



Full wwPDB X-ray Structure Validation Report ⓘ

May 14, 2020 – 07:11 am BST

PDB ID : 6BGN
Title : Crystal Structure of 4-Oxalocrotonate Tautomerase After Incubation with 5-Fluoro-2-hydroxy-2,4-pentadienoate
Authors : Zhang, Y.; Li, W.; Stack, T.
Deposited on : 2017-10-29
Resolution : 1.51 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

<https://www.wwpdb.org/validation/2017/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:

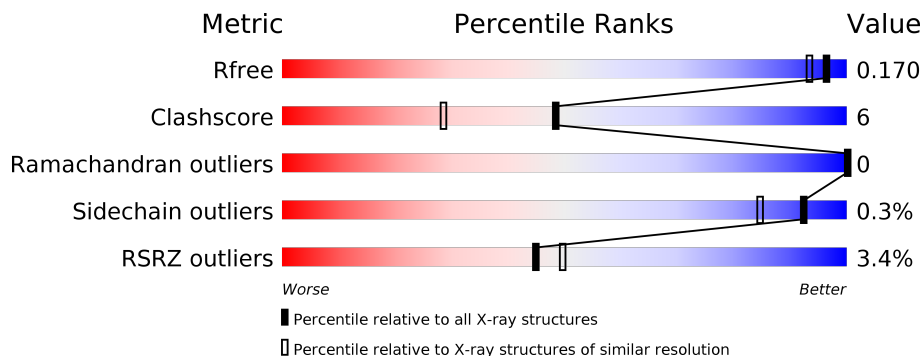
MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.11
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.11

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 1.51 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}	130704	4009 (1.54-1.50)
Clashscore	141614	4249 (1.54-1.50)
Ramachandran outliers	138981	4148 (1.54-1.50)
Sidechain outliers	138945	4146 (1.54-1.50)
RSRZ outliers	127900	3943 (1.54-1.50)

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 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	60	
1	B	60	
1	C	60	
1	D	60	
1	E	60	
1	F	60	

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	G	60	<p>2% 93% 7%</p>
1	H	60	<p>5% 90% 8%</p>
1	I	60	<p>3% 80% 17%</p>
1	J	60	<p>7% 85% 15%</p>
1	K	60	<p>2% 92% 8%</p>
1	L	60	<p>5% 92% 8%</p>
1	M	60	<p>2% 88% 8%</p>
1	N	60	<p>5% 90% 7%</p>
1	O	60	<p>3% 88% 10%</p>

2 Entry composition i

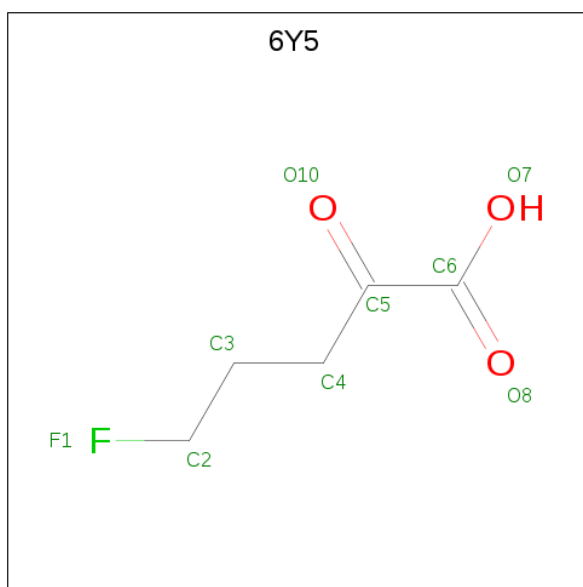
There are 5 unique types of molecules in this entry. The entry contains 7904 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 2-hydroxymuconate tautomerase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	59	479	299	85	94	1	0	4	0
1	B	60	468	294	81	92	1	0	3	0
1	C	59	456	284	80	91	1	0	2	0
1	D	60	488	307	87	93	1	0	5	0
1	E	58	466	292	85	88	1	0	4	0
1	F	59	471	296	80	94	1	0	4	0
1	G	60	486	306	84	95	1	0	5	0
1	H	59	472	296	83	92	1	0	4	0
1	I	58	469	293	86	89	1	0	4	0
1	J	60	461	288	81	91	1	0	1	0
1	K	60	460	289	81	89	1	0	1	0
1	L	60	469	293	84	91	1	0	2	0
1	M	58	461	287	84	89	1	0	3	0
1	N	59	448	279	80	88	1	0	0	0
1	O	59	454	283	80	90	1	0	1	0

- Molecule 2 is 5-fluoranyl-2-oxidanylidene-pentanoic acid (three-letter code: 6Y5) (formula: C₅H₇FO₃).



