



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 12:00 PM GMT

PDB ID : 3QPE
Title : Crystal structure of Galacturonate Dehydratase from GEOBACILLUS SP.
complexed with D-Galacturonate and 5-keto-4-deoxy-D-Galacturonate
Authors : Fedorov, A.A.; Fedorov, E.V.; Mills-Groninger, F.; Gerlt, J.A.; Almo, S.C.
Deposited on : 2011-02-12
Resolution : 1.80 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

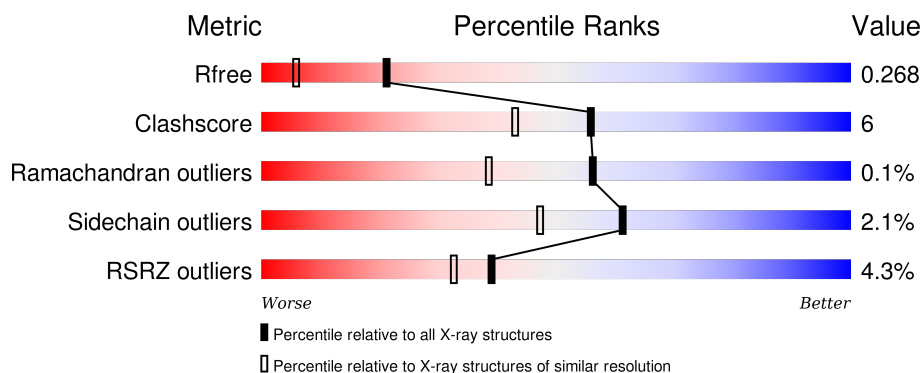
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.80 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	4533 (1.80-1.80)
Clashscore	102246	5383 (1.80-1.80)
Ramachandran outliers	100387	5320 (1.80-1.80)
Sidechain outliers	100360	5319 (1.80-1.80)
RSRZ outliers	91569	4547 (1.80-1.80)

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	392	<div> <div>2%</div> <div>86%</div> <div>11%</div> <div>••</div> </div>
1	B	392	<div> <div>8%</div> <div>80%</div> <div>14%</div> <div>• 5%</div> </div>
1	C	392	<div> <div>5%</div> <div>83%</div> <div>12%</div> <div>••</div> </div>
1	D	392	<div> <div>2%</div> <div>88%</div> <div>10%</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
2	MG	B	393	-	-	-	X
2	MG	B	394	-	-	-	X
2	MG	C	393	-	-	-	X
2	MG	C	394	-	-	-	X
2	MG	D	394	-	-	-	X
3	DGU	A	401	-	-	X	-
4	D54	D	401	-	-	-	X
5	GOL	C	395	-	-	X	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 12829 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 Mandelate racemase/muconate lactonizing protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	385	Total	C	N	O	S	0	2	0
			3053	1930	536	577	10			
1	B	371	Total	C	N	O	S	0	0	0
			2936	1860	512	554	10			
1	C	376	Total	C	N	O	S	0	2	0
			2989	1892	520	567	10			
1	D	385	Total	C	N	O	S	0	0	0
			3033	1919	531	573	10			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	MET	-	EXPRESSION TAG	UNP D3EID5
A	2	SER	-	EXPRESSION TAG	UNP D3EID5
A	3	LEU	-	EXPRESSION TAG	UNP D3EID5
A	385	GLU	-	EXPRESSION TAG	UNP D3EID5
A	386	GLY	-	EXPRESSION TAG	UNP D3EID5
A	387	HIS	-	EXPRESSION TAG	UNP D3EID5
A	388	HIS	-	EXPRESSION TAG	UNP D3EID5
A	389	HIS	-	EXPRESSION TAG	UNP D3EID5
A	390	HIS	-	EXPRESSION TAG	UNP D3EID5
A	391	HIS	-	EXPRESSION TAG	UNP D3EID5
A	392	HIS	-	EXPRESSION TAG	UNP D3EID5
B	1	MET	-	EXPRESSION TAG	UNP D3EID5
B	2	SER	-	EXPRESSION TAG	UNP D3EID5
B	3	LEU	-	EXPRESSION TAG	UNP D3EID5
B	385	GLU	-	EXPRESSION TAG	UNP D3EID5
B	386	GLY	-	EXPRESSION TAG	UNP D3EID5
B	387	HIS	-	EXPRESSION TAG	UNP D3EID5
B	388	HIS	-	EXPRESSION TAG	UNP D3EID5
B	389	HIS	-	EXPRESSION TAG	UNP D3EID5
B	390	HIS	-	EXPRESSION TAG	UNP D3EID5
B	391	HIS	-	EXPRESSION TAG	UNP D3EID5

Continued on next page...

