



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 11:38 AM GMT

PDB ID : 3PKQ
Title : Q83D Variant of S. Enterica RmlA with dGTP
Authors : Chang, A.; Moretti, R.; Bingman, C.A.; Thorson, J.S.; Phillips Jr., G.N.;
Center for Eukaryotic Structural Genomics (CESG)
Deposited on : 2010-11-11
Resolution : 2.40 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

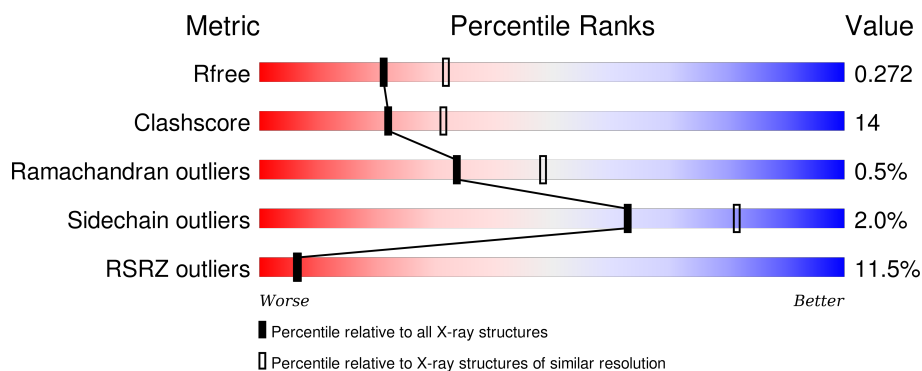
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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	292	 3% 76% 21% ..
1	B	292	 4% 72% 25% ..
1	C	292	 17% 71% 25% ..
1	D	292	 20% 72% 23% 5%

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 crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	PEG	A	293	-	-	-	X
4	PEG	A	294	-	-	X	X
4	PEG	C	293	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 9278 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.

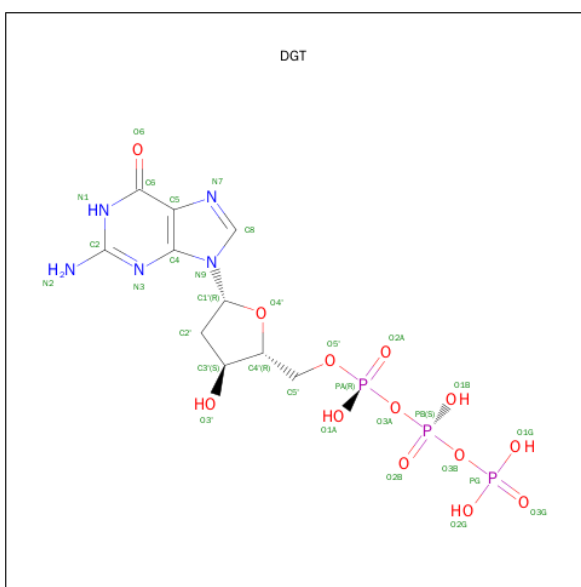
- Molecule 1 is a protein called Glucose-1-phosphate thymidyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	285	Total	C	N	O	S	0	3	0
			2251	1440	372	428	11			
1	B	286	Total	C	N	O	S	0	3	0
			2259	1446	374	427	12			
1	C	284	Total	C	N	O	S	0	0	0
			2221	1424	367	419	11			
1	D	278	Total	C	N	O	S	0	0	0
			2172	1394	358	409	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	ASP	GLN	ENGINEERED MUTATION	UNP P26393
B	83	ASP	GLN	ENGINEERED MUTATION	UNP P26393
C	83	ASP	GLN	ENGINEERED MUTATION	UNP P26393
D	83	ASP	GLN	ENGINEERED MUTATION	UNP P26393

- Molecule 2 is 2'-DEOXYGUANOSINE-5'-TRIPHOSPHATE (three-letter code: DGT) (formula: C₁₀H₁₆N₅O₁₃P₃).

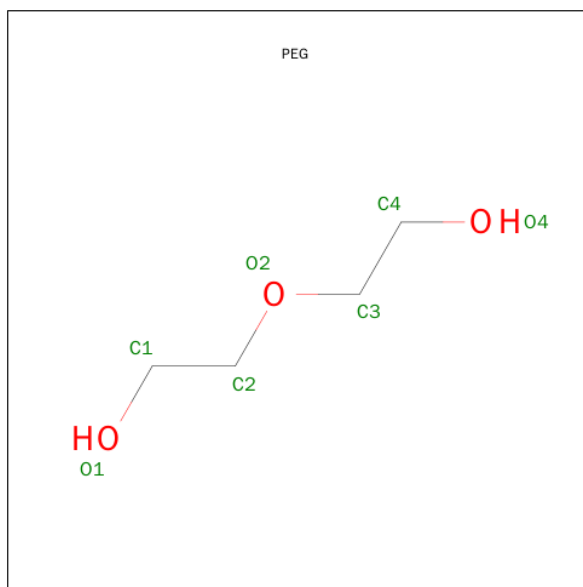


Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
2	A	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	B	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	C	1	Total	C	N	O	P	0	0
			31	10	5	13	3		
2	D	1	Total	C	N	O	P	0	0
			31	10	5	13	3		

- Molecule 3 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	2	Total	Mg	0	0
			2	2		
3	A	1	Total	Mg	0	0
			1	1		
3	D	1	Total	Mg	0	0
			1	1		
3	C	1	Total	Mg	0	0
			1	1		

- Molecule 4 is DI(HYDROXYETHYL)ETHER (three-letter code: PEG) (formula: C₄H₁₀O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			7	4	3		
4	A	1	Total	C	O	0	0
			7	4	3		
4	C	1	Total	C	O	0	0
			7	4	3		