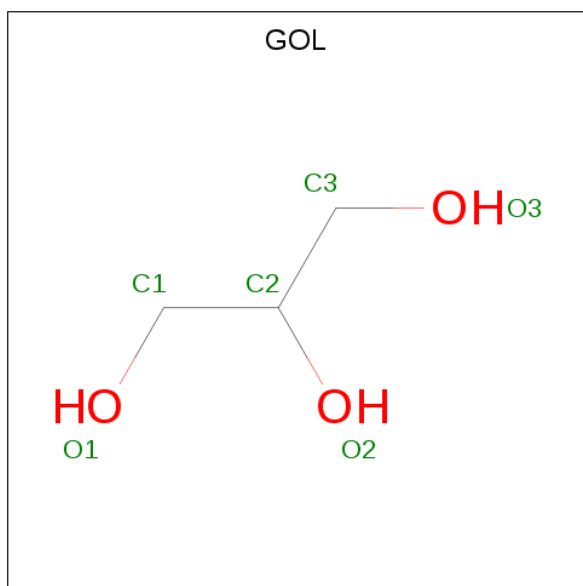
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	F	O	0	0
			9	5	1	3		
2	B	1	Total	C	F	O	0	0
			9	5	1	3		
2	C	1	Total	C	F	O	0	0
			9	5	1	3		
2	D	1	Total	C	F	O	0	0
			9	5	1	3		
2	E	1	Total	C	F	O	0	0
			9	5	1	3		
2	F	1	Total	C	F	O	0	0
			9	5	1	3		
2	G	1	Total	C	F	O	0	0
			9	5	1	3		
2	H	1	Total	C	F	O	0	0
			9	5	1	3		
2	I	1	Total	C	F	O	0	0
			9	5	1	3		
2	J	1	Total	C	F	O	0	0
			9	5	1	3		
2	K	1	Total	C	F	O	0	0
			9	5	1	3		
2	L	1	Total	C	F	O	0	0
			9	5	1	3		
2	M	1	Total	C	F	O	0	0
			9	5	1	3		
2	N	1	Total	C	F	O	0	0
			9	5	1	3		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	F	O		
2	O	1	9	5	1	3	0	0

- Molecule 3 is GLYCEROL (three-letter code: GOL) (formula: C₃H₈O₃).



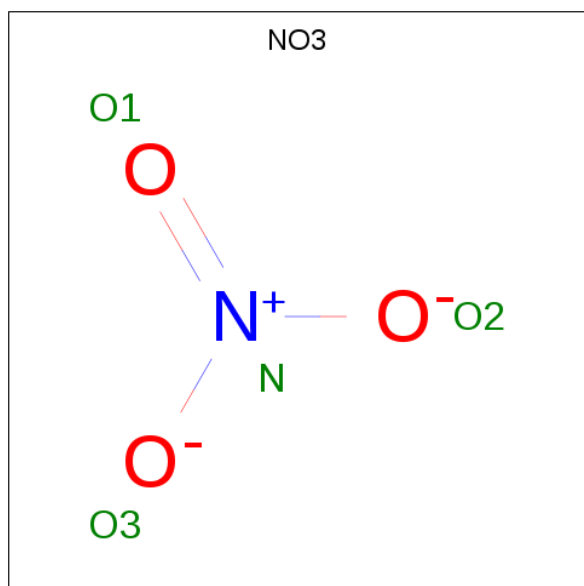
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
			Total	C	O		
3	B	1	6	3	3	0	0
3	B	1	6	3	3	0	0
3	B	1	6	3	3	0	0
3	D	1	6	3	3	0	0
3	D	1	6	3	3	0	0
3	E	1	6	3	3	0	0
3	F	1	6	3	3	0	0
3	G	1	6	3	3	0	0
3	G	1	6	3	3	0	0
3	H	1	6	3	3	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	H	1	Total	C	O	0	0
			6	3	3		
3	I	1	Total	C	O	0	0
			6	3	3		
3	J	1	Total	C	O	0	0
			6	3	3		
3	K	1	Total	C	O	0	0
			6	3	3		
3	L	1	Total	C	O	0	0
			6	3	3		
3	M	1	Total	C	O	0	0
			6	3	3		
3	N	1	Total	C	O	0	0
			6	3	3		
3	O	1	Total	C	O	0	0
			6	3	3		

- Molecule 4 is NITRATE ION (three-letter code: NO3) (formula: NO₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	G	1	Total	N	O	0	0
			4	1	3		
4	H	1	Total	N	O	0	0
			4	1	3		
4	J	1	Total	N	O	0	0
			4	1	3		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	46	Total 46	O 46	0	0
5	B	53	Total 54	O 54	0	1
5	C	59	Total 59	O 59	0	0
5	D	50	Total 51	O 51	0	1
5	E	44	Total 44	O 44	0	0
5	F	47	Total 47	O 47	0	0
5	G	47	Total 48	O 48	0	1
5	H	54	Total 54	O 54	0	0
5	I	37	Total 37	O 37	0	0
5	J	32	Total 32	O 32	0	0
5	K	31	Total 31	O 31	0	0
5	L	29	Total 30	O 30	0	1
5	M	33	Total 33	O 33	0	0
5	N	43	Total 43	O 43	0	0
5	O	32	Total 32	O 32	0	0

3 Residue-property plots [i](#)

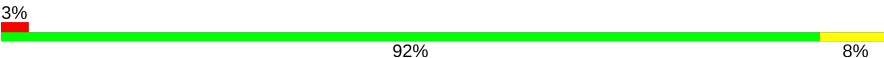
These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are 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: 2-hydroxymuconate tautomerase

Chain A: 



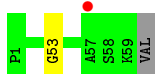
- Molecule 1: 2-hydroxymuconate tautomerase

Chain B: 




- Molecule 1: 2-hydroxymuconate tautomerase

Chain C: 




- Molecule 1: 2-hydroxymuconate tautomerase

Chain D: 