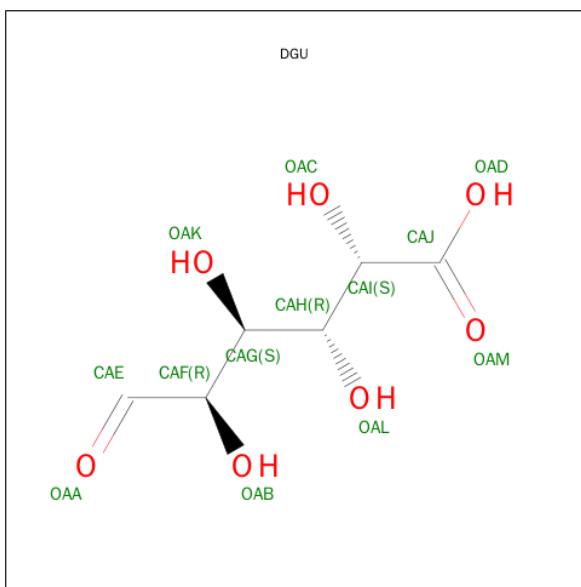
Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	392	HIS	-	EXPRESSION TAG	UNP D3EID5
C	1	MET	-	EXPRESSION TAG	UNP D3EID5
C	2	SER	-	EXPRESSION TAG	UNP D3EID5
C	3	LEU	-	EXPRESSION TAG	UNP D3EID5
C	385	GLU	-	EXPRESSION TAG	UNP D3EID5
C	386	GLY	-	EXPRESSION TAG	UNP D3EID5
C	387	HIS	-	EXPRESSION TAG	UNP D3EID5
C	388	HIS	-	EXPRESSION TAG	UNP D3EID5
C	389	HIS	-	EXPRESSION TAG	UNP D3EID5
C	390	HIS	-	EXPRESSION TAG	UNP D3EID5
C	391	HIS	-	EXPRESSION TAG	UNP D3EID5
C	392	HIS	-	EXPRESSION TAG	UNP D3EID5
D	1	MET	-	EXPRESSION TAG	UNP D3EID5
D	2	SER	-	EXPRESSION TAG	UNP D3EID5
D	3	LEU	-	EXPRESSION TAG	UNP D3EID5
D	385	GLU	-	EXPRESSION TAG	UNP D3EID5
D	386	GLY	-	EXPRESSION TAG	UNP D3EID5
D	387	HIS	-	EXPRESSION TAG	UNP D3EID5
D	388	HIS	-	EXPRESSION TAG	UNP D3EID5
D	389	HIS	-	EXPRESSION TAG	UNP D3EID5
D	390	HIS	-	EXPRESSION TAG	UNP D3EID5
D	391	HIS	-	EXPRESSION TAG	UNP D3EID5
D	392	HIS	-	EXPRESSION TAG	UNP D3EID5

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

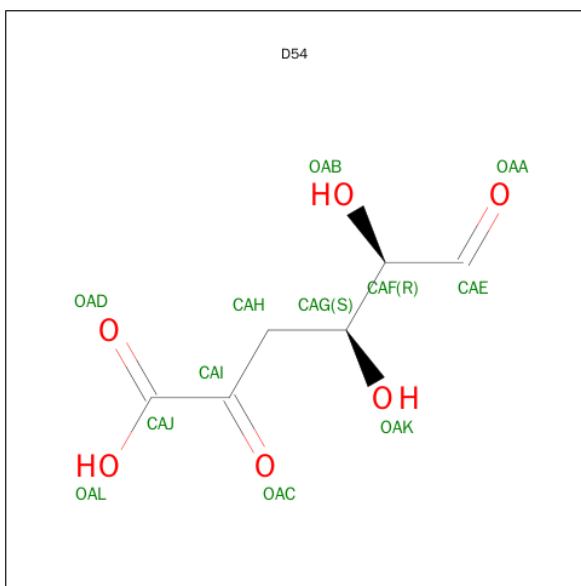
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	B	2	Total Mg 2 2	0	0
2	A	2	Total Mg 2 2	0	0
2	D	2	Total Mg 2 2	0	0
2	C	2	Total Mg 2 2	0	0

- Molecule 3 is D-GALACTURONIC ACID (three-letter code: DGU) (formula: C₆H₁₀O₇).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			13	6	7		

- Molecule 4 is 4-DEOXY-L-THREO-HEX-5-ULOSURONIC ACID (three-letter code: D54) (formula: $C_6H_8O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	B	1	Total	C	O	0	0
			12	6	6		
4	C	1	Total	C	O	0	0
			12	6	6		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	D	1	Total	C	O	0	0
			12	6	6		

- Molecule 5 is GLYCEROL (three-letter code: GOL) (formula: $C_3H_8O_3$).



