



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 07:46 AM GMT

PDB ID : 3C4Q
Title : Structure of the retaining glycosyltransferase MshA : The first step in mycothiol biosynthesis. Organism : Corynebacterium glutamicum- Complex with UDP
Authors : Vetting, M.W.; Frantom, P.A.; Blanchard, J.S.
Deposited on : 2008-01-30
Resolution : 2.80 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

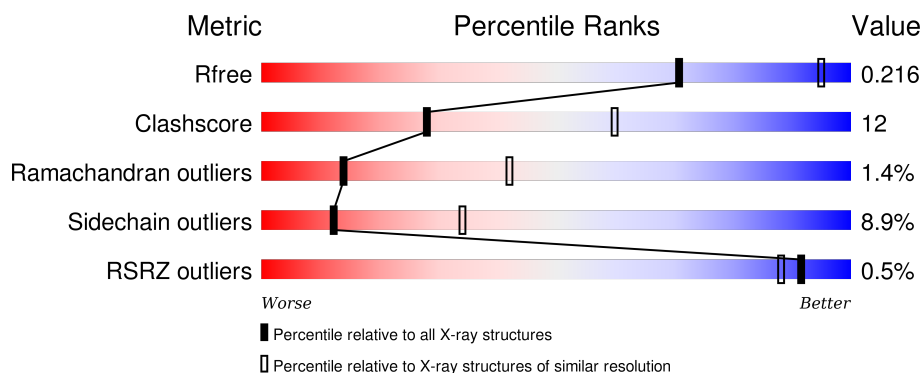
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION



The reported resolution of this entry is 2.80 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	2393 (2.80-2.80)
Clashscore	102246	2827 (2.80-2.80)
Ramachandran outliers	100387	2782 (2.80-2.80)
Sidechain outliers	100360	2784 (2.80-2.80)
RSRZ outliers	91569	2404 (2.80-2.80)

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	426	 69% 18% • • 8%
1	B	426	 73% 15% • • 8%

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	602	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 6189 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 Predicted glycosyltransferases.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	393	Total	C	N	O	S	0	0	0
			3026	1896	540	578	12			
1	B	393	Total	C	N	O	S	0	3	0
			3046	1915	540	578	13			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	419	LEU	-	EXPRESSION TAG	UNP Q8NTA6
A	420	GLU	-	EXPRESSION TAG	UNP Q8NTA6
A	421	HIS	-	EXPRESSION TAG	UNP Q8NTA6
A	422	HIS	-	EXPRESSION TAG	UNP Q8NTA6
A	423	HIS	-	EXPRESSION TAG	UNP Q8NTA6
A	424	HIS	-	EXPRESSION TAG	UNP Q8NTA6
A	425	HIS	-	EXPRESSION TAG	UNP Q8NTA6
A	426	HIS	-	EXPRESSION TAG	UNP Q8NTA6
B	419	LEU	-	EXPRESSION TAG	UNP Q8NTA6
B	420	GLU	-	EXPRESSION TAG	UNP Q8NTA6
B	421	HIS	-	EXPRESSION TAG	UNP Q8NTA6
B	422	HIS	-	EXPRESSION TAG	UNP Q8NTA6
B	423	HIS	-	EXPRESSION TAG	UNP Q8NTA6
B	424	HIS	-	EXPRESSION TAG	UNP Q8NTA6
B	425	HIS	-	EXPRESSION TAG	UNP Q8NTA6
B	426	HIS	-	EXPRESSION TAG	UNP Q8NTA6