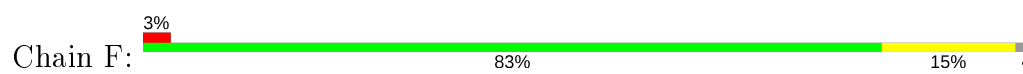


- Molecule 1: 2-hydroxymuconate tautomerase

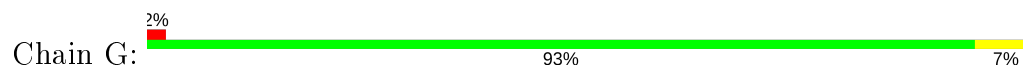
Chain E: 



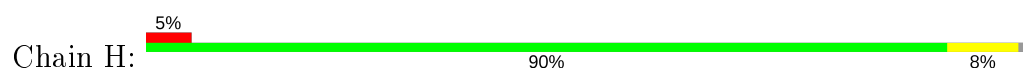
- Molecule 1: 2-hydroxymuconate tautomerase



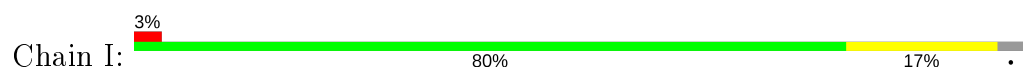
- Molecule 1: 2-hydroxymuconate tautomerase



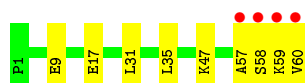
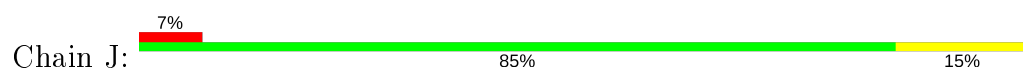
- Molecule 1: 2-hydroxymuconate tautomerase



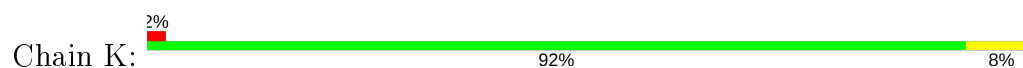
- Molecule 1: 2-hydroxymuconate tautomerase



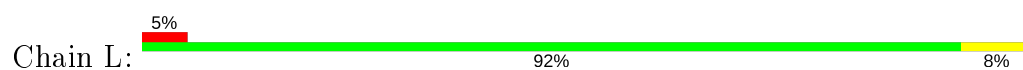
- Molecule 1: 2-hydroxymuconate tautomerase



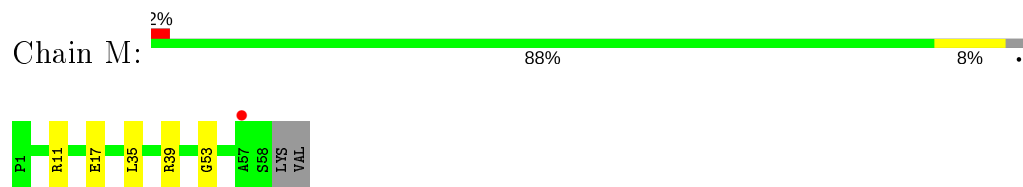
- Molecule 1: 2-hydroxymuconate tautomerase



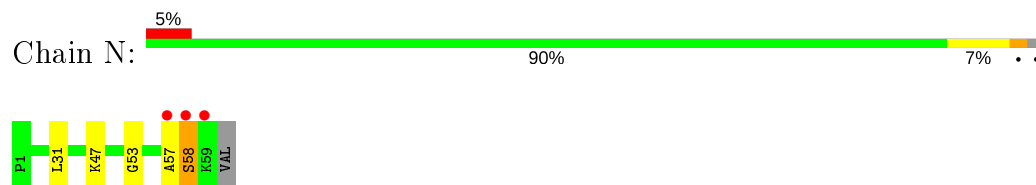
- Molecule 1: 2-hydroxymuconate tautomerase



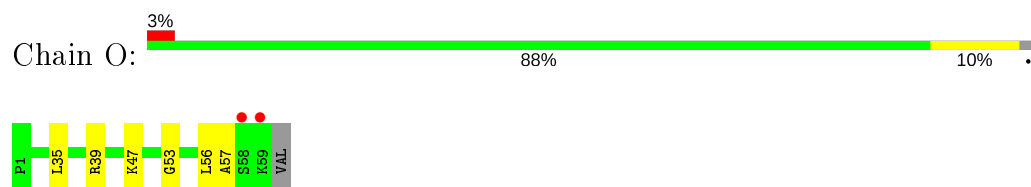
- Molecule 1: 2-hydroxymuconate tautomerase



- Molecule 1: 2-hydroxymuconate tautomerase



- Molecule 1: 2-hydroxymuconate tautomerase



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	87.41Å 88.01Å 112.67Å 90.00° 98.26° 90.00°	Depositor
Resolution (Å)	43.29 – 1.51 43.25 – 1.51	Depositor EDS
% Data completeness (in resolution range)	99.4 (43.29-1.51) 99.5 (43.25-1.51)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.84 (at 1.51Å)	Xtrriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.116 , 0.169 0.116 , 0.170	Depositor DCC
R_{free} test set	6595 reflections (5.03%)	wwPDB-VP
Wilson B-factor (Å ²)	13.0	Xtrriage
Anisotropy	0.641	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.39 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.98	EDS
Total number of atoms	7904	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 12.40% 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, 0.333 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: GOL, 6Y5, NO3

