



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 4, 2016 – 07:13 PM EDT

PDB ID : 5FX8
Title : Complete structure of manganese lipxygenase of *Gaeumannomyces graminis*
and partial structure of zonadhesin of *Komagataella pastoris*
Authors : Chen, Y.; Wennman, A.; Karkehanadi, S.; Engstrom, A.; Oliw, E.H.
Deposited on : 2016-02-25
Resolution : 2.60 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
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) : rb-20027939

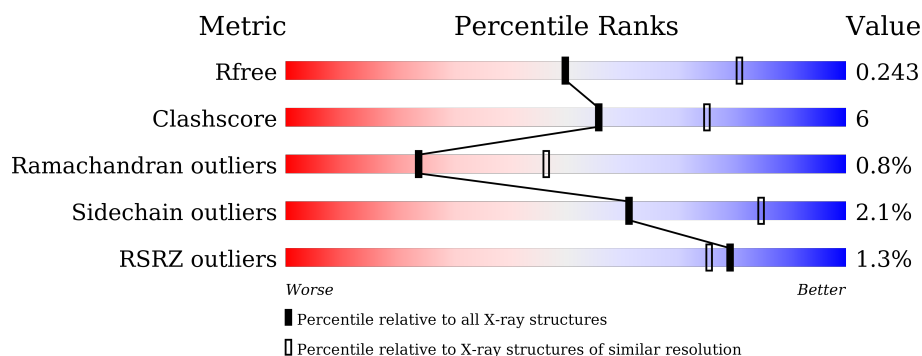
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	618	
1	B	618	
2	U	320	

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	MN	B	1000	-	-	-	X
4	NAG	B	1001	-	-	-	X
4	NAG	B	1002	-	-	-	X
5	NAG	A	1005	-	-	-	X
6	NAG	B	1006	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 11543 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 LINOLEATE 11-LIPOXYGENASE.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	563	Total	C	N	O	S	0	0	0
			4397	2807	780	799	11			
1	B	556	Total	C	N	O	S	0	0	0
			4353	2783	772	787	11			

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	52	ASN	LYS	CONFLICT	UNP Q8X151
A	158	CYS	TYR	CONFLICT	UNP Q8X151
B	52	ASN	LYS	CONFLICT	UNP Q8X151
B	158	CYS	TYR	CONFLICT	UNP Q8X151

- Molecule 2 is a protein called ZONADHESIN.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	U	309	Total	C	N	O	S	0	0	0
			2344	1491	351	500	2			

- Molecule 3 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	B	1	Total	Mn	0	0
			1	1		
3	A	1	Total	Mn	0	0
			1	1		

- Molecule 4 is a polymer of unknown type called SUGAR (2-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		

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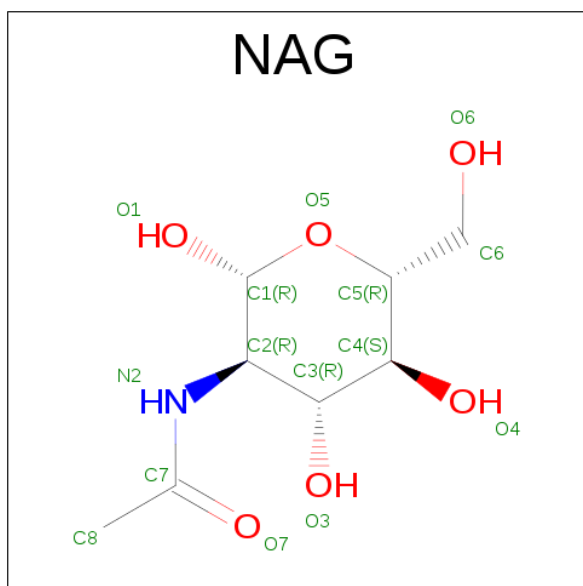
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	2	Total	C	N	O	0	0
			28	16	2	10		
4	B	2	Total	C	N	O	0	0
			28	16	2	10		
4	B	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 5 is a polymer of unknown type called SUGAR (3-MER).

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	3	Total	C	N	O	0	0
			42	24	3	15		

- Molecule 6 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	A	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		
6	B	1	Total	C	N	O	0	0
			14	8	1	5		