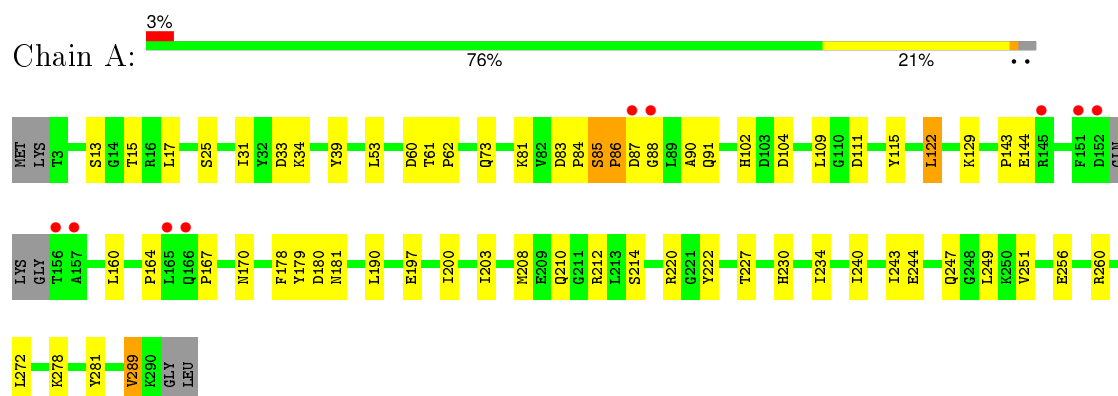
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	98	Total	O	0	0
			98	98		
5	B	83	Total	O	0	0
			83	83		
5	C	28	Total	O	0	0
			28	28		
5	D	16	Total	O	0	0
			16	16		

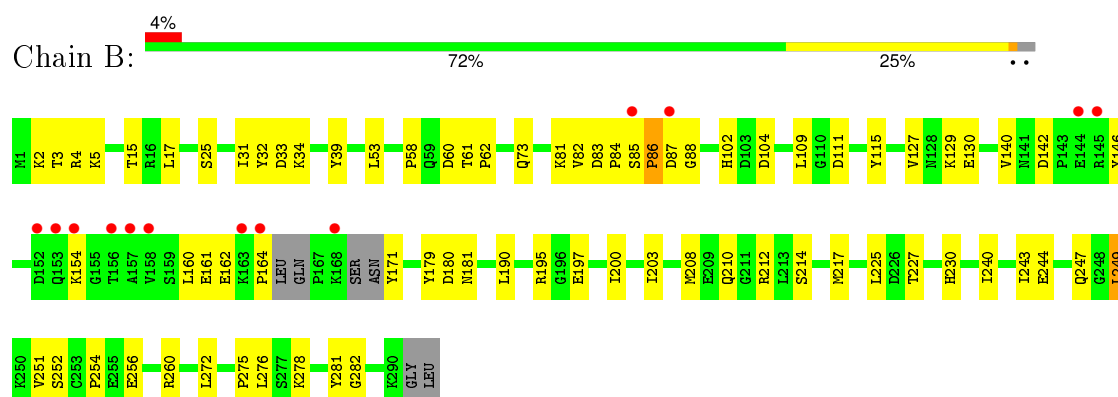
3 Residue-property plots [i](#)

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.

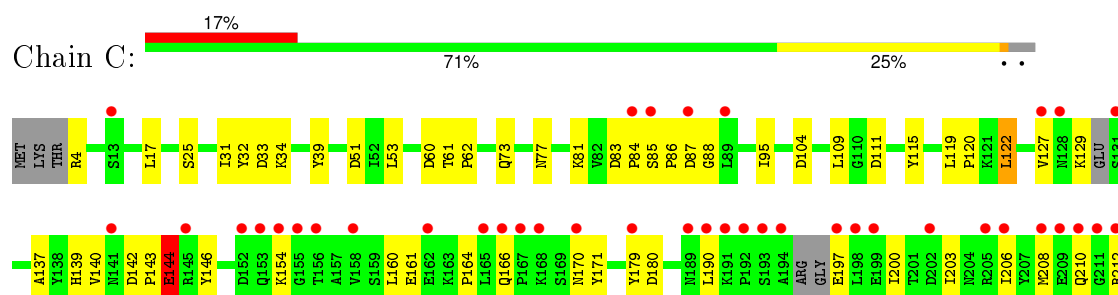
- Molecule 1: Glucose-1-phosphate thymidyltransferase

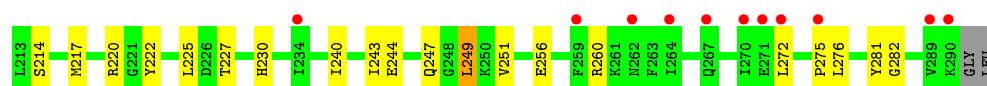


- Molecule 1: Glucose-1-phosphate thymidyltransferase

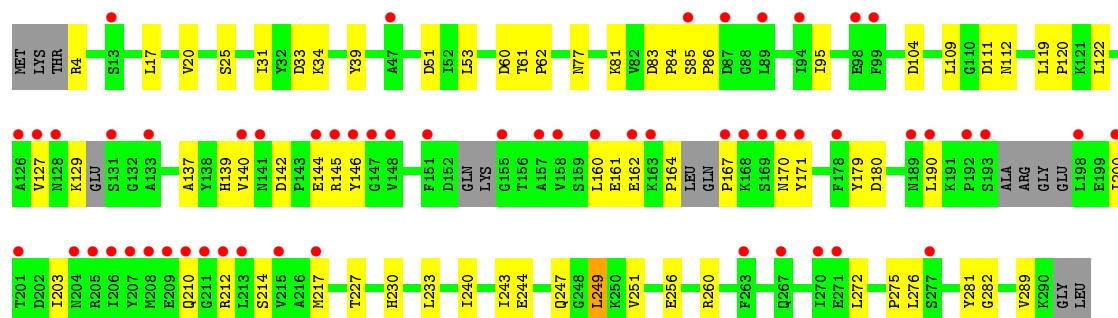


- Molecule 1: Glucose-1-phosphate thymidyltransferase





● Molecule 1: Glucose-1-phosphate thymidyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 41	Depositor
Cell constants a, b, c, α , β , γ	109.40Å 109.40Å 110.08Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.71 – 2.40 44.71 – 2.40	Depositor EDS
% Data completeness (in resolution range)	97.4 (44.71-2.40) 97.4 (44.71-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.32 (at 2.39Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.6.4_486)	Depositor
R, R_{free}	0.212 , 0.271 0.213 , 0.272	Depositor DCC
R_{free} test set	2516 reflections (5.37%)	DCC
Wilson B-factor (Å ²)	43.2	Xtriage
Anisotropy	0.025	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 54.8	EDS
Estimated twinning fraction	0.025 for -h,-l,-k 0.014 for -h,l,k 0.013 for l,-k,h 0.026 for -l,-k,-h 0.064 for h,-k,-l	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.47$, $\langle L^2 \rangle = 0.30$	Xtriage
Outliers	0 of 49380 reflections	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	9278	wwPDB-VP
Average B, all atoms (Å ²)	57.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% of the height of the origin peak. No significant pseudotranslation is detected.*

¹ Intensities estimated from amplitudes.

² Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.375 respectively for untwinned datasets, and 0.333, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: MG, PEG, DGT

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	0.53	0/2298	0.60	0/3113
1	B	0.48	0/2305	0.57	0/3116
1	C	0.39	0/2266	0.57	2/3066 (0.1%)
1	D	0.37	0/2215	0.56	0/2994
All	All	0.45	0/9084	0.58	2/12289 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	144	GLU	CA-CB-CG	5.55	125.62	113.40
1	C	225	LEU	CA-CB-CG	5.29	127.46	115.30

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	2251	0	2243	75	0
1	B	2259	0	2262	78	0
1	C	2221	0	2222	68	0
1	D	2172	0	2170	54	0
2	A	31	0	12	6	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	B	31	0	12	2	0
2	C	31	0	12	1	0
2	D	31	0	12	2	0
3	A	1	0	0	0	0
3	B	2	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	14	0	20	6	0
4	C	7	0	10	3	0
5	A	98	0	0	3	0
5	B	83	0	0	7	0
5	C	28	0	0	1	0
5	D	16	0	0	3	0
All	All	9278	0	8975	251	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 14.

All (251) 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:86[B]:PRO:HB2	1:B:87[B]:ASP:HA	1.27	1.15
1:C:87:ASP:HB3	1:C:197:GLU:HG3	1.17	1.09
1:C:33:ASP:HB2	1:D:230:HIS:ND1	1.77	1.00
1:B:86[B]:PRO:HB2	1:B:87[B]:ASP:CA	1.93	0.99
1:D:142:ASP:HB2	1:D:144:GLU:OE2	1.62	0.98
1:A:87[A]:ASP:HB3	1:A:197:GLU:HG3	1.46	0.95
1:A:200:ILE:HB	5:A:380:HOH:O	1.67	0.93
1:A:234:ILE:HB	4:A:294:PEG:H11	1.48	0.92
1:A:33:ASP:HB2	1:B:230:HIS:ND1	1.84	0.91
1:A:230:HIS:ND1	1:B:33:ASP:HB2	1.87	0.90
1:C:33:ASP:CB	1:D:230:HIS:ND1	2.36	0.88
1:A:87[B]:ASP:HB3	1:A:197:GLU:HG3	1.53	0.88
1:C:87:ASP:HB3	1:C:197:GLU:CG	2.04	0.87
1:A:88:GLY:N	1:A:197:GLU:HG2	1.90	0.86
1:B:88:GLY:N	1:B:197:GLU:HG2	1.91	0.85
1:A:33:ASP:CB	1:B:230:HIS:ND1	2.40	0.85
4:C:293:PEG:H41	1:D:233:LEU:HD23	1.61	0.82
1:B:247:GLN:NE2	1:C:115:TYR:HE2	1.76	0.82
1:C:88:GLY:N	1:C:197:GLU:HG2	1.95	0.81
1:B:247:GLN:NE2	1:C:115:TYR:CE2	2.50	0.80