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

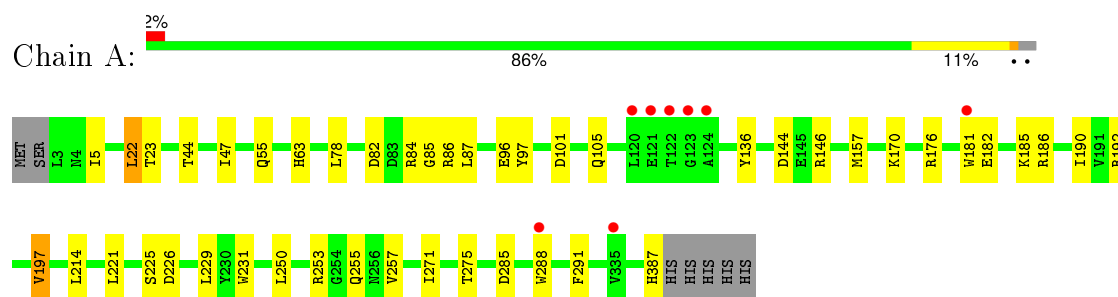
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	249	Total	O	0	0
			249	249		
6	B	129	Total	O	0	0
			129	129		
6	C	145	Total	O	0	0
			145	145		
6	D	232	Total	O	0	0
			232	232		

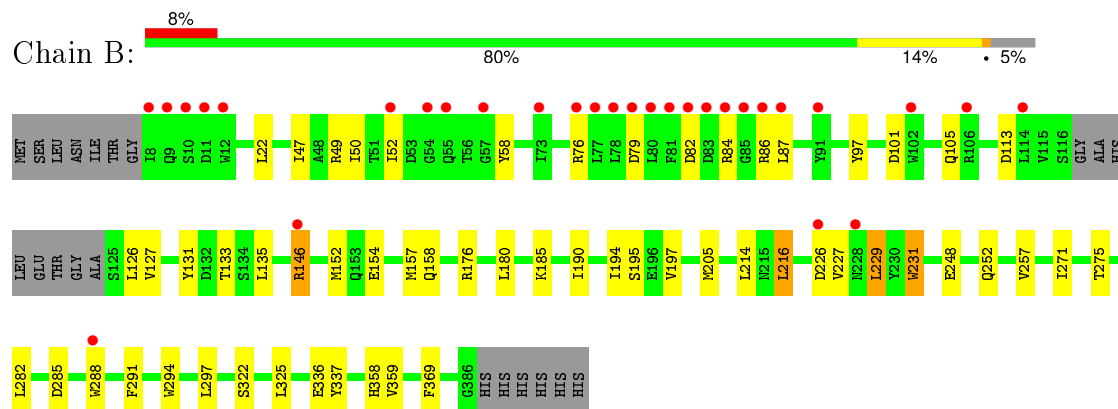
3 Residue-property plots [i](#)

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.

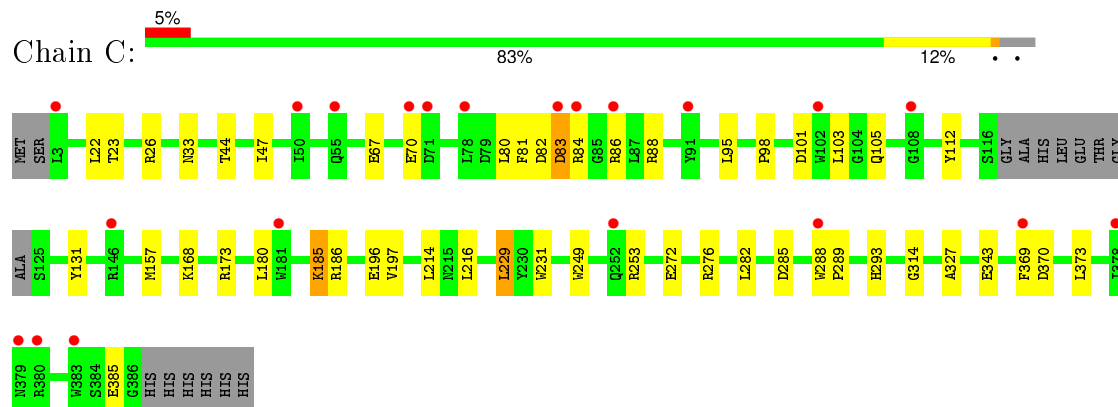
- Molecule 1: Mandelate racemase/muconate lactonizing protein