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	0.56	0/489	0.65	1/655 (0.2%)
1	B	0.55	0/481	0.79	1/646 (0.2%)
1	C	0.58	0/466	0.67	0/625
1	D	0.53	0/507	0.67	0/679
1	E	0.53	0/482	0.70	0/646
1	F	0.56	0/487	0.70	0/653
1	G	0.53	0/505	0.61	0/677
1	H	0.54	0/488	0.68	0/654
1	I	0.46	0/482	0.61	0/646
1	J	0.54	1/468 (0.2%)	0.62	0/628
1	K	0.46	0/467	0.61	0/627
1	L	0.46	0/479	0.61	0/642
1	M	0.46	0/474	0.56	0/635
1	N	0.47	0/452	0.63	0/606
1	O	0.47	0/461	0.61	0/618
All	All	0.52	1/7188 (0.0%)	0.65	2/9637 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	J	9	GLU	CD-OE2	5.58	1.31	1.25

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	29	ARG	NE-CZ-NH1	5.35	122.98	120.30
1	B	11	ARG	NE-CZ-NH2	-5.10	117.75	120.30

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	479	0	498	3	0
1	B	468	0	493	5	0
1	C	456	0	473	1	0
1	D	488	0	522	19	0
1	E	466	0	496	6	0
1	F	471	0	493	9	0
1	G	486	0	515	4	0
1	H	472	0	498	5	0
1	I	469	0	495	10	0
1	J	461	0	479	10	0
1	K	460	0	484	4	0
1	L	469	0	492	4	0
1	M	461	0	483	6	0
1	N	448	0	464	5	0
1	O	454	0	470	7	0
2	A	9	0	0	0	0
2	B	9	0	0	0	0
2	C	9	0	0	0	0
2	D	9	0	0	0	0
2	E	9	0	0	0	0
2	F	9	0	0	1	0
2	G	9	0	0	0	0
2	H	9	0	0	0	0
2	I	9	0	0	0	0
2	J	9	0	0	1	0
2	K	9	0	0	0	0
2	L	9	0	0	1	0
2	M	9	0	0	0	0
2	N	9	0	0	0	0
2	O	9	0	0	0	0
3	B	18	0	24	0	0
3	D	12	0	16	3	0
3	E	6	0	8	0	0
3	F	6	0	8	2	0
3	G	12	0	16	3	0
3	H	12	0	16	2	0
3	I	6	0	8	0	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	J	6	0	8	0	0
3	K	6	0	8	0	0
3	L	6	0	8	0	0
3	M	6	0	8	0	0
3	N	6	0	8	0	0
3	O	6	0	8	0	0
4	G	4	0	0	0	0
4	H	4	0	0	0	0
4	J	4	0	0	0	0
5	A	46	0	0	0	0
5	B	54	0	0	4	3
5	C	59	0	0	0	0
5	D	51	0	0	6	0
5	E	44	0	0	3	1
5	F	47	0	0	2	3
5	G	48	0	0	0	1
5	H	54	0	0	5	0
5	I	37	0	0	4	1
5	J	32	0	0	3	0
5	K	31	0	0	0	0
5	L	30	0	0	3	1
5	M	33	0	0	1	0
5	N	43	0	0	2	1
5	O	32	0	0	3	0
All	All	7904	0	7499	88	6

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 (88) 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:42:ILE:HG13	5:B:249:HOH:O	1.22	1.28
1:D:32:ASP:HB3	5:D:226:HOH:O	1.66	0.94
1:I:11[B]:ARG:HD3	1:I:15[B]:GLN:OE1	1.70	0.90
1:D:11[B]:ARG:HH11	1:D:11[B]:ARG:HG3	1.37	0.87
3:G:102:GOL:H11	5:H:226:HOH:O	1.74	0.86
1:O:57:ALA:HB3	5:O:201:HOH:O	1.77	0.84
1:J:47:LYS:HB3	1:J:58:SER:CB	2.12	0.79
1:I:15[B]:GLN:NE2	5:I:201:HOH:O	2.14	0.79
1:D:32:ASP:CB	5:D:226:HOH:O	2.27	0.79