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:86[B]:PRO:CB	1:A:87[B]:ASP:HA	2.12	0.79
1:A:230:HIS:ND1	1:B:33:ASP:CB	2.46	0.79
1:B:115:TYR:HE2	1:C:247:GLN:NE2	1.83	0.77
1:B:86[B]:PRO:HD3	2:B:500:DGT:O6	1.85	0.76
1:A:86[B]:PRO:HD2	2:A:500:DGT:O6	1.86	0.75
1:C:230:HIS:ND1	1:D:33:ASP:HB2	2.03	0.74
1:A:86[B]:PRO:HB3	1:A:87[B]:ASP:C	2.08	0.73
1:B:115:TYR:CE2	1:C:247:GLN:NE2	2.57	0.73
1:C:33:ASP:HB2	1:D:230:HIS:CE1	2.24	0.73
1:A:86[B]:PRO:HB3	1:A:88:GLY:N	2.04	0.73
1:A:86[B]:PRO:CB	1:A:87[B]:ASP:CA	2.66	0.72
1:A:87[B]:ASP:HB3	1:A:197:GLU:CG	2.19	0.72
1:A:87[A]:ASP:HB3	1:A:197:GLU:CG	2.20	0.71
1:B:87[B]:ASP:HB3	1:B:197:GLU:HG3	1.73	0.71
1:B:85[A]:SER:N	1:B:86[A]:PRO:HD3	2.05	0.70
1:B:86[B]:PRO:CB	1:B:87[B]:ASP:CA	2.71	0.69
1:B:247:GLN:HE22	1:C:115:TYR:HE2	1.42	0.67
1:D:142:ASP:CB	1:D:144:GLU:OE2	2.38	0.67
1:B:86[B]:PRO:HB3	1:B:88:GLY:N	2.10	0.66
1:B:86[B]:PRO:CB	1:B:88:GLY:N	2.57	0.66
1:A:115:TYR:HE2	1:D:247:GLN:NE2	1.94	0.65
1:A:86[B]:PRO:HB3	1:A:87[B]:ASP:CA	2.27	0.65
1:A:33:ASP:HB2	1:B:230:HIS:CE1	2.31	0.65
1:B:115:TYR:HE2	1:C:247:GLN:HE22	1.45	0.65
1:A:86[B]:PRO:HB3	1:A:87[B]:ASP:HA	1.81	0.63
1:A:234:ILE:CB	4:A:294:PEG:H11	2.24	0.62
1:A:230:HIS:CE1	1:B:33:ASP:HB2	2.34	0.62
1:C:32:TYR:O	4:C:293:PEG:H42	2.00	0.62
1:B:58:PRO:HA	1:B:82:VAL:HG11	1.81	0.62
1:C:144:GLU:CD	1:C:144:GLU:H	2.03	0.61
1:C:85:SER:N	1:C:86:PRO:HD3	2.14	0.61
1:A:86[B]:PRO:HB2	1:A:87[B]:ASP:HA	1.81	0.61
1:D:85:SER:N	1:D:86:PRO:HD3	2.15	0.61
1:A:84:PRO:C	1:A:86[A]:PRO:HD3	2.21	0.61
1:B:84:PRO:O	1:B:85[B]:SER:HB2	2.02	0.60
1:A:86[B]:PRO:HG2	2:A:500:DGT:O6	2.02	0.59
1:D:109:LEU:HB3	2:D:500:DGT:H4'	1.85	0.58
1:C:230:HIS:ND1	1:D:33:ASP:CB	2.66	0.58
1:B:86[B]:PRO:HB2	1:B:88:GLY:N	2.19	0.57
1:B:243:ILE:HG23	1:B:247:GLN:OE1	2.03	0.57
1:D:83:ASP:C	1:D:85:SER:H	2.07	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:15:THR:HB	5:B:358:HOH:O	2.05	0.57
1:C:83:ASP:C	1:C:85:SER:H	2.08	0.56
1:B:249:LEU:HB3	1:C:220:ARG:HG3	1.87	0.56
1:B:160:LEU:HD12	1:B:208:MET:HE2	1.87	0.56
1:D:210:GLN:OE1	1:D:212:ARG:HD3	2.06	0.56
1:C:34:LYS:HE2	1:C:251:VAL:O	2.05	0.56
1:B:61:THR:OG1	1:B:82:VAL:HG22	2.06	0.56
1:A:115:TYR:CE2	1:D:247:GLN:NE2	2.73	0.55
1:C:144:GLU:OE1	1:C:144:GLU:N	2.38	0.55
1:C:210:GLN:OE1	1:C:212:ARG:HD3	2.06	0.55
1:C:109:LEU:HB3	2:C:500:DGT:H4'	1.87	0.55
1:A:17:LEU:HD23	1:A:230:HIS:HD2	1.71	0.55
1:B:142:ASP:OD1	1:B:142:ASP:N	2.39	0.55
1:D:17:LEU:HD23	1:D:230:HIS:HD2	1.72	0.55
1:D:144:GLU:N	1:D:144:GLU:OE1	2.30	0.55
1:C:160:LEU:HD12	1:C:208:MET:HE2	1.89	0.54
4:A:294:PEG:H12	1:B:32:TYR:HA	1.89	0.54
1:B:109:LEU:HB3	2:B:500:DGT:H4'	1.88	0.54
1:C:142:ASP:OD1	1:C:142:ASP:N	2.40	0.54
1:D:256:GLU:O	1:D:260:ARG:HG2	2.07	0.54
1:C:17:LEU:HD23	1:C:230:HIS:HD2	1.73	0.54
1:D:167:PRO:CD	5:D:308:HOH:O	2.56	0.54
1:B:2:LYS:HG2	5:B:319:HOH:O	2.07	0.54
1:B:225:LEU:CD2	5:B:366:HOH:O	2.55	0.54
1:C:53:LEU:HD11	1:C:81:LYS:HG3	1.90	0.54
1:A:179:TYR:O	4:A:293:PEG:H31	2.07	0.54
1:B:87[B]:ASP:HB3	1:B:197:GLU:CG	2.38	0.53
1:D:53:LEU:HD11	1:D:81:LYS:HG3	1.91	0.53
1:A:210:GLN:OE1	1:A:212:ARG:HD3	2.08	0.53
1:A:86[B]:PRO:CD	2:A:500:DGT:O6	2.53	0.53
1:C:32:TYR:HA	4:C:293:PEG:H31	1.90	0.53
1:A:53:LEU:HD11	1:A:81:LYS:HG3	1.90	0.53
1:D:111:ASP:HB2	1:D:227:THR:OG1	2.08	0.53
1:B:111:ASP:HB2	1:B:227:THR:OG1	2.09	0.53
1:C:111:ASP:HB2	1:C:227:THR:OG1	2.09	0.53