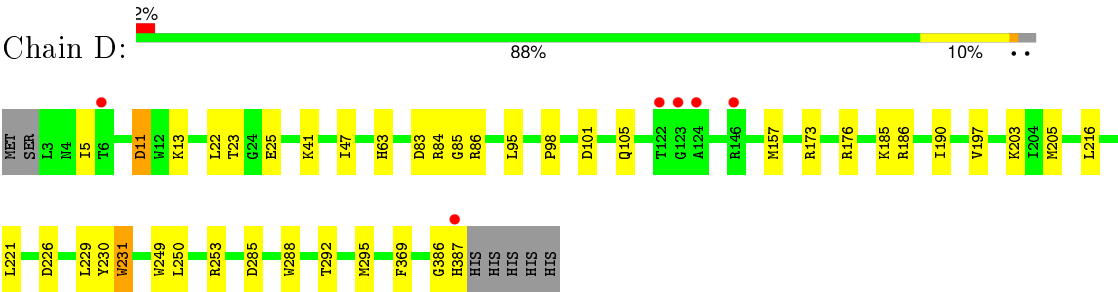
- Molecule 1: Mandelate racemase/muconate lactonizing protein



- Molecule 1: Mandelate racemase/muconate lactonizing protein



● Molecule 1: Mandelate racemase/muconate lactonizing protein



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	158.02Å 66.27Å 154.61Å 90.00° 95.73° 90.00°	Depositor
Resolution (Å)	39.03 – 1.80 39.03 – 1.80	Depositor EDS
% Data completeness (in resolution range)	99.4 (39.03-1.80) 99.4 (39.03-1.80)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.13 (at 1.79Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.221 , 0.270 0.220 , 0.268	Depositor DCC
R_{free} test set	7389 reflections (5.27%)	DCC
Wilson B-factor (Å ²)	24.0	Xtriage
Anisotropy	0.507	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.5	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	0 of 147568 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	12829	wwPDB-VP
Average B, all atoms (Å ²)	32.0	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 25.84 % 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 2.9428e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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, MG, D54, DGU

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	0/3124	0.56	0/4234
1	B	0.32	0/3004	0.50	0/4070
1	C	0.33	0/3057	0.52	0/4142
1	D	0.38	0/3104	0.55	0/4208
All	All	0.35	0/12289	0.53	0/16654

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	3053	0	2942	28	0
1	B	2936	0	2832	41	0
1	C	2989	0	2880	44	0
1	D	3033	0	2925	34	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
3	A	13	0	9	6	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	B	12	0	7	0	0
4	C	12	0	7	1	0
4	D	12	0	7	0	0
5	C	6	0	8	4	0
6	A	249	0	0	3	0
6	B	129	0	0	0	0
6	C	145	0	0	0	0
6	D	232	0	0	1	0
All	All	12829	0	11617	147	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 6.

All (147) 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:26:ARG:HH22	5:C:395:GOL:H12	1.16	1.09
1:D:22:LEU:HD22	1:D:47:ILE:HD12	1.47	0.94
1:C:26:ARG:HH22	5:C:395:GOL:C1	1.83	0.91
1:B:22:LEU:HD22	1:B:47:ILE:HD12	1.58	0.85
1:B:82:ASP:HB2	1:B:86:ARG:H	1.40	0.84
1:C:26:ARG:NH2	5:C:395:GOL:H12	1.95	0.81
3:A:401:DGU:OAL	3:A:401:DGU:HAE	1.80	0.80
1:C:22:LEU:HD22	1:C:47:ILE:HD12	1.61	0.80
1:A:84:ARG:HD3	1:A:86:ARG:HH21	1.49	0.78
1:D:84:ARG:HD3	1:D:86:ARG:HH21	1.50	0.76
1:A:157:MET:SD	1:A:197:VAL:HG13	2.30	0.71
1:D:5:ILE:HD13	1:D:85:GLY:HA2	1.74	0.69
1:D:22:LEU:HD22	1:D:47:ILE:CD1	2.24	0.68
1:A:5:ILE:HD13	1:A:85:GLY:HA2	1.76	0.67
1:D:292:THR:HA	1:D:295:MET:HE2	1.77	0.66
1:A:170:LYS:NZ	3:A:401:DGU:HAI	2.12	0.64
1:D:157:MET:SD	1:D:197:VAL:HG13	2.37	0.64
1:C:82:ASP:C	1:C:84:ARG:H	2.02	0.63
1:B:101:ASP:O	1:B:105:GLN:HG2	1.97	0.63
1:D:173:ARG:HD3	1:D:186:ARG:HG2	1.81	0.63
1:B:84:ARG:HD3	1:B:86:ARG:HH21	1.65	0.62
1:D:47:ILE:HD13	1:D:369:PHE:CE1	2.35	0.61
1:B:127:VAL:HG22	1:B:358:HIS:CD2	2.35	0.61
1:C:84:ARG:HD3	1:C:86:ARG:HH21	1.66	0.61
1:B:82:ASP:HB3	1:B:84:ARG:H	1.65	0.61