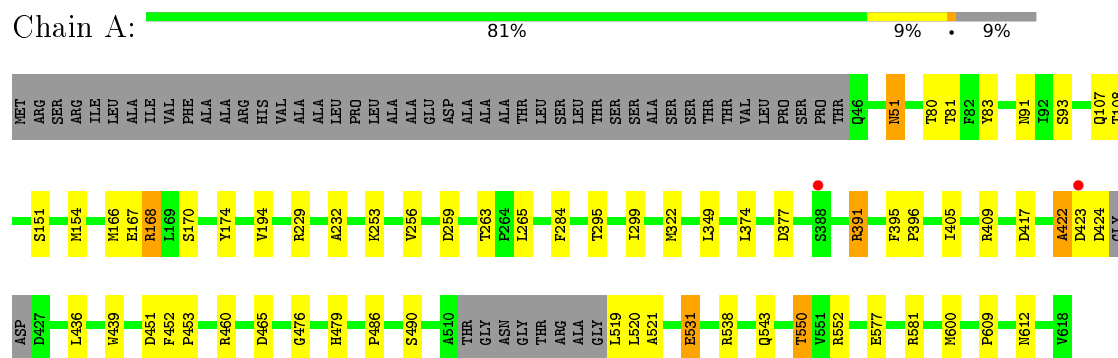
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	125	Total 125	O 125	0	0
7	B	72	Total 72	O 72	0	0
7	U	26	Total 26	O 26	0	0

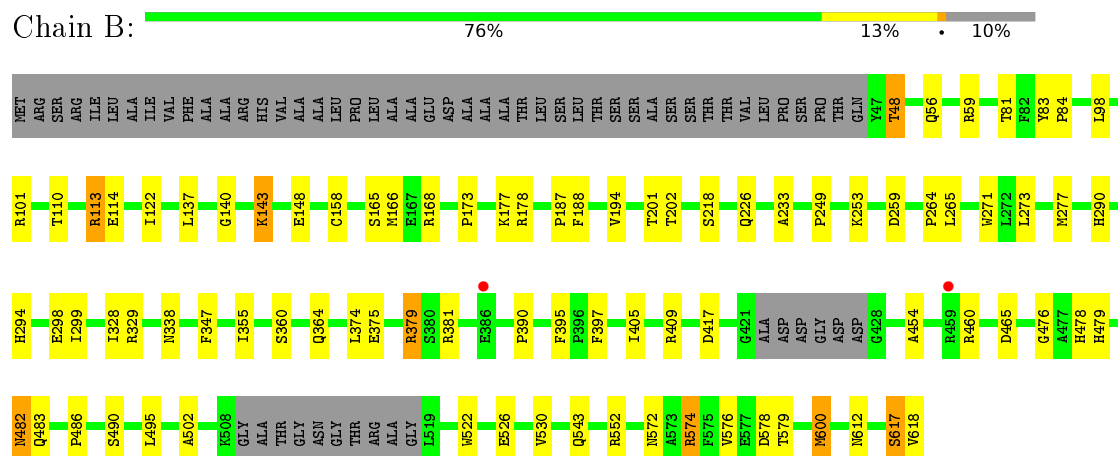
3 Residue-property plots

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.

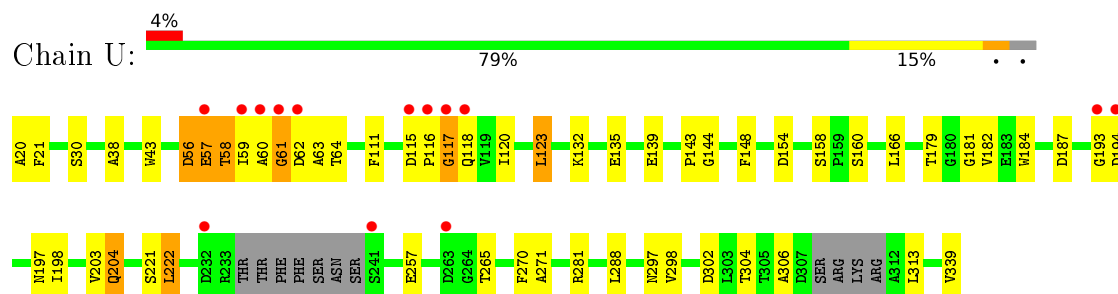
• Molecule 1: LINOLEATE 11-LIPOXYGENASE



• Molecule 1: LINOLEATE 11-LIPOXYGENASE



• Molecule 2: ZONADHESIN



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	226.31Å 50.47Å 177.62Å 90.00° 91.28° 90.00°	Depositor
Resolution (Å)	43.16 – 2.60 43.16 – 2.60	Depositor EDS
% Data completeness (in resolution range)	96.0 (43.16-2.60) 96.0 (43.16-2.60)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.33 (at 2.61Å)	Xtriage
Refinement program	PHENIX (PHENIX.REFINE)	Depositor
R, R_{free}	0.195 , 0.245 0.192 , 0.243	Depositor DCC
R_{free} test set	3049 reflections (5.06%)	DCC
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.529	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for -h,-k,l	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	11543	wwPDB-VP
Average B, all atoms (Å ²)	23.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.46% 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: MN, NAG