1:A:85[B]:SER:O	1:A:86[B]:PRO:O	2.27	0.53
1:B:17:LEU:HD23	1:B:230:HIS:HD2	1.73	0.53
1:B:87[A]:ASP:HB3	1:B:197:GLU:HG3	1.90	0.53
1:D:142:ASP:OD1	1:D:142:ASP:N	2.42	0.53
1:B:86[B]:PRO:HB2	1:B:87[B]:ASP:C	2.28	0.53
1:B:256:GLU:O	1:B:260:ARG:HG2	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:34:LYS:HE2	1:D:251:VAL:O	2.09	0.52
1:B:210:GLN:OE1	1:B:212:ARG:HD3	2.09	0.52
1:A:111:ASP:HB2	1:A:227:THR:OG1	2.08	0.52
1:B:243:ILE:CD1	1:C:243:ILE:HD11	2.40	0.52
1:A:160:LEU:HD12	1:A:208:MET:HE2	1.92	0.52
1:B:225:LEU:HD23	5:B:366:HOH:O	2.09	0.52
1:D:171:TYR:HE2	1:D:217:MET:HG3	1.75	0.52
1:C:256:GLU:O	1:C:260:ARG:HG2	2.09	0.52
1:B:195:ARG:NH1	1:B:197:GLU:OE1	2.43	0.52
1:A:256:GLU:O	1:A:260:ARG:HG2	2.11	0.51
1:B:84:PRO:C	1:B:86[A]:PRO:HD3	2.30	0.51
1:D:25:SER:HB2	1:D:60:ASP:CG	2.30	0.51
1:B:86[B]:PRO:CB	1:B:87[B]:ASP:C	2.79	0.51
1:D:167:PRO:HD3	5:D:308:HOH:O	2.12	0.50
1:A:178:PHE:HB3	4:A:293:PEG:H32	1.91	0.50
1:B:58:PRO:CA	1:B:82:VAL:HG11	2.40	0.50
1:A:220:ARG:HG3	1:D:249:LEU:HB3	1.93	0.50
1:B:25:SER:HB2	1:B:60:ASP:CG	2.31	0.50
1:B:171:TYR:HE2	1:B:217:MET:HG3	1.77	0.50
1:B:102:HIS:HA	1:B:181:ASN:ND2	2.26	0.50
1:B:85[A]:SER:N	1:B:86[A]:PRO:CD	2.74	0.49
1:A:129:LYS:HE3	1:A:214:SER:OG	2.13	0.49
1:B:84:PRO:O	1:B:85[B]:SER:CB	2.57	0.49
1:B:243:ILE:CD1	1:C:243:ILE:CD1	2.91	0.49
1:D:190:LEU:HD22	1:D:203:ILE:HG13	1.94	0.49
1:A:109:LEU:HB3	2:A:500:DGT:H4'	1.94	0.49
1:A:234:ILE:HB	4:A:294:PEG:C1	2.33	0.49
1:C:171:TYR:HE2	1:C:217:MET:HG3	1.78	0.48
1:D:84:PRO:C	1:D:86:PRO:HD3	2.33	0.48
1:C:119:LEU:HB3	1:C:120:PRO:HD3	1.95	0.48
1:C:243:ILE:HG23	1:C:247:GLN:OE1	2.13	0.48
1:A:122:LEU:HD22	1:A:222:TYR:OH	2.14	0.48
1:D:31:ILE:HB	1:D:39:TYR:CE1	2.48	0.48
1:A:34:LYS:HE2	1:A:251:VAL:O	2.14	0.48
1:B:179:TYR:OH	1:B:200:ILE:HD11	2.13	0.48
1:C:31:ILE:HB	1:C:39:TYR:CE1	2.50	0.47
1:A:86[B]:PRO:CG	2:A:500:DGT:O6	2.62	0.47
1:D:272:LEU:O	1:D:275:PRO:HD2	2.13	0.47
1:B:243:ILE:HD11	1:C:243:ILE:CD1	2.44	0.47
1:D:243:ILE:HG23	1:D:247:GLN:OE1	2.14	0.47
1:D:249:LEU:HD23	1:D:249:LEU:H	1.79	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:289:VAL:O	1:A:289:VAL:HG13	2.13	0.47
1:D:240:ILE:O	1:D:244:GLU:HG3	2.15	0.47
1:C:230:HIS:O	5:C:314:HOH:O	2.20	0.47
1:A:25:SER:HB2	1:A:60:ASP:CG	2.34	0.47
1:A:85[A]:SER:N	1:A:86[A]:PRO:HD3	2.30	0.47
1:C:25:SER:HB2	1:C:60:ASP:CG	2.34	0.47
1:A:61:THR:HB	1:A:62:PRO:HD3	1.96	0.47
1:C:272:LEU:O	1:C:275:PRO:HD2	2.14	0.47
1:C:190:LEU:HD22	1:C:203:ILE:HG13	1.95	0.47
1:C:84:PRO:C	1:C:86:PRO:HD3	2.33	0.47
1:B:3:THR:HB	1:B:5:LYS:HE3	1.97	0.47
1:D:161:GLU:O	1:D:164:PRO:HD3	2.15	0.47
1:A:164:PRO:HG2	1:A:167:PRO:HB3	1.97	0.47
1:B:53:LEU:HD11	1:B:81:LYS:HG3	1.96	0.46
1:A:86[B]:PRO:HD2	2:A:500:DGT:C6	2.44	0.46
1:C:164:PRO:C	1:C:166:GLN:N	2.66	0.46
1:B:2:LYS:HE3	5:B:354:HOH:O	2.16	0.46
1:A:83:ASP:OD2	1:A:86[B]:PRO:HD3	2.16	0.46
1:B:34:LYS:HE2	1:B:251:VAL:O	2.16	0.46
1:C:164:PRO:HB2	1:C:166:GLN:C	2.36	0.46
1:B:190:LEU:HD22	1:B:203:ILE:HG13	1.97	0.46
1:B:61:THR:HB	1:B:62:PRO:HD3	1.97	0.46
1:B:140:VAL:HG11	1:B:146:TYR:CE2	2.51	0.46
1:A:85[A]:SER:N	1:A:86[A]:PRO:CD	2.79	0.45
1:C:61:THR:HB	1:C:62:PRO:HD3	1.97	0.45
1:A:17:LEU:CD2	1:A:230:HIS:HD2	2.30	0.45
1:C:179:TYR:OH	1:C:200:ILE:HD11	2.16	0.45
1:D:81:LYS:HD3	1:D:95:ILE:HG22	1.99	0.45
1:A:73:GLN:HB2	1:A:272:LEU:HD21	1.98	0.45
1:D:179:TYR:OH	1:D:200:ILE:HD11	2.17	0.45
1:C:240:ILE:O	1:C:244:GLU:HG3	2.17	0.45