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:47:ILE:CD1	1:D:369:PHE:CE1	2.85	0.60
1:B:285:ASP:HB3	1:B:288:TRP:O	2.01	0.60
1:D:221:LEU:HD13	1:D:250:LEU:HD21	1.83	0.60
1:D:84:ARG:HD3	1:D:86:ARG:NH2	2.17	0.59
1:C:214:LEU:HD23	1:D:176:ARG:HG3	1.84	0.59
1:B:135:LEU:HD13	1:B:194:ILE:HD13	1.86	0.58
1:C:285:ASP:HB3	1:C:288:TRP:O	2.04	0.57
1:C:101:ASP:O	1:C:105:GLN:HG2	2.04	0.57
1:C:249:TRP:O	1:C:253:ARG:HG3	2.04	0.57
1:B:82:ASP:C	1:B:84:ARG:H	2.07	0.57
1:A:55:GLN:HB2	6:A:592:HOH:O	2.05	0.56
1:D:25:GLU:OE1	1:D:41:LYS:HE3	2.06	0.55
1:B:146:ARG:HH11	1:B:146:ARG:HB2	1.71	0.55
1:C:47:ILE:CD1	1:C:369:PHE:CE1	2.90	0.55
1:A:176:ARG:HG3	1:B:214:LEU:HD23	1.88	0.55
1:D:249:TRP:CZ2	1:D:253:ARG:HD2	2.42	0.54
1:A:185:LYS:HE3	6:A:517:HOH:O	2.07	0.54
1:C:157:MET:SD	1:C:197:VAL:HG13	2.47	0.54
1:A:181:TRP:CH2	1:A:185:LYS:HD3	2.43	0.54
1:C:173:ARG:HD3	1:C:186:ARG:HG2	1.89	0.54
1:A:23:THR:HG22	1:A:44:THR:HG22	1.90	0.53
1:B:195:SER:HB2	1:B:227:VAL:HG13	1.91	0.53
1:B:47:ILE:HD13	1:B:369:PHE:CE1	2.44	0.52
1:A:253:ARG:HG3	6:A:492:HOH:O	2.08	0.52
1:B:282:LEU:HD22	1:B:282:LEU:N	2.24	0.52
1:D:386:GLY:C	1:D:387:HIS:CG	2.82	0.52
3:A:401:DGU:OAL	3:A:401:DGU:CAE	2.56	0.51
1:C:84:ARG:CD	1:C:86:ARG:HH21	2.23	0.51
1:B:76:ARG:HB2	1:B:79:ASP:OD2	2.11	0.51
1:C:84:ARG:HD3	1:C:86:ARG:NH2	2.24	0.51
1:C:23:THR:HG22	1:C:44:THR:HG22	1.92	0.51
1:D:47:ILE:CD1	1:D:369:PHE:HE1	2.24	0.50
1:D:249:TRP:O	1:D:253:ARG:HG3	2.11	0.50
1:A:101:ASP:O	1:A:105:GLN:HG2	2.12	0.50
1:C:82:ASP:OD2	1:C:86:ARG:HB2	2.11	0.50
1:D:285:ASP:HB3	1:D:288:TRP:O	2.11	0.50
1:B:82:ASP:OD2	1:B:86:ARG:HB2	2.12	0.50
1:B:84:ARG:CD	1:B:86:ARG:HH21	2.24	0.49
1:D:288:TRP:O	1:D:288:TRP:CE3	2.66	0.49
1:A:285:ASP:HB3	1:A:288:TRP:O	2.12	0.49
1:C:81:PHE:HZ	1:C:103:LEU:HD11	1.77	0.49