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

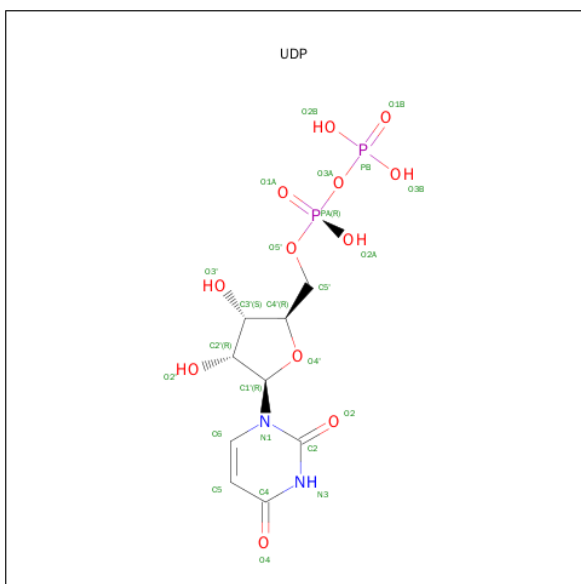
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	B	1	Total	Mg	0	0
			1	1		
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	B	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is URIDINE-5'-DIPHOSPHATE (three-letter code: UDP) (formula: C₉H₁₄N₂O₁₂P₂).



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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	P	0	0
			25	9	2	12	2		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	28	Total	O	0	0
			28	28		
5	B	27	Total	O	0	0
			27	27		

4 Data and refinement statistics

Property	Value	Source
Space group	I 4 2 2	Depositor
Cell constants a, b, c, α , β , γ	224.25Å 224.25Å 125.11Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	78.25 – 2.80 78.25 – 2.80	Depositor EDS
% Data completeness (in resolution range)	95.5 (78.25-2.80) 95.5 (78.25-2.80)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.35 (at 2.82Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.184 , 0.218 0.183 , 0.216	Depositor DCC
R_{free} test set	1885 reflections (5.28%)	DCC
Wilson B-factor (Å ²)	54.6	Xtriage
Anisotropy	0.498	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 53.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 37594 reflections	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	6189	wwPDB-VP
Average B, all atoms (Å ²)	28.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.66% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: UDP, MG, SO4

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	0.69	0/3086	0.86	6/4199 (0.1%)
1	B	0.60	0/3117	0.75	3/4239 (0.1%)
All	All	0.65	0/6203	0.81	9/8438 (0.1%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	4
1	B	0	4
All	All	0	8

There are no bond length outliers.

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	318	PHE	N-CA-C	-7.08	91.89	111.00
1	B	205	GLY	N-CA-C	-6.73	96.27	113.10
1	A	18	THR	N-CA-C	6.40	128.29	111.00
1	A	389	PHE	C-N-CA	6.25	137.34	121.70
1	B	388	THR	N-CA-C	6.20	127.73	111.00
1	A	121	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	A	17	GLY	N-CA-C	-5.99	98.12	113.10
1	A	289	ARG	NE-CZ-NH2	5.09	122.85	120.30
1	B	388	THR	CA-C-N	5.07	128.35	117.20

There are no chirality outliers.

All (8) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	16	PRO	Peptide
1	A	17	GLY	Peptide
1	A	317	SER	Peptide
1	A	392	ALA	Peptide
1	B	318[A]	PHE	Peptide
1	B	318[B]	PHE	Peptide
1	B	388	THR	Peptide

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	3026	0	2988	56	1
1	B	3046	0	3014	89	0
2	A	1	0	0	0	0
2	B	1	0	0	0	0
3	A	5	0	0	0	0
3	B	5	0	0	0	0
4	A	25	0	11	0	0
4	B	25	0	11	1	0
5	A	28	0	0	1	0
5	B	27	0	0	0	1
All	All	6189	0	6024	142	1

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 12.

All (142) 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:318[B]:PHE:CE2	1:B:343:ALA:HB2	1.72	1.22
1:B:323[A]:MET:HG2	1:B:389[A]:PHE:CE1	1.74	1.22
1:B:320:LEU:N	1:B:320:LEU:HD23	1.58	1.14
1:B:323[B]:MET:HE3	1:B:389[B]:PHE:CD2	1.84	1.12
1:A:316:GLU:HG3	1:A:317:SER:O	1.49	1.11
1:B:316:GLU:HG3	1:B:317:SER:H	1.00	1.09
1:B:323[A]:MET:HG2	1:B:389[A]:PHE:CZ	1.94	1.02