1:A:243:ILE:HG23	1:A:247:GLN:OE1	2.16	0.45
1:B:104:ASP:OD1	1:B:180:ASP:HA	2.17	0.45
1:C:122:LEU:HD22	1:C:222:TYR:OH	2.17	0.45
1:B:83:ASP:HA	1:B:84:PRO:HD3	1.81	0.45
1:C:249:LEU:HD23	1:C:249:LEU:H	1.82	0.44
1:A:144:GLU:CD	1:A:144:GLU:H	2.21	0.44
1:D:104:ASP:OD1	1:D:180:ASP:HA	2.16	0.44
1:D:4:ARG:CZ	1:D:127:VAL:HG11	2.48	0.44
1:D:61:THR:HB	1:D:62:PRO:HD3	1.99	0.44
1:A:31:ILE:HB	1:A:39:TYR:CE1	2.52	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:85[B]:SER:HA	1:A:86[B]:PRO:HD2	1.67	0.44
1:C:104:ASP:OD1	1:C:180:ASP:HA	2.17	0.44
1:B:252:SER:O	1:B:254:PRO:HD3	2.17	0.44
1:A:83:ASP:HA	1:A:84:PRO:HD3	1.81	0.44
1:D:140:VAL:HG11	1:D:146:TYR:CE2	2.52	0.44
1:A:102:HIS:HA	1:A:181:ASN:ND2	2.31	0.44
1:C:206:ILE:O	1:C:210:GLN:HG3	2.17	0.44
1:D:137:ALA:HB1	1:D:171:TYR:HB3	2.00	0.44
1:B:87[A]:ASP:HB3	1:B:197:GLU:CG	2.48	0.43
1:A:86[B]:PRO:CB	1:A:87[B]:ASP:C	2.82	0.43
1:D:109:LEU:HD13	2:D:500:DGT:H5'A	2.00	0.43
1:D:129:LYS:HE3	1:D:214:SER:OG	2.18	0.43
1:A:17:LEU:HD23	1:A:230:HIS:CD2	2.53	0.43
1:A:278:LYS:HB2	5:A:302:HOH:O	2.18	0.43
1:D:119:LEU:HB3	1:D:120:PRO:HD3	2.01	0.43
1:C:73:GLN:HB2	1:C:272:LEU:HD21	2.00	0.43
1:C:276:LEU:O	1:C:282:GLY:HA3	2.18	0.43
1:D:51:ASP:OD2	1:D:77:ASN:HB3	2.19	0.43
1:B:73:GLN:HB2	1:B:272:LEU:HD21	2.01	0.43
1:C:140:VAL:HG11	1:C:146:TYR:CE2	2.54	0.43
1:B:278:LYS:HB2	5:B:299:HOH:O	2.19	0.43
1:A:179:TYR:OH	1:A:200:ILE:HD11	2.19	0.43
1:A:104:ASP:OD1	1:A:180:ASP:HA	2.19	0.43
1:C:33:ASP:OD1	1:C:34:LYS:NZ	2.47	0.42
1:A:190:LEU:HD22	1:A:203:ILE:HG13	2.00	0.42
1:D:139:HIS:CE1	1:D:170:ASN:HB3	2.54	0.42
1:B:31:ILE:HB	1:B:39:TYR:CE1	2.53	0.42
1:C:139:HIS:CE1	1:C:170:ASN:HB3	2.53	0.42
1:C:83:ASP:OD2	1:C:85:SER:HA	2.19	0.42
1:C:85:SER:N	1:C:86:PRO:CD	2.82	0.42
1:C:137:ALA:HB1	1:C:171:TYR:HB3	2.02	0.42
1:C:87:ASP:C	1:C:197:GLU:HG2	2.39	0.42
1:C:129:LYS:HE3	1:C:214:SER:OG	2.19	0.42
1:B:276:LEU:O	1:B:282:GLY:HA3	2.19	0.42
1:A:90:ALA:HB1	1:A:203:ILE:HD12	2.02	0.42
1:D:276:LEU:O	1:D:282:GLY:HA3	2.19	0.42
1:A:83:ASP:C	1:A:85[B]:SER:H	2.22	0.42
1:C:51:ASP:OD2	1:C:77:ASN:HB3	2.20	0.42
1:D:144:GLU:HG2	1:D:145:ARG:HG2	2.01	0.42
1:B:225:LEU:HD22	5:B:366:HOH:O	2.20	0.42
1:D:83:ASP:OD2	1:D:85:SER:HA	2.20	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:161:GLU:O	1:C:164:PRO:HD3	2.18	0.41
5:A:372:HOH:O	1:B:15:THR:HB	2.19	0.41
1:B:272:LEU:O	1:B:275:PRO:HD2	2.21	0.41
1:A:143:PRO:HG3	1:A:170:ASN:HA	2.03	0.41
1:D:83:ASP:HA	1:D:84:PRO:HD3	1.82	0.41
1:B:4:ARG:CZ	1:B:127:VAL:HG11	2.51	0.41
1:A:86[A]:PRO:HB2	1:A:91:GLN:OE1	2.20	0.41
1:B:247:GLN:HB2	1:B:249:LEU:CD1	2.51	0.41
1:C:81:LYS:HD3	1:C:95:ILE:HG22	2.02	0.41
1:D:167:PRO:HD2	5:D:308:HOH:O	2.18	0.41
1:B:129:LYS:HE3	1:B:214:SER:OG	2.21	0.41
1:C:4:ARG:CZ	1:C:127:VAL:HG11	2.51	0.41
1:C:83:ASP:HA	1:C:84:PRO:HD3	1.82	0.40
1:B:240:ILE:O	1:B:244:GLU:HG3	2.21	0.40
1:B:161:GLU:O	1:B:164:PRO:HD3	2.20	0.40
1:D:17:LEU:O	1:D:20:VAL:HG22	2.21	0.40
1:D:144:GLU:H	1:D:144:GLU:CD	2.18	0.40
1:C:143:PRO:HG3	1:C:170:ASN:HA	2.03	0.40
1:A:83:ASP:C	1:A:85[A]:SER:H	2.24	0.40
1:C:247:GLN:HB2	1:C:249:LEU:CD2	2.51	0.40
1:D:17:LEU:HD23	1:D:230:HIS:CD2	2.54	0.40
1:A:13:SER:CB	1:A:15:THR:HG23	2.52	0.40
1:A:240:ILE:O	1:A:244:GLU:HG3	2.21	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	284/292 (97%)	275 (97%)	5 (2%)	4 (1%)	14 19
1	B	283/292 (97%)	269 (95%)	11 (4%)	3 (1%)	17 25