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:180:LEU:HD22	1:D:216:LEU:HG	1.94	0.49
4:C:401:D54:HAH	4:C:401:D54:HAE	1.57	0.48
1:C:314:GLY:HA2	5:C:395:GOL:H11	1.95	0.48
1:C:84:ARG:NE	1:C:86:ARG:HH21	2.12	0.48
1:B:205:MET:HG2	1:B:231:TRP:CG	2.49	0.48
1:D:5:ILE:CD1	1:D:85:GLY:HA2	2.44	0.48
1:C:289:PRO:HB2	1:C:293:HIS:CG	2.49	0.48
1:C:82:ASP:O	1:C:84:ARG:N	2.43	0.47
1:C:81:PHE:CZ	1:C:103:LEU:HD11	2.49	0.47
1:C:370:ASP:HB3	1:C:373:LEU:HB3	1.94	0.47
1:A:170:LYS:HZ1	3:A:401:DGU:HAI	1.79	0.47
1:B:248:GLU:O	1:B:252:GLN:HG2	2.15	0.47
1:C:272[A]:GLU:HG2	1:C:276:ARG:NH1	2.29	0.47
1:B:22:LEU:HD22	1:B:47:ILE:CD1	2.36	0.47
1:B:146:ARG:HB2	1:B:146:ARG:NH1	2.30	0.47
1:B:205:MET:HG2	1:B:231:TRP:CD2	2.49	0.47
1:B:50:ILE:HD13	1:B:52:ILE:HD11	1.97	0.47
3:A:401:DGU:HOAL	3:A:401:DGU:HAE	1.79	0.47
1:A:22:LEU:HD22	1:A:47:ILE:HG13	1.97	0.47
1:B:157:MET:SD	1:B:197:VAL:HG13	2.55	0.46
1:D:205:MET:HG2	1:D:231:TRP:CG	2.51	0.46
1:A:181:TRP:CE3	1:A:182[A]:GLU:HG3	2.50	0.46
1:C:82:ASP:C	1:C:84:ARG:N	2.69	0.46
1:A:186:ARG:O	1:A:190:ILE:HG12	2.15	0.46
1:D:95:LEU:C	1:D:98:PRO:HD2	2.37	0.45
1:C:180:LEU:HD11	1:C:216:LEU:HD11	1.99	0.45
1:B:271:ILE:O	1:B:275:THR:HG23	2.16	0.45
1:C:249:TRP:CE2	1:C:253:ARG:HD2	2.52	0.45
1:B:49:ARG:HD3	1:B:58:TYR:CZ	2.52	0.45
1:D:186:ARG:O	1:D:190:ILE:HG12	2.16	0.45
1:B:229:LEU:HB3	1:B:257:VAL:HG22	1.99	0.45
1:C:249:TRP:CZ2	1:C:253:ARG:HD2	2.52	0.45
1:D:47:ILE:HD11	1:D:369:PHE:HE1	1.82	0.44
1:D:203:LYS:HD3	1:D:230:TYR:CD1	2.52	0.44
1:A:214:LEU:HD23	1:B:176:ARG:HG3	1.99	0.44
1:D:185:LYS:HE2	1:D:185:LYS:HB3	1.41	0.44
1:A:170:LYS:HZ2	3:A:401:DGU:HAI	1.81	0.44
1:A:82:ASP:OD2	1:A:86:ARG:HB2	2.18	0.44
1:B:231:TRP:C	1:B:231:TRP:CD1	2.91	0.44
1:A:97:TYR:CZ	1:A:291:PHE:HB2	2.52	0.44
1:D:47:ILE:HD11	1:D:369:PHE:CE1	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:249:TRP:CE2	1:D:253:ARG:HD2	2.53	0.44
1:A:221:LEU:HD13	1:A:250:LEU:HD21	2.00	0.44
1:B:154:GLU:O	1:B:158:GLN:HG3	2.19	0.43
1:D:11:ASP:O	1:D:13:LYS:HG3	2.18	0.43
1:D:23:THR:HG23	6:D:477:HOH:O	2.18	0.43
1:A:181:TRP:HE3	1:A:182[A]:GLU:HG3	1.83	0.43
1:C:272[A]:GLU:CG	1:C:276:ARG:HH12	2.32	0.43
1:C:112:TYR:HB2	1:C:327:ALA:CB	2.49	0.43
1:D:101:ASP:O	1:D:105:GLN:HG2	2.19	0.43
1:D:226:ASP:OD1	1:D:226:ASP:N	2.44	0.43
1:C:47:ILE:HD13	1:C:369:PHE:CE1	2.54	0.43
1:B:205:MET:HG2	1:B:231:TRP:CD1	2.54	0.43
1:B:294:TRP:CZ3	1:B:297:LEU:HD23	2.54	0.43
1:B:282:LEU:CD2	1:B:282:LEU:N	2.83	0.42
1:C:70:GLU:HG2	1:C:385:GLU:OE1	2.18	0.42
1:C:80:LEU:O	1:C:88:ARG:HG3	2.19	0.42
1:B:180:LEU:HD11	1:B:216:LEU:HD11	2.02	0.42
1:A:255:GLN:HG2	1:A:257:VAL:HG23	2.00	0.42
1:C:282:LEU:N	1:C:282:LEU:HD22	2.35	0.42
1:A:144:ASP:OD1	1:A:146:ARG:HB2	2.19	0.42
1:B:131:TYR:CE1	1:B:336:GLU:HG3	2.55	0.42
1:B:133:THR:HG22	1:B:337:TYR:O	2.20	0.42
1:A:136:TYR:CZ	1:A:170:LYS:HE2	2.55	0.42
1:C:95:LEU:C	1:C:98:PRO:HD2	2.39	0.42
1:C:67:GLU:O	1:C:70:GLU:HB2	2.20	0.41
1:C:229:LEU:HA	1:C:229:LEU:HD12	1.89	0.41
1:C:33:ASN:OD1	1:C:33:ASN:C	2.58	0.41
1:C:22:LEU:CD2	1:C:47:ILE:HD12	2.43	0.41
1:B:152:MET:HG3	1:B:190:ILE:HD12	2.03	0.41
1:C:185:LYS:HE2	1:C:185:LYS:HB3	1.85	0.41
1:B:97:TYR:CZ	1:B:291:PHE:HB2	2.56	0.41
1:B:322:SER:O	1:B:325:LEU:HB3	2.20	0.41
1:B:205:MET:HG2	1:B:231:TRP:CE2	2.56	0.41
1:C:131:TYR:CE1	1:C:168:LYS:HE2	2.55	0.41
1:D:157:MET:SD	1:D:197:VAL:CG1	3.07	0.40
1:A:87:LEU:CD2	1:A:96:GLU:HA	2.51	0.40
1:B:126:LEU:HB3	1:B:359:VAL:HB	2.03	0.40
1:A:271:ILE:O	1:A:275:THR:HG23	2.21	0.40
1:C:23:THR:O	1:C:343:GLU:HG2	2.21	0.40
1:A:192[B]:ARG:NH2	1:A:226:ASP:OD1	2.55	0.40