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:L:101:6Y5:O10	5:L:201:HOH:O	2.00	0.79
1:D:11[B]:ARG:NH1	1:D:11[B]:ARG:HG3	1.92	0.79
2:J:101:6Y5:O10	5:J:201:HOH:O	2.01	0.78
1:I:11[B]:ARG:CD	1:I:15[B]:GLN:OE1	2.36	0.74
1:J:47:LYS:HB3	1:J:58:SER:HB2	1.70	0.73
1:H:47:LYS:HB3	1:H:58:SER:HB3	1.71	0.72
1:D:8:LEU:O	1:D:11[B]:ARG:NH1	2.23	0.71
1:J:47:LYS:HB3	1:J:58:SER:HB3	1.76	0.68
1:B:59:LYS:HD2	5:B:236:HOH:O	1.94	0.68
3:D:103:GOL:H11	5:E:218:HOH:O	1.96	0.66
3:D:103:GOL:C1	5:E:218:HOH:O	2.44	0.65
1:B:8[B]:LEU:HD13	5:B:248:HOH:O	1.98	0.63
3:G:102:GOL:C1	5:H:226:HOH:O	2.38	0.63
1:D:11[B]:ARG:CG	1:D:11[B]:ARG:HH11	2.10	0.62
1:I:39:ARG:HD2	5:I:202:HOH:O	2.01	0.61
1:B:8[B]:LEU:CD1	5:B:248:HOH:O	2.48	0.60
1:M:17[B]:GLU:HG2	1:O:56:LEU:HD11	1.84	0.60
1:O:47:LYS:O	5:O:201:HOH:O	2.16	0.60
1:B:8[B]:LEU:HD21	1:B:57:ALA:HB1	1.84	0.59
1:G:17:GLU:HG3	5:I:219:HOH:O	2.03	0.58
1:O:39:ARG:HD2	5:O:202:HOH:O	2.04	0.57
1:D:59:LYS:HD2	5:D:244[B]:HOH:O	2.04	0.57
1:J:57:ALA:HB3	5:J:203:HOH:O	2.05	0.56
1:N:47:LYS:HD3	1:N:58:SER:HB2	1.88	0.56
1:D:31:LEU:HD22	1:E:11[A]:ARG:HD3	1.86	0.55
1:E:47:LYS:HB3	1:E:58:SER:HB3	1.87	0.55
1:D:57:ALA:HA	1:D:60:VAL:CG1	2.37	0.55
1:J:60:VAL:HG12	1:J:60:VAL:O	2.06	0.55
1:L:47:LYS:HB3	1:L:58:SER:HB3	1.90	0.54
1:F:35:LEU:O	1:H:53:GLY:HA2	2.08	0.54
3:H:103:GOL:H32	5:H:206:HOH:O	2.08	0.53
1:K:35:LEU:O	1:M:53:GLY:HA2	2.09	0.53
1:J:35:LEU:O	1:L:53:GLY:HA2	2.09	0.52
2:F:101:6Y5:O10	5:F:201:HOH:O	2.19	0.52
1:J:60:VAL:HG21	5:J:211:HOH:O	2.10	0.51
1:M:35:LEU:O	1:O:53:GLY:HA2	2.11	0.51
1:D:47:LYS:HB3	1:D:58:SER:HB3	1.93	0.51
1:F:20:ILE:HG13	1:F:42[B]:ILE:HD11	1.92	0.51
1:A:35:LEU:O	1:C:53:GLY:HA2	2.12	0.49
1:M:11:ARG:HD3	1:N:31:LEU:HD22	1.94	0.49
1:L:35:LEU:O	1:N:53:GLY:HA2	2.13	0.48

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:17[B]:GLU:HG2	1:F:56:LEU:HD11	1.95	0.48
3:D:103:GOL:O2	5:D:201:HOH:O	2.17	0.48
1:I:57:ALA:HB3	5:I:203:HOH:O	2.13	0.48
1:D:56:LEU:O	1:D:60:VAL:HG12	2.14	0.48
1:D:57:ALA:HA	1:D:60:VAL:HG12	1.96	0.48
1:A:47:LYS:HE2	5:D:218:HOH:O	2.13	0.48
5:E:205:HOH:O	1:I:17:GLU:HG3	2.15	0.46
1:L:39:ARG:HD2	5:L:201:HOH:O	2.15	0.46
1:D:53:GLY:HA2	1:H:35:LEU:O	2.16	0.46
1:K:53:GLY:HA2	1:O:35:LEU:O	2.16	0.45
1:A:56:LEU:HD12	1:A:59:LYS:HE3	1.98	0.45
1:G:35:LEU:O	1:I:53:GLY:HA2	2.17	0.45
1:E:35:LEU:O	1:G:53:GLY:HA2	2.16	0.44
1:D:35:LEU:O	1:F:53:GLY:HA2	2.18	0.44
1:N:47:LYS:HB2	5:N:202:HOH:O	2.17	0.44
1:E:19:LEU:HD23	1:E:42[A]:ILE:HD12	2.00	0.44
1:H:47:LYS:HB3	1:H:58:SER:CB	2.46	0.44
1:D:60:VAL:HG13	1:D:60:VAL:O	2.18	0.43
1:F:47:LYS:HB3	1:F:58:SER:CB	2.48	0.43
1:F:39:ARG:HD2	5:F:201:HOH:O	2.18	0.43
3:F:102:GOL:H12	5:H:209:HOH:O	2.17	0.43
1:J:60:VAL:CG1	1:J:60:VAL:O	2.67	0.43
1:M:39:ARG:HD2	5:M:201:HOH:O	2.18	0.43
1:D:25:GLU:OE1	5:D:202:HOH:O	2.21	0.43
1:G:4:GLN:HB2	3:G:102:GOL:H12	2.01	0.43
1:H:4:GLN:HB2	3:H:103:GOL:H31	1.99	0.43
1:F:47:LYS:HB3	1:F:58:SER:HB3	2.01	0.42
1:J:17:GLU:HG3	5:L:207:HOH:O	2.19	0.42
1:D:11[A]:ARG:HD3	1:E:31:LEU:HD22	2.01	0.42
3:F:102:GOL:C1	5:H:209:HOH:O	2.67	0.42
1:F:11:ARG:HD3	1:I:31:LEU:HD22	2.02	0.41
1:J:31:LEU:HD22	1:K:11:ARG:HD3	2.01	0.41
1:M:17[B]:GLU:CG	1:O:56:LEU:HD11	2.49	0.41
1:I:47:LYS:HB3	1:I:58:SER:HB3	2.01	0.41
1:E:53:GLY:HA2	1:I:35:LEU:O	2.20	0.41
1:N:57:ALA:HB3	5:N:204:HOH:O	2.21	0.41
1:D:17[B]:GLU:CG	1:F:56:LEU:HD11	2.52	0.40
1:K:56:LEU:HD12	1:K:59:LYS:HE3	2.03	0.40