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	C	278/292 (95%)	265 (95%)	13 (5%)	0	100	100
1	D	268/292 (92%)	255 (95%)	12 (4%)	1 (0%)	39	56
All	All	1113/1168 (95%)	1064 (96%)	41 (4%)	8 (1%)	34	38

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	86[A]	PRO
1	A	86[B]	PRO
1	B	86[A]	PRO
1	B	86[B]	PRO
1	A	85[A]	SER
1	A	85[B]	SER
1	D	162	GLU
1	B	162	GLU

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	243/245 (99%)	239 (98%)	4 (2%)	70	86
1	B	243/245 (99%)	239 (98%)	4 (2%)	70	86
1	C	239/245 (98%)	234 (98%)	5 (2%)	61	80
1	D	234/245 (96%)	228 (97%)	6 (3%)	54	74
All	All	959/980 (98%)	940 (98%)	19 (2%)	63	81

All (19) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	122	LEU
1	A	249	LEU
1	A	281	TYR
1	A	289	VAL

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Mol	Chain	Res	Type
1	B	130	GLU
1	B	154	LYS
1	B	249	LEU
1	B	281	TYR
1	C	122	LEU
1	C	144	GLU
1	C	154	LYS
1	C	249	LEU
1	C	281	TYR
1	D	112	ASN
1	D	122	LEU
1	D	160	LEU
1	D	249	LEU
1	D	281	TYR
1	D	289	VAL

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	B	27	GLN
1	C	27	GLN
1	D	27	GLN

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](#)

Of 12 ligands modelled in this entry, 5 are monoatomic - leaving 7 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	$\# Z > 2$
4	PEG	A	293	-	6,6,6	0.54	0	5,5,5	0.64	0
4	PEG	A	294	-	6,6,6	0.68	0	5,5,5	0.25	0
2	DGT	A	500	3	25,33,33	1.09	2 (8%)	35,52,52	1.78	8 (22%)
2	DGT	B	500	3	25,33,33	1.08	2 (8%)	35,52,52	1.67	8 (22%)
4	PEG	C	293	-	6,6,6	0.50	0	5,5,5	0.28	0
2	DGT	C	500	3	25,33,33	1.08	2 (8%)	35,52,52	1.74	8 (22%)
2	DGT	D	500	3	25,33,33	1.06	2 (8%)	35,52,52	1.75	8 (22%)

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
4	PEG	A	293	-	-	0/4/4/4	0/0/0/0
4	PEG	A	294	-	-	0/4/4/4	0/0/0/0
2	DGT	A	500	3	-	0/18/34/34	0/3/3/3
2	DGT	B	500	3	-	0/18/34/34	0/3/3/3
4	PEG	C	293	-	-	0/4/4/4	0/0/0/0
2	DGT	C	500	3	-	0/18/34/34	0/3/3/3
2	DGT	D	500	3	-	0/18/34/34	0/3/3/3

All (8) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	D	500	DGT	C5-C4	3.01	1.47	1.40
2	B	500	DGT	C5-C4	3.04	1.47	1.40
2	C	500	DGT	C5-C4	3.06	1.47	1.40
2	A	500	DGT	C5-C4	3.07	1.47	1.40
2	A	500	DGT	C6-C5	3.49	1.48	1.41
2	B	500	DGT	C6-C5	3.54	1.48	1.41
2	C	500	DGT	C6-C5	3.57	1.48	1.41
2	D	500	DGT	C6-C5	3.58	1.48	1.41

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	D	500	DGT	C5-C6-N1	-4.10	117.98	123.59
2	A	500	DGT	C5-C6-N1	-4.05	118.06	123.59
2	B	500	DGT	C5-C6-N1	-3.99	118.14	123.59
2	C	500	DGT	C5-C6-N1	-3.93	118.21	123.59
2	C	500	DGT	C6-C5-C4	-3.59	116.60	120.90
2	A	500	DGT	C6-C5-C4	-3.45	116.78	120.90
2	D	500	DGT	C6-C5-C4	-3.25	117.01	120.90
2	A	500	DGT	PA-O3A-PB	-3.24	123.62	132.73
2	C	500	DGT	PB-O3B-PG	-3.23	121.85	132.67
2	D	500	DGT	PB-O3B-PG	-3.13	122.17	132.67
2	A	500	DGT	PB-O3B-PG	-3.08	122.35	132.67
2	B	500	DGT	C6-C5-C4	-3.07	117.23	120.90
2	C	500	DGT	N3-C2-N1	-3.06	122.78	127.44
2	A	500	DGT	N3-C2-N1	-3.01	122.87	127.44
2	D	500	DGT	PA-O3A-PB	-2.99	124.33	132.73
2	C	500	DGT	PA-O3A-PB	-2.95	124.45	132.73
2	B	500	DGT	PA-O3A-PB	-2.91	124.54	132.73
2	D	500	DGT	N3-C2-N1	-2.88	123.06	127.44
2	B	500	DGT	C4-C5-N7	-2.87	106.84	109.48
2	D	500	DGT	C4-C5-N7	-2.87	106.84	109.48
2	B	500	DGT	PB-O3B-PG	-2.68	123.69	132.67
2	B	500	DGT	N3-C2-N1	-2.66	123.39	127.44
2	A	500	DGT	C2'-C1'-N9	-2.46	108.19	114.16
2	B	500	DGT	C2'-C1'-N9	-2.40	108.31	114.16
2	C	500	DGT	C4-C5-N7	-2.39	107.28	109.48
2	A	500	DGT	C4-C5-N7	-2.35	107.31	109.48
2	D	500	DGT	C2'-C1'-N9	-2.34	108.46	114.16
2	C	500	DGT	C2'-C1'-N9	-2.15	108.92	114.16
2	B	500	DGT	C6-N1-C2	4.17	121.73	115.94
2	D	500	DGT	C6-N1-C2	4.51	122.19	115.94
2	A	500	DGT	C6-N1-C2	4.51	122.19	115.94
2	C	500	DGT	C6-N1-C2	4.51	122.20	115.94

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

7 monomers are involved in 20 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	293	PEG	2	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	A	294	PEG	4	0
2	A	500	DGT	6	0
2	B	500	DGT	2	0
4	C	293	PEG	3	0
2	C	500	DGT	1	0
2	D	500	DGT	2	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	285/292 (97%)	0.05	9 (3%) 51 51	20, 43, 86, 115	0
1	B	286/292 (97%)	0.15	13 (4%) 37 38	22, 44, 102, 138	0
1	C	284/292 (97%)	0.77	51 (17%) 2 2	28, 59, 110, 162	0
1	D	278/292 (95%)	0.95	57 (20%) 1 1	28, 62, 105, 160	0
All	All	1133/1168 (97%)	0.48	130 (11%) 6 6	20, 52, 102, 162	0