There are no symmetry-related clashes.

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	385/392 (98%)	381 (99%)	4 (1%)	0	100	100
1	B	367/392 (94%)	355 (97%)	12 (3%)	0	100	100
1	C	374/392 (95%)	366 (98%)	7 (2%)	1 (0%)	46	29
1	D	383/392 (98%)	376 (98%)	7 (2%)	0	100	100
All	All	1509/1568 (96%)	1478 (98%)	30 (2%)	1 (0%)	56	38

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	83	ASP

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	311/316 (98%)	303 (97%)	8 (3%)	54	37
1	B	300/316 (95%)	292 (97%)	8 (3%)	52	36
1	C	306/316 (97%)	301 (98%)	5 (2%)	70	59
1	D	309/316 (98%)	304 (98%)	5 (2%)	70	59
All	All	1226/1264 (97%)	1200 (98%)	26 (2%)	61	47

All (26) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	22	LEU
1	A	63	HIS
1	A	78	LEU
1	A	197	VAL
1	A	225	SER
1	A	229	LEU
1	A	231	TRP
1	A	387	HIS
1	B	87	LEU
1	B	113	ASP
1	B	146	ARG
1	B	185	LYS
1	B	216	LEU
1	B	226	ASP
1	B	229	LEU
1	B	231	TRP
1	C	83	ASP
1	C	185	LYS
1	C	196	GLU
1	C	229	LEU
1	C	231	TRP
1	D	11	ASP
1	D	63	HIS
1	D	83	ASP
1	D	229	LEU
1	D	231	TRP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (1) such sidechains are listed below:

Mol	Chain	Res	Type
1	B	358	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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](#)

Of 13 ligands modelled in this entry, 8 are monoatomic - leaving 5 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	DGU	A	401	2	8,12,12	1.16	1 (12%)	10,16,16	0.60	0
4	D54	B	401	2	8,11,11	1.31	2 (25%)	4,14,14	0.83	0
5	GOL	C	395	-	5,5,5	0.31	0	5,5,5	0.30	0
4	D54	C	401	2	8,11,11	1.39	2 (25%)	4,14,14	0.81	0
4	D54	D	401	2	8,11,11	1.74	3 (37%)	4,14,14	1.34	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
3	DGU	A	401	2	-	0/12/18/18	0/0/0/0
4	D54	B	401	2	-	0/8/14/14	0/0/0/0
5	GOL	C	395	-	-	0/4/4/4	0/0/0/0
4	D54	C	401	2	-	0/8/14/14	0/0/0/0
4	D54	D	401	2	-	0/8/14/14	0/0/0/0