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:320:LEU:CD2	1:B:320:LEU:H	1.64	1.01
1:B:316:GLU:HG3	1:B:317:SER:N	1.75	1.00
1:B:320:LEU:H	1:B:320:LEU:HD23	0.78	0.95
1:B:323[B]:MET:CE	1:B:389[B]:PHE:CD2	2.51	0.93
1:B:316:GLU:CG	1:B:317:SER:H	1.83	0.92
1:B:323[A]:MET:CG	1:B:389[A]:PHE:CZ	2.54	0.88
1:B:318[B]:PHE:CE2	1:B:343:ALA:CB	2.56	0.88
1:A:326:GLN:HG3	1:A:382:ALA:HB1	1.60	0.84
1:B:318[B]:PHE:HE2	1:B:343:ALA:HB2	1.39	0.81
1:B:34:GLU:HG2	1:B:392:ALA:HA	1.63	0.79
1:A:316:GLU:CG	1:A:317:SER:O	2.30	0.79
1:A:18:THR:HG23	1:A:264:GLY:HA3	1.67	0.77
1:B:320:LEU:N	1:B:320:LEU:CD2	2.30	0.75
1:B:316:GLU:O	1:B:317:SER:HB3	1.85	0.73
1:A:280:GLU:HB3	1:A:285:GLU:HG2	1.70	0.72
1:A:121:ARG:NH2	1:A:164:ASN:O	2.22	0.72
1:B:318[B]:PHE:CD2	1:B:343:ALA:HB2	2.23	0.71
1:B:195:PRO:HB2	1:B:318[A]:PHE:CE2	2.26	0.70
1:B:318[B]:PHE:HE2	1:B:343:ALA:CB	1.97	0.70
1:B:280:GLU:HB3	1:B:285:GLU:HG2	1.76	0.68
1:B:206:ASN:HB3	1:B:209:ALA:HB2	1.74	0.67
1:B:280:GLU:HA	1:B:285:GLU:HG3	1.77	0.67
1:A:196:GLY:HA2	1:A:389:PHE:HB2	1.76	0.66
1:A:217:LEU:O	1:A:289:ARG:NH1	2.26	0.66
1:A:18:THR:CG2	1:A:264:GLY:HA3	2.27	0.64
1:B:195:PRO:HG2	1:B:318[A]:PHE:CD2	2.34	0.64
1:B:323[B]:MET:CE	1:B:389[B]:PHE:CG	2.80	0.63
1:A:280:GLU:HA	1:A:285:GLU:HG3	1.80	0.62
1:B:195:PRO:CB	1:B:318[A]:PHE:CE2	2.83	0.62
1:B:18:THR:HG23	1:B:293:PRO:HG3	1.83	0.61
1:B:318[A]:PHE:H	1:B:318[A]:PHE:HD1	0.76	0.60
1:A:390:SER:O	1:A:393:ALA:HB3	2.01	0.59
1:B:316:GLU:O	1:B:317:SER:CB	2.50	0.59
1:B:323[A]:MET:HG3	1:B:389[A]:PHE:CZ	2.37	0.59
1:A:205:GLY:O	1:A:206:ASN:CB	2.50	0.59
1:B:323[B]:MET:HE1	1:B:389[B]:PHE:CG	2.38	0.59
1:B:186:ASP:HB3	1:B:189:ARG:HG3	1.85	0.58
1:A:148:THR:HB	1:A:150:GLU:OE2	2.04	0.58
1:B:205:GLY:O	1:B:206:ASN:HB2	2.04	0.56
1:A:1:MET:HE2	1:A:40:ILE:HG12	1.87	0.56
1:B:18:THR:CG2	1:B:264:GLY:HA3	2.34	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:363:ASP:O	1:A:367:THR:HG23	2.05	0.56
1:A:18:THR:HG23	1:A:293:PRO:HG3	1.87	0.56
1:B:258:ARG:CZ	1:B:287:ARG:HH21	2.19	0.56
1:A:17:GLY:HA2	1:A:18:THR:O	2.06	0.55
1:B:205:GLY:O	1:B:206:ASN:CB	2.54	0.55
1:A:17:GLY:CA	1:A:21:SER:O	2.55	0.55
1:B:317:SER:HA	1:B:339:GLY:H	1.72	0.55
1:B:280:GLU:HB3	1:B:285:GLU:CG	2.37	0.54
1:A:204:PRO:HB2	1:A:205:GLY:HA2	1.90	0.54
1:A:315:ASN:O	1:A:316:GLU:HB2	2.09	0.53
1:A:24:MET:HG3	1:A:133:HIS:CG	2.44	0.53
1:B:280:GLU:CA	1:B:285:GLU:HG3	2.39	0.52
1:B:323[A]:MET:HA	1:B:389[A]:PHE:HZ	1.74	0.52
1:B:323[A]:MET:CG	1:B:389[A]:PHE:CE1	2.67	0.52
1:A:229:VAL:HA	1:A:262:CYS:O	2.10	0.51
1:A:389:PHE:HA	5:A:624:HOH:O	2.10	0.51
1:B:204:PRO:HA	1:B:328:SER:O	2.10	0.51
1:B:18:THR:HG23	1:B:264:GLY:HA3	1.93	0.51
1:B:388:THR:CA	1:B:389[A]:PHE:HB3	2.41	0.50
1:A:170:VAL:HG11	1:A:179:LEU:HD22	1.93	0.50
1:A:205:GLY:O	1:A:206:ASN:HB3	2.10	0.50
1:A:115:GLN:HE21	1:A:157:CYS:HB3	1.75	0.50