All (130) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	157	ALA	9.1
1	C	198	LEU	6.9
1	C	194	ALA	6.6
1	C	87	ASP	6.3
1	D	163	LYS	6.2
1	D	89	LEU	5.9
1	C	154	LYS	5.8
1	D	198	LEU	5.5
1	C	289	VAL	5.3
1	A	151	PHE	5.3
1	D	147	GLY	5.2
1	D	87	ASP	5.0
1	D	85	SER	4.9
1	B	153	GLN	4.8
1	D	160	LEU	4.7
1	C	155	GLY	4.7
1	D	145	ARG	4.6
1	C	156	THR	4.5
1	D	170	ASN	4.4
1	C	193	SER	4.4
1	A	156	THR	4.3

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Mol	Chain	Res	Type	RSRZ
1	B	156	THR	4.2
1	D	99	PHE	4.2
1	C	191	LYS	4.2
1	D	131	SER	4.1
1	D	146	TYR	4.0
1	C	158	VAL	4.0
1	C	153	GLN	4.0
1	C	272	LEU	4.0
1	D	267	GLN	4.0
1	D	213	LEU	3.9
1	D	171	TYR	3.9
1	B	154	LYS	3.8
1	C	165	LEU	3.8
1	D	211	GLY	3.7
1	D	151	PHE	3.7
1	D	200	ILE	3.7
1	D	169	SER	3.5
1	D	217	MET	3.5
1	D	155	GLY	3.5
1	B	157	ALA	3.4
1	D	208	MET	3.4
1	C	166	GLN	3.4
1	C	267	GLN	3.4
1	C	197	GLU	3.4
1	D	127	VAL	3.4
1	D	158	VAL	3.4
1	D	148	VAL	3.3
1	C	152	ASP	3.3
1	D	144	GLU	3.2
1	C	131	SER	3.1
1	B	163	LYS	3.1
1	C	212	ARG	3.1
1	D	178	PHE	3.1
1	D	270	ILE	3.1
1	D	263	PHE	3.0
1	C	271	GLU	3.0
1	C	211	GLY	3.0
1	D	277	SER	2.9
1	D	206	ILE	2.9
1	B	164	PRO	2.9
1	C	192	PRO	2.9
1	C	208	MET	2.9

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Mol	Chain	Res	Type	RSRZ
1	D	162	GLU	2.9
1	D	140	VAL	2.9
1	C	190	LEU	2.8
1	D	13	SER	2.8
1	B	152	ASP	2.8
1	C	202	ASP	2.8
1	D	212	ARG	2.8
1	D	98	GLU	2.7
1	C	209	GLU	2.7
1	D	210	GLN	2.7
1	A	165	LEU	2.7
1	D	190	LEU	2.7
1	D	128	ASN	2.7
1	B	145	ARG	2.7
1	B	158	VAL	2.7
1	B	144	GLU	2.6
1	C	84	PRO	2.6
1	D	167	PRO	2.6
1	C	210	GLN	2.6
1	D	271	GLU	2.6
1	B	168	LYS	2.6
1	C	290	LYS	2.6
1	C	162	GLU	2.5
1	D	209	GLU	2.5
1	D	193	SER	2.5
1	D	205	ARG	2.5
1	C	141	ASN	2.5
1	C	262	ASN	2.5
1	D	47	ALA	2.4
1	B	87[A]	ASP	2.4
1	C	128	ASN	2.4
1	D	201	THR	2.4
1	D	204	ASN	2.4
1	C	170	ASN	2.3
1	D	168	LYS	2.3
1	C	89	LEU	2.3
1	D	94	ILE	2.3
1	D	133	ALA	2.3
1	C	199	GLU	2.3
1	A	145	ARG	2.3
1	D	192	PRO	2.3
1	D	126	ALA	2.3

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Mol	Chain	Res	Type	RSRZ
1	C	13	SER	2.2
1	C	85	SER	2.2
1	D	207	TYR	2.2
1	C	275	PRO	2.2
1	C	205	ARG	2.2
1	C	259	PHE	2.2
1	C	168	LYS	2.2
1	D	157	ALA	2.2
1	C	234	ILE	2.2
1	C	264	ILE	2.2
1	C	167	PRO	2.2
1	A	87[A]	ASP	2.2
1	C	206	ILE	2.2
1	C	270	ILE	2.2
1	B	85[A]	SER	2.1
1	A	152	ASP	2.1
1	D	141	ASN	2.1
1	D	189	ASN	2.1
1	A	88	GLY	2.1
1	D	215	VAL	2.1
1	A	166	GLN	2.0
1	C	127	VAL	2.0
1	C	145	ARG	2.0
1	C	179	TYR	2.0
1	C	189	ASN	2.0

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

6.4 Ligands ⓘ

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
4	PEG	C	293	7/7	0.81	0.35	4.54	48,67,78,93	0
4	PEG	A	293	7/7	0.81	0.21	3.54	46,52,61,72	0
4	PEG	A	294	7/7	0.90	0.26	2.80	27,58,72,99	0
2	DGT	A	500	31/31	0.87	0.22	1.20	34,65,102,108	31
2	DGT	C	500	31/31	0.87	0.19	0.20	47,75,101,104	31
2	DGT	D	500	31/31	0.93	0.17	-0.14	47,72,92,113	31
2	DGT	B	500	31/31	0.95	0.12	-1.02	36,69,89,104	31
3	MG	B	502	1/1	0.85	0.13	-	64,64,64,64	0
3	MG	C	501	1/1	0.70	0.28	-	64,64,64,64	0
3	MG	A	501	1/1	0.76	0.25	-	77,77,77,77	0
3	MG	B	501	1/1	0.51	0.27	-	75,75,75,75	0
3	MG	D	502	1/1	0.82	0.21	-	73,73,73,73	0

6.5 Other polymers [i](#)

There are no such residues in this entry.