335	GLU	2.3
1	A	105	ARG	2.2
1	B	100	ASN	2.1
1	C	318	SER	2.1
1	C	330	SER	2.1
1	C	311	VAL	2.1
1	B	130	ASN	2.1
1	C	148	GLU	2.1
1	B	239	GLY	2.1
1	A	86	ILE	2.1
1	C	131	GLU	2.1
1	B	303	SER	2.1
1	C	303	SER	2.0
1	C	72	HIS	2.0
1	A	128	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, 95th 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	A	350	11/12	0.88	0.34	-	63,76,82,85	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	MLY	C	89	11/12	0.96	0.23	-	41,62,63,66	0
1	MLY	B	155	11/12	0.90	0.31	-	40,43,57,57	0
1	MLY	C	175	11/12	0.96	0.16	-	20,35,42,42	0
1	MLY	A	269	11/12	0.82	0.27	-	64,68,87,89	0
1	MLY	B	173	11/12	0.95	0.20	-	23,54,58,58	0
1	MLY	B	175	11/12	0.93	0.28	-	44,52,79,79	0
1	MLY	C	112	11/12	0.86	0.19	-	51,68,80,91	0
1	MLY	C	98	11/12	0.84	0.49	-	80,85,97,98	0
1	MLY	A	351	11/12	0.90	0.21	-	62,73,87,87	0
1	MLY	B	89	11/12	0.95	0.15	-	14,41,52,59	0
1	MLY	C	116	11/12	0.91	0.19	-	49,52,83,83	0
1	MLY	A	94	11/12	0.90	0.24	-	77,92,98,98	0
1	MLY	A	249	11/12	0.95	0.23	-	16,35,46,46	0
1	MLY	A	112	11/12	0.91	0.34	-	70,72,83,92	0
1	MLY	C	249	11/12	0.94	0.19	-	14,36,42,54	0
1	MLY	B	329	11/12	0.93	0.25	-	48,58,79,81	0
1	MLY	A	173	11/12	0.92	0.22	-	38,45,63,69	0
1	MLY	B	261	11/12	0.89	0.22	-	53,58,70,81	0
1	MLY	C	132	11/12	0.67	0.46	-	75,85,93,104	0
1	MLY	B	132	11/12	0.75	0.56	-	54,62,84,98	0
1	MLY	B	116	11/12	0.95	0.20	-	30,39,66,73	0
1	MLY	C	261	11/12	0.89	0.30	-	59,64,76,80	0
1	MLY	A	261	11/12	0.90	0.22	-	36,49,67,67	0
1	MLY	A	244	11/12	0.96	0.23	-	21,33,62,62	0
1	MLY	A	89	11/12	0.86	0.28	-	64,80,91,92	0
1	MLY	C	155	11/12	0.94	0.23	-	44,47,62,62	0
1	MLY	B	144	11/12	0.92	0.22	-	35,42,64,64	0
1	MLY	A	132	11/12	0.74	0.57	-	81,92,106,107	0
1	MLY	A	116	11/12	0.88	0.38	-	60,81,99,104	0
1	MLY	B	98	11/12	0.78	0.46	-	56,66,77,79	0
1	MLY	B	112	11/12	0.91	0.24	-	31,43,58,58	0
1	MLY	B	249	11/12	0.94	0.19	-	24,45,50,68	0
1	MLY	C	260	11/12	0.94	0.18	-	40,56,65,71	0
1	MLY	A	144	11/12	0.89	0.30	-	75,78,93,93	0
1	MLY	C	168	11/12	0.92	0.20	-	20,37,50,64	0
1	MLY	B	350	11/12	0.92	0.22	-	14,46,65,65	0
1	MLY	C	269	11/12	0.69	0.51	-	81,85,93,99	0
1	MLY	A	175	11/12	0.95	0.20	-	15,40,53,53	0
1	MLY	B	269	11/12	0.84	0.44	-	73,78,83,83	0
1	MLY	A	329	11/12	0.94	0.31	-	48,59,79,79	0
1	MLY	C	173	11/12	0.94	0.21	-	26,39,63,66	0
1	MLY	C	351	11/12	0.75	0.48	-	121,124,126,130	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
1	MLY	B	94	11/12	0.94	0.21	-	50,52,67,69	0
1	MLY	B	260	11/12	0.91	0.30	-	48,55,73,80	0
1	MLY	A	260	11/12	0.93	0.15	-	29,43,74,75	0
1	MLY	B	351	11/12	0.89	0.27	-	49,62,81,90	0
1	MLY	A	230	11/12	0.92	0.26	-	18,48,76,85	0
1	MLY	C	230	11/12	0.87	0.27	-	39,49,74,82	0
1	MLY	C	144	11/12	0.82	0.39	-	64,72,85,85	0
1	MLY	C	329	11/12	0.79	0.47	-	112,115,124,130	0
1	MLY	A	168	11/12	0.93	0.22	-	18,34,56,59	0
1	MLY	C	94	11/12	0.88	0.30	-	53,69,75,76	0
1	MLY	C	244	11/12	0.97	0.21	-	33,40,76,76	0
1	MLY	B	244	11/12	0.95	0.19	-	33,41,45,45	0
1	MLY	A	98	11/12	0.77	0.32	-	83,96,102,106	0
1	MLY	B	230	11/12	0.93	0.26	-	34,47,70,71	0
1	MLY	C	350	11/12	0.79	0.46	-	119,124,125,126	0
1	MLY	A	155	11/12	0.95	0.24	-	34,44,51,53	0
1	MLY	B	168	11/12	0.91	0.23	-	37,46,57,59	0

6.3 Carbohydrates [i](#)

There are no carbohydrates 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. 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, 95th 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(\AA^2)	Q<0.9
3	GOL	B	1356	6/6	0.71	0.45	10.15	90,90,90,90	0
3	GOL	A	1357	6/6	0.62	0.30	-	87,87,87,87	0
2	ACT	A	1356	4/4	0.64	0.51	-	95,95,95,95	0

6.5 Other polymers [i](#)

There are no such residues in this entry.