1:B:318[A]:PHE:CE2	1:B:320:LEU:HD22	2.48	0.49
1:B:243:LYS:HG3	1:B:278:MET:CE	2.43	0.49
1:A:207:ASP:OD2	1:A:207:ASP:N	2.46	0.49
1:B:320:LEU:HA	1:B:323[A]:MET:HB2	1.95	0.49
1:A:298:GLU:HG2	1:B:51:PRO:HG2	1.95	0.49
1:B:323[B]:MET:HE3	1:B:389[B]:PHE:HD2	1.66	0.48
1:B:171:ASN:HB3	1:B:195:PRO:HG3	1.96	0.48
1:A:170:VAL:CG1	1:A:179:LEU:HD22	2.43	0.48
1:B:26:VAL:HG11	4:B:600:UDP:O3'	2.14	0.48
1:B:346:GLU:HB2	1:B:352:LEU:HD12	1.95	0.48
1:A:223:THR:HA	1:A:256:ASN:OD1	2.13	0.48
1:B:363:ASP:O	1:B:367:THR:HG23	2.14	0.47
1:A:280:GLU:HA	1:A:285:GLU:CG	2.43	0.47
1:B:384:GLU:OE2	1:B:387:ARG:NH2	2.45	0.47
1:A:1:MET:HA	1:A:104:ASP:OD2	2.14	0.47
1:A:26:VAL:HG22	1:A:320:LEU:HD21	1.96	0.47
1:B:195:PRO:HG2	1:B:318[A]:PHE:CG	2.48	0.47
1:A:51:PRO:HG2	1:B:298:GLU:HG2	1.95	0.47
1:B:5:MET:HA	1:B:107:HIS:O	2.14	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:HIS:O	1:A:113:SER:HB2	2.15	0.47
1:B:388:THR:N	1:B:389[A]:PHE:HB3	2.30	0.46
1:B:194:SER:HA	1:B:195:PRO:HD3	1.74	0.46
1:B:318[B]:PHE:CE2	1:B:343:ALA:CA	2.99	0.46
1:A:226:VAL:HG23	1:A:257:LEU:HD21	1.97	0.45
1:A:316:GLU:HB3	1:A:338:GLY:HA3	1.98	0.45
1:B:202:TYR:CD2	1:B:324:GLU:HG2	2.52	0.44
1:A:79:GLU:H	1:A:79:GLU:CD	2.21	0.44
1:A:294:ARG:HB2	1:A:295:PRO:HD2	2.00	0.44
1:A:233:GLN:HG2	1:A:235:PHE:CE1	2.53	0.43
1:A:316:GLU:OE2	1:A:316:GLU:HA	2.18	0.43
1:B:121:ARG:HB2	1:B:126:ILE:O	2.19	0.43
1:A:334:ALA:HB1	1:A:340:LEU:HD13	2.00	0.43
1:A:186:ASP:HA	1:A:187:PRO:HD3	1.90	0.43
1:B:402:TYR:O	1:B:406:ILE:HG12	2.18	0.43
1:A:45:TYR:CD1	1:A:92:MET:HG2	2.54	0.43
1:A:17:GLY:HA2	1:A:21:SER:O	2.19	0.43
1:A:76:LEU:HD12	1:A:76:LEU:HA	1.90	0.43
1:B:311:VAL:HG22	1:B:311:VAL:O	2.18	0.42
1:A:311:VAL:O	1:A:311:VAL:CG2	2.67	0.42
1:B:18:THR:HG22	1:B:264:GLY:HA3	2.00	0.42
1:A:74:GLU:OE1	1:B:294:ARG:NH1	2.40	0.42
1:A:211:GLU:HB2	1:A:215:ARG:HH22	1.85	0.42
1:B:150:GLU:CD	1:B:150:GLU:H	2.23	0.42
1:B:353:VAL:HG11	1:B:361:TRP:NE1	2.35	0.41
1:A:80:GLU:C	1:A:82:PRO:HD2	2.41	0.41
1:A:27:TYR:CD2	1:A:27:TYR:C	2.93	0.41
1:B:333:ILE:HD12	1:B:365:LEU:HD23	2.01	0.41
1:A:127:PRO:HA	1:A:166:ASP:OD2	2.20	0.41
1:B:24:MET:HE2	1:B:24:MET:HB3	1.95	0.41
1:B:323[B]:MET:HE3	1:B:389[B]:PHE:CG	2.39	0.41
1:A:385:HIS:O	1:A:388:THR:HG23	2.20	0.41
1:A:237:GLY:N	1:A:238:PRO:CD	2.84	0.40
1:B:111:TRP:HZ3	1:B:157:CYS:HG	1.66	0.40
1:B:318[B]:PHE:HZ	1:B:342:ILE:HG22	1.85	0.40
1:B:318[A]:PHE:HB2	1:B:323[A]:MET:CE	2.52	0.40
1:A:15:GLN:NE2	1:A:16:PRO:HD2	2.36	0.40
1:B:27:TYR:HD1	1:B:318[A]:PHE:HZ	1.67	0.40
1:B:224:LYS:HA	1:B:307:ASP:OD2	2.21	0.40
1:B:325:ALA:O	1:B:328:SER:HB2	2.22	0.40
1:B:259:VAL:HB	1:B:288:ILE:HG12	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:61:GLU:O	1:B:62:ASN:HB2	2.22	0.40
1:A:401:LEU:HD12	1:A:401:LEU:HA	1.69	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:155:ARG:NH2	5:B:605:HOH:O[7_555]	2.19	0.01