All (6) 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)
5:E:231:HOH:O	5:E:231:HOH:O 2_557]	1.91	0.29
5:I:236:HOH:O	5:L:217:HOH:O 2_557]	2.03	0.17
5:B:218:HOH:O	5:F:247:HOH:O 2_657]	2.06	0.14
5:B:252:HOH:O	5:F:230:HOH:O 2_657]	2.07	0.13
5:B:252:HOH:O	5:F:222:HOH:O 2_657]	2.08	0.12
5:G:242:HOH:O	5:N:223:HOH:O 2_557]	2.10	0.10

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	61/60 (102%)	61 (100%)	0	0	100	100
1	B	61/60 (102%)	60 (98%)	1 (2%)	0	100	100
1	C	59/60 (98%)	59 (100%)	0	0	100	100
1	D	63/60 (105%)	61 (97%)	2 (3%)	0	100	100
1	E	60/60 (100%)	60 (100%)	0	0	100	100
1	F	61/60 (102%)	59 (97%)	2 (3%)	0	100	100
1	G	63/60 (105%)	63 (100%)	0	0	100	100
1	H	61/60 (102%)	61 (100%)	0	0	100	100
1	I	60/60 (100%)	60 (100%)	0	0	100	100
1	J	59/60 (98%)	59 (100%)	0	0	100	100
1	K	59/60 (98%)	59 (100%)	0	0	100	100
1	L	60/60 (100%)	58 (97%)	2 (3%)	0	100	100
1	M	59/60 (98%)	59 (100%)	0	0	100	100
1	N	57/60 (95%)	57 (100%)	0	0	100	100
1	O	58/60 (97%)	58 (100%)	0	0	100	100
All	All	901/900 (100%)	894 (99%)	7 (1%)	0	100	100

There are no Ramachandran outliers to report.

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	53/50 (106%)	53 (100%)	0	100	100
1	B	53/50 (106%)	53 (100%)	0	100	100
1	C	51/50 (102%)	51 (100%)	0	100	100
1	D	55/50 (110%)	55 (100%)	0	100	100
1	E	52/50 (104%)	52 (100%)	0	100	100
1	F	53/50 (106%)	53 (100%)	0	100	100
1	G	55/50 (110%)	55 (100%)	0	100	100
1	H	53/50 (106%)	53 (100%)	0	100	100
1	I	52/50 (104%)	52 (100%)	0	100	100
1	J	51/50 (102%)	50 (98%)	1 (2%)	55	24
1	K	51/50 (102%)	51 (100%)	0	100	100
1	L	52/50 (104%)	52 (100%)	0	100	100
1	M	51/50 (102%)	51 (100%)	0	100	100
1	N	49/50 (98%)	48 (98%)	1 (2%)	55	24
1	O	50/50 (100%)	50 (100%)	0	100	100
All	All	781/750 (104%)	779 (100%)	2 (0%)	92	84

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	J	59	LYS
1	N	58	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