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	401	D54	CAH-CAI	2.11	1.54	1.51
4	C	401	D54	CAH-CAI	2.14	1.54	1.51
4	B	401	D54	CAF-CAE	2.22	1.54	1.50
4	D	401	D54	CAG-CAF	2.36	1.55	1.53

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	401	D54	CAF-CAE	2.52	1.54	1.50
4	C	401	D54	CAF-CAE	2.54	1.54	1.50
3	A	401	DGU	CAF-CAE	2.69	1.55	1.50
4	D	401	D54	CAH-CAI	2.71	1.55	1.51

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	401	DGU	6	0
5	C	395	GOL	4	0
4	C	401	D54	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	385/392 (98%)	0.11	8 (2%) 67 62	17, 25, 41, 69	0
1	B	371/392 (94%)	0.65	30 (8%) 15 11	23, 37, 56, 92	0
1	C	376/392 (95%)	0.45	21 (5%) 28 22	22, 33, 52, 77	0
1	D	385/392 (98%)	0.03	6 (1%) 74 71	19, 27, 43, 63	0
All	All	1517/1568 (96%)	0.30	65 (4%) 39 32	17, 30, 52, 92	0

All (65) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	124	ALA	6.0
1	B	84	ARG	5.8
1	B	86	ARG	5.6
1	A	181	TRP	5.4
1	B	8	ILE	5.2
1	C	181	TRP	5.1
1	B	102	TRP	4.8
1	C	83	ASP	4.8
1	B	83	ASP	4.5
1	B	82	ASP	4.3
1	B	73	ILE	4.2
1	C	288	TRP	4.1
1	B	288	TRP	4.0
1	C	86	ARG	3.9
1	D	387	HIS	3.9
1	B	12	TRP	3.8
1	A	122	THR	3.6
1	B	80	LEU	3.5
1	C	3	LEU	3.5
1	A	121	GLU	3.4
1	B	77	LEU	3.3

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	C	84	ARG	3.3
1	B	226	ASP	3.3
1	B	146	ARG	3.2
1	B	52	ILE	3.1
1	A	120	LEU	3.1
1	C	70	GLU	3.0
1	B	78	LEU	2.9
1	B	76	ARG	2.9
1	B	79	ASP	2.8
1	D	123	GLY	2.8
1	A	123	GLY	2.7
1	C	380	ARG	2.6
1	B	106	ARG	2.6
1	B	11	ASP	2.6
1	B	57	GLY	2.5
1	C	146	ARG	2.5
1	B	228	ASN	2.4
1	C	91	TYR	2.4
1	C	78	LEU	2.4
1	B	91	TYR	2.4
1	D	124	ALA	2.4
1	D	6	THR	2.4
1	B	9	GLN	2.4
1	B	81	PHE	2.3
1	C	55	GLN	2.3
1	B	114	LEU	2.3
1	C	378	ILE	2.3
1	D	146	ARG	2.3
1	C	383	TRP	2.3
1	C	379	ASN	2.3
1	C	71	ASP	2.3
1	C	252	GLN	2.3
1	A	288	TRP	2.2
1	C	102	TRP	2.2
1	C	108	GLY	2.2
1	B	54	GLY	2.2
1	B	85	GLY	2.2
1	D	122	THR	2.2
1	B	10	SER	2.1
1	C	50	ILE	2.1
1	C	369	PHE	2.1
1	B	55	GLN	2.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	335	VAL	2.0
1	B	87	LEU	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. 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
5	GOL	C	395	6/6	0.83	0.29	9.51	25,40,42,45	0
2	MG	C	394	1/1	0.97	0.18	6.55	27,27,27,27	0
2	MG	B	394	1/1	0.97	0.19	4.47	26,26,26,26	0
4	D54	D	401	12/12	0.84	0.16	2.85	25,32,42,42	0
2	MG	B	393	1/1	0.97	0.23	2.63	29,29,29,29	0
2	MG	D	394	1/1	0.99	0.13	2.33	25,25,25,25	0
2	MG	C	393	1/1	0.98	0.17	2.32	22,22,22,22	0
4	D54	C	401	12/12	0.81	0.16	1.77	23,33,40,47	0
2	MG	A	394	1/1	0.97	0.12	1.40	23,23,23,23	0
2	MG	A	393	1/1	0.96	0.15	1.23	26,26,26,26	0
2	MG	D	393	1/1	0.99	0.12	0.73	23,23,23,23	0
3	DGU	A	401	13/13	0.90	0.13	0.64	20,29,38,44	0
4	D54	B	401	12/12	0.88	0.13	-0.57	26,33,38,43	0

6.5 Other polymers [i](#)

There are no such residues in this entry.