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	387/426 (91%)	365 (94%)	16 (4%)	6 (2%)	12	38
1	B	390/426 (92%)	371 (95%)	12 (3%)	7 (2%)	11	34
All	All	777/852 (91%)	736 (95%)	28 (4%)	13 (2%)	14	36

All (13) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	18	THR
1	A	206	ASN
1	A	390	SER
1	A	393	ALA
1	B	206	ASN
1	B	318[A]	PHE
1	B	318[B]	PHE
1	A	263	GLY
1	A	316	GLU
1	B	317	SER
1	B	389[A]	PHE

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Mol	Chain	Res	Type
1	B	389[B]	PHE
1	B	195	PRO

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	319/348 (92%)	290 (91%)	29 (9%)	12	33
1	B	322/348 (92%)	292 (91%)	30 (9%)	11	32
All	All	641/696 (92%)	582 (91%)	59 (9%)	12	32

All (59) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	LEU
1	A	26	VAL
1	A	50	ARG
1	A	58	ARG
1	A	76	LEU
1	A	93	LEU
1	A	102	THR
1	A	121	ARG
1	A	179	LEU
1	A	207	ASP
1	A	221	LEU
1	A	233	GLN
1	A	254	ASP
1	A	255	ARG
1	A	257	LEU
1	A	274	THR
1	A	285	GLU
1	A	286	LYS
1	A	287	ARG
1	A	297	SER
1	A	299	LEU