36 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	6Y5	J	101	1	5,8,8	0.77	0	5,9,9	1.15	0
2	6Y5	I	101	1	5,8,8	0.68	0	5,9,9	1.92	3 (60%)
2	6Y5	H	101	1	5,8,8	0.71	0	5,9,9	0.89	0
2	6Y5	D	101	1	5,8,8	0.63	0	5,9,9	0.99	0
3	GOL	J	102	-	5,5,5	0.68	0	5,5,5	0.69	0
2	6Y5	B	101	1	5,8,8	0.69	0	5,9,9	1.33	0
3	GOL	D	103	-	5,5,5	0.41	0	5,5,5	0.49	0
3	GOL	N	102	-	5,5,5	0.53	0	5,5,5	0.55	0
3	GOL	B	102	-	5,5,5	0.63	0	5,5,5	0.42	0
3	GOL	K	102	-	5,5,5	0.52	0	5,5,5	0.45	0
3	GOL	M	102	-	5,5,5	0.61	0	5,5,5	0.56	0
2	6Y5	M	101	1	5,8,8	0.52	0	5,9,9	0.67	0
3	GOL	H	102	-	5,5,5	0.45	0	5,5,5	0.52	0
4	NO3	J	103	-	1,3,3	0.10	0	0,3,3	0.00	-
3	GOL	G	103	-	5,5,5	0.46	0	5,5,5	0.77	0
3	GOL	I	102	-	5,5,5	0.48	0	5,5,5	0.70	0
3	GOL	O	102	-	5,5,5	0.46	0	5,5,5	0.72	0
4	NO3	H	104	-	1,3,3	0.12	0	0,3,3	0.00	-
3	GOL	H	103	-	5,5,5	0.28	0	5,5,5	0.35	0
3	GOL	B	103	-	5,5,5	0.55	0	5,5,5	0.44	0
2	6Y5	C	101	1	5,8,8	0.92	0	5,9,9	1.90	2 (40%)
3	GOL	L	102	-	5,5,5	0.62	0	5,5,5	0.56	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	GOL	F	102	-	5,5,5	0.59	0	5,5,5	0.55	0
3	GOL	D	102	-	5,5,5	0.73	0	5,5,5	0.71	0
2	6Y5	L	101	1	5,8,8	0.44	0	5,9,9	1.10	0
2	6Y5	K	101	1	5,8,8	0.65	0	5,9,9	0.86	0
3	GOL	G	102	-	5,5,5	0.42	0	5,5,5	0.20	0
3	GOL	E	102	-	5,5,5	0.41	0	5,5,5	0.57	0
2	6Y5	F	101	1	5,8,8	0.57	0	5,9,9	1.21	0
3	GOL	B	104	-	5,5,5	0.38	0	5,5,5	0.52	0
2	6Y5	E	101	1	5,8,8	0.73	0	5,9,9	1.03	0
2	6Y5	O	101	1	5,8,8	0.48	0	5,9,9	1.57	1 (20%)
2	6Y5	A	101	1	5,8,8	0.81	0	5,9,9	1.37	0
4	NO3	G	104	-	1,3,3	0.10	0	0,3,3	0.00	-
2	6Y5	N	101	1	5,8,8	0.72	0	5,9,9	0.99	0
2	6Y5	G	101	1	5,8,8	0.68	0	5,9,9	1.28	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
2	6Y5	J	101	1	-	2/4/8/8	-
2	6Y5	I	101	1	-	0/4/8/8	-
2	6Y5	H	101	1	-	1/4/8/8	-
2	6Y5	D	101	1	-	1/4/8/8	-
3	GOL	J	102	-	-	0/4/4/4	-
2	6Y5	B	101	1	-	0/4/8/8	-
3	GOL	D	103	-	-	2/4/4/4	-
3	GOL	N	102	-	-	0/4/4/4	-
3	GOL	B	102	-	-	0/4/4/4	-
3	GOL	K	102	-	-	0/4/4/4	-
3	GOL	M	102	-	-	0/4/4/4	-
2	6Y5	M	101	1	-	1/4/8/8	-
3	GOL	H	102	-	-	0/4/4/4	-
3	GOL	G	103	-	-	0/4/4/4	-
3	GOL	I	102	-	-	0/4/4/4	-
3	GOL	O	102	-	-	0/4/4/4	-
3	GOL	H	103	-	-	0/4/4/4	-
3	GOL	B	103	-	-	0/4/4/4	-
2	6Y5	C	101	1	-	0/4/8/8	-
3	GOL	L	102	-	-	0/4/4/4	-
3	GOL	F	102	-	-	0/4/4/4	-

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	GOL	D	102	-	-	0/4/4/4	-
2	6Y5	L	101	1	-	0/4/8/8	-
2	6Y5	K	101	1	-	1/4/8/8	-
3	GOL	G	102	-	-	4/4/4/4	-
3	GOL	E	102	-	-	0/4/4/4	-
2	6Y5	F	101	1	-	0/4/8/8	-
3	GOL	B	104	-	-	0/4/4/4	-
2	6Y5	E	101	1	-	0/4/8/8	-
2	6Y5	O	101	1	-	1/4/8/8	-
2	6Y5	A	101	1	-	0/4/8/8	-
2	6Y5	N	101	1	-	0/4/8/8	-
2	6Y5	G	101	1	-	0/4/8/8	-

There are no bond length outliers.

All (6) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	101	6Y5	O10-C5-C4	2.86	125.25	120.38
2	C	101	6Y5	C4-C5-C6	-2.65	114.73	121.32
2	I	101	6Y5	O10-C5-C4	2.53	124.70	120.38
2	I	101	6Y5	C4-C5-C6	-2.30	115.58	121.32
2	I	101	6Y5	C2-C3-C4	-2.22	106.06	112.60
2	O	101	6Y5	C4-C5-C6	-2.15	115.97	121.32

There are no chirality outliers.

All (13) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	J	101	6Y5	F1-C2-C3-C4
2	H	101	6Y5	F1-C2-C3-C4
3	D	103	GOL	C1-C2-C3-O3
2	M	101	6Y5	F1-C2-C3-C4
2	K	101	6Y5	F1-C2-C3-C4
3	G	102	GOL	C1-C2-C3-O3
2	J	101	6Y5	C2-C3-C4-C5
3	D	103	GOL	O2-C2-C3-O3
3	G	102	GOL	O2-C2-C3-O3
3	G	102	GOL	O1-C1-C2-O2
2	D	101	6Y5	C2-C3-C4-C5
2	O	101	6Y5	C2-C3-C4-C5
3	G	102	GOL	O1-C1-C2-C3

There are no ring outliers.