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Mol	Chain	Res	Type
1	A	311	VAL
1	A	316	GLU
1	A	317	SER
1	A	326	GLN
1	A	387	ARG
1	A	389	PHE
1	A	390	SER
1	A	399	SER
1	B	13	LEU
1	B	18	THR
1	B	26	VAL
1	B	61	GLU
1	B	93	LEU
1	B	94	SER
1	B	97	ARG
1	B	100	LYS
1	B	121	ARG
1	B	172	THR
1	B	199	VAL
1	B	215	ARG
1	B	236	LYS
1	B	257	LEU
1	B	285	GLU
1	B	286	LYS
1	B	287	ARG
1	B	293	PRO
1	B	297	SER
1	B	300	VAL
1	B	311	VAL
1	B	318[A]	PHE
1	B	318[B]	PHE
1	B	320	LEU
1	B	357	SER
1	B	384	GLU
1	B	388	THR
1	B	389[A]	PHE
1	B	389[B]	PHE
1	B	399	SER

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	115	GLN
1	A	326	GLN
1	A	385	HIS
1	A	403	ASN
1	B	9	HIS
1	B	38	GLN
1	B	173	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 6 ligands modelled in this entry, 2 are monoatomic - leaving 4 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	UDP	A	600	-	18,26,26	1.26	3 (16%)	26,40,40	1.81	3 (11%)
3	SO4	A	603	-	4,4,4	0.20	0	6,6,6	0.47	0
4	UDP	B	600	-	18,26,26	1.13	1 (5%)	26,40,40	1.77	4 (15%)
3	SO4	B	603	-	4,4,4	0.11	0	6,6,6	0.37	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
4	UDP	A	600	-	-	0/12/32/32	0/2/2/2
3	SO4	A	603	-	-	0/0/0/0	0/0/0/0
4	UDP	B	600	-	-	0/12/32/32	0/2/2/2
3	SO4	B	603	-	-	0/0/0/0	0/0/0/0

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	600	UDP	PB-O3B	-2.35	1.46	1.54
4	A	600	UDP	PB-O2B	-2.29	1.46	1.54
4	A	600	UDP	C4-N3	2.48	1.37	1.33
4	B	600	UDP	C4-N3	2.74	1.38	1.33

All (7) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	600	UDP	PA-O3A-PB	-6.60	110.55	132.67
4	B	600	UDP	PA-O3A-PB	-4.42	117.85	132.67
4	A	600	UDP	O4'-C4'-C5'	-2.12	101.75	109.32
4	B	600	UDP	O3B-PB-O3A	2.07	114.49	105.09
4	B	600	UDP	C4'-O4'-C1'	2.75	112.74	109.72
4	A	600	UDP	C4-N3-C2	4.37	118.47	114.14
4	B	600	UDP	C4-N3-C2	5.34	119.43	114.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	B	600	UDP	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues

There are no chain breaks in this entry.

6 Fit of model and data [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	393/426 (92%)	0.22	1 (0%) 94 92	5, 24, 39, 49	0
1	B	393/426 (92%)	0.31	3 (0%) 87 81	18, 32, 43, 55	0
All	All	786/852 (92%)	0.27	4 (0%) 91 88	5, 28, 42, 55	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	318[A]	PHE	5.7
1	B	359	HIS	2.6
1	B	315	ASN	2.3
1	A	249	PHE	2.1

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(\AA^2)	Q<0.9
2	MG	B	602	1/1	0.88	0.23	2.10	32,32,32,32	0
3	SO4	B	603	5/5	0.91	0.24	0.23	81,81,81,82	0
2	MG	A	602	1/1	0.83	0.19	-0.29	42,42,42,42	0
3	SO4	A	603	5/5	0.95	0.20	-0.48	50,50,52,52	0
4	UDP	B	600	25/25	0.95	0.15	-1.27	17,28,52,54	0
4	UDP	A	600	25/25	0.95	0.15	-2.15	13,19,48,49	0

6.5 Other polymers [i](#)

There are no such residues in this entry.