7 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	J	101	6Y5	1	0
3	D	103	GOL	3	0
3	H	103	GOL	2	0
3	F	102	GOL	2	0
2	L	101	6Y5	1	0
3	G	102	GOL	3	0
2	F	101	6Y5	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

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	59/60 (98%)	-0.39	0 100 100	9, 14, 43, 89	0
1	B	60/60 (100%)	-0.30	2 (3%) 46 51	10, 14, 37, 68	0
1	C	59/60 (98%)	-0.39	1 (1%) 70 74	9, 13, 38, 80	0
1	D	60/60 (100%)	-0.18	3 (5%) 28 31	9, 15, 49, 77	0
1	E	58/60 (96%)	-0.41	2 (3%) 45 50	10, 16, 44, 62	0
1	F	59/60 (98%)	-0.34	2 (3%) 45 50	11, 15, 36, 69	0
1	G	60/60 (100%)	-0.26	1 (1%) 70 74	12, 17, 45, 103	0
1	H	59/60 (98%)	-0.33	3 (5%) 28 30	10, 15, 39, 79	0
1	I	58/60 (96%)	-0.38	2 (3%) 45 50	12, 18, 41, 73	0
1	J	60/60 (100%)	-0.05	4 (6%) 17 19	13, 21, 63, 76	0
1	K	60/60 (100%)	-0.09	1 (1%) 70 74	15, 23, 47, 97	0
1	L	60/60 (100%)	-0.10	3 (5%) 28 31	14, 23, 60, 94	0
1	M	58/60 (96%)	-0.31	1 (1%) 70 74	14, 20, 46, 63	0
1	N	59/60 (98%)	-0.31	3 (5%) 28 30	13, 19, 53, 73	0
1	O	59/60 (98%)	-0.33	2 (3%) 45 50	14, 21, 54, 108	0
All	All	888/900 (98%)	-0.28	30 (3%) 45 50	9, 18, 49, 108	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	K	60	VAL	10.6
1	G	60	VAL	10.4
1	J	60	VAL	7.7
1	D	60	VAL	6.6
1	L	60	VAL	5.9
1	B	60	VAL	5.7
1	J	58	SER	4.2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	L	58	SER	3.9
1	J	59	LYS	3.8
1	E	58	SER	3.8
1	N	59	LYS	3.7
1	O	59	LYS	3.5
1	N	58	SER	3.4
1	L	59	LYS	2.9
1	N	57	ALA	2.9
1	M	57	ALA	2.8
1	D	57	ALA	2.8
1	H	59	LYS	2.8
1	D	58	SER	2.6
1	F	59	LYS	2.6
1	B	58	SER	2.6
1	E	57	ALA	2.5
1	H	57	ALA	2.5
1	I	57	ALA	2.4
1	I	58	SER	2.2
1	O	58	SER	2.2
1	C	57	ALA	2.2
1	F	58	SER	2.1
1	J	57	ALA	2.1
1	H	58	SER	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

There are no non-standard protein/DNA/RNA residues in this entry.

6.3 Carbohydrates [i](#)

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. 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.

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	GOL	H	103	6/6	0.83	0.18	48,61,73,78	0
2	6Y5	B	101	9/9	0.84	0.15	24,35,58,59	5
3	GOL	D	103	6/6	0.86	0.13	35,42,57,73	0
2	6Y5	D	101	9/9	0.86	0.16	34,46,58,63	0
2	6Y5	M	101	9/9	0.88	0.15	43,55,70,81	0
2	6Y5	K	101	9/9	0.88	0.16	41,51,61,63	0
4	NO3	J	103	4/4	0.90	0.14	32,37,54,61	0
2	6Y5	J	101	9/9	0.90	0.15	37,45,57,63	6
2	6Y5	I	101	9/9	0.90	0.17	35,46,53,56	0
2	6Y5	H	101	9/9	0.91	0.16	34,64,87,103	0
3	GOL	G	102	6/6	0.91	0.12	41,45,56,73	0
4	NO3	G	104	4/4	0.91	0.11	35,44,52,62	0
2	6Y5	O	101	9/9	0.92	0.14	32,34,49,51	1
2	6Y5	C	101	9/9	0.92	0.14	24,35,88,103	1
4	NO3	H	104	4/4	0.93	0.08	28,38,43,44	0
2	6Y5	A	101	9/9	0.93	0.12	28,34,73,137	0
2	6Y5	G	101	9/9	0.93	0.13	23,31,49,60	1
2	6Y5	L	101	9/9	0.94	0.18	42,66,83,96	0
2	6Y5	N	101	9/9	0.94	0.13	28,41,54,64	2
2	6Y5	F	101	9/9	0.94	0.14	27,37,66,66	0
2	6Y5	E	101	9/9	0.95	0.10	21,34,47,50	1
3	GOL	M	102	6/6	0.96	0.08	18,22,28,29	0
3	GOL	G	103	6/6	0.96	0.09	17,21,25,26	0
3	GOL	N	102	6/6	0.96	0.07	19,25,28,34	0
3	GOL	L	102	6/6	0.97	0.07	21,22,28,29	0
3	GOL	D	102	6/6	0.97	0.08	14,17,22,23	0
3	GOL	O	102	6/6	0.97	0.08	19,23,27,34	0
3	GOL	H	102	6/6	0.97	0.07	14,16,20,21	0
3	GOL	J	102	6/6	0.98	0.07	19,22,30,30	0
3	GOL	B	102	6/6	0.98	0.07	13,14,20,21	0
3	GOL	I	102	6/6	0.98	0.05	18,19,26,29	0
3	GOL	K	102	6/6	0.98	0.06	19,21,29,32	0
3	GOL	E	102	6/6	0.98	0.07	18,19,23,26	0
3	GOL	F	102	6/6	0.98	0.06	14,16,21,24	0
3	GOL	B	104	6/6	0.99	0.06	13,14,19,21	0
3	GOL	B	103	6/6	0.99	0.09	13,14,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.