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	0.68	2/4513 (0.0%)	0.70	2/6132 (0.0%)
1	B	0.58	0/4469	0.64	1/6072 (0.0%)
2	U	0.59	0/2397	0.64	0/3283
All	All	0.62	2/11379 (0.0%)	0.66	3/15487 (0.0%)

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	451	ASP	C-N	-6.29	1.19	1.34
1	A	174	TYR	CD1-CE1	-5.53	1.31	1.39

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	ARG	NE-CZ-NH1	6.52	123.56	120.30
1	B	143	LYS	CD-CE-NZ	-6.33	97.15	111.70
1	A	322	MET	CG-SD-CE	-5.07	92.10	100.20

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	4397	0	4296	46	0
1	B	4353	0	4266	55	0
2	U	2344	0	2176	36	0
3	A	1	0	0	0	0
3	B	1	0	0	1	0
4	A	56	0	50	0	0
4	B	56	0	50	3	0
5	A	42	0	37	1	0
6	A	28	0	26	1	0
6	B	42	0	39	0	0
7	A	125	0	0	6	0
7	B	72	0	0	5	0
7	U	26	0	0	0	0
All	All	11543	0	10940	139	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 (139) 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)
2:U:61:GLY:O	2:U:63:ALA:N	1.87	1.06
1:A:263:THR:HG22	1:A:265:LEU:H	1.34	0.90
7:A:2079:HOH:O	1:B:101:ARG:NH2	2.13	0.80
1:A:577:GLU:OE1	7:A:2119:HOH:O	1.99	0.79
1:A:519:LEU:HD13	1:A:520:LEU:N	2.00	0.77
2:U:194:ASP:OD1	2:U:306:ALA:N	2.18	0.76
1:B:454:ALA:O	7:B:2062:HOH:O	2.04	0.75
2:U:60:ALA:HB3	2:U:120:ILE:HD13	1.67	0.75
1:A:519:LEU:HD12	1:A:521:ALA:H	1.50	0.74
1:B:81:THR:CG2	1:B:299:ILE:HB	2.19	0.73
1:B:574:ARG:NH1	1:B:578:ASP:OD1	2.22	0.72
1:A:81:THR:CG2	1:A:299:ILE:HB	2.18	0.72
2:U:203:VAL:HG12	2:U:265:THR:HG22	1.73	0.70
2:U:60:ALA:HA	2:U:61:GLY:O	1.92	0.69
1:A:423:ASP:OD1	1:A:423:ASP:O	2.11	0.68
1:B:618:VAL:N	7:B:2013:HOH:O	2.15	0.68
1:B:166:MET:HB3	1:B:600:MET:HE2	1.76	0.68
2:U:203:VAL:HG22	2:U:298:VAL:CG1	2.26	0.66
1:A:81:THR:HG21	1:A:299:ILE:HB	1.78	0.66
1:B:194:VAL:HG13	1:B:265:LEU:HD12	1.77	0.65
2:U:221:SER:OG	2:U:222:LEU:N	2.29	0.65

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:140:GLY:C	1:B:143:LYS:HZ1	2.00	0.65
1:B:618:VAL:O	7:B:2043:HOH:O	2.15	0.64
1:B:486:PRO:HA	1:B:490:SER:HB2	1.80	0.64
4:B:1004:NAG:H83	4:B:1004:NAG:H3	1.79	0.64
1:A:519:LEU:CD1	1:A:521:ALA:H	2.11	0.62
1:B:81:THR:HG21	1:B:299:ILE:HB	1.79	0.62
1:B:178:ARG:NH2	1:B:390:PRO:O	2.33	0.62
1:B:218:SER:HA	1:B:233:ALA:HB1	1.82	0.62
3:B:1000:MN:MN	7:B:2043:HOH:O	1.56	0.61
5:A:1005:NAG:H83	5:A:1005:NAG:H3	1.83	0.61
2:U:193:GLY:HA2	2:U:194:ASP:HB3	1.83	0.61
2:U:203:VAL:HG22	2:U:298:VAL:HG12	1.84	0.60
1:A:424:ASP:C	1:A:460:ARG:HD2	2.22	0.60
1:A:396:PRO:HG2	1:A:600:MET:HE3	1.84	0.59
1:B:298:GLU:OE1	1:B:329:ARG:NH2	2.34	0.59
2:U:193:GLY:CA	2:U:194:ASP:HB3	2.32	0.59
1:B:165:SER:HB3	1:B:249:PRO:HD3	1.83	0.59
1:B:166:MET:HB3	1:B:600:MET:CE	2.32	0.58
1:A:550:THR:HG23	1:A:609:PRO:O	2.03	0.58
2:U:204:GLN:HE21	2:U:297:ASN:HD22	1.51	0.58
1:B:110:THR:O	1:B:114:GLU:HG3	2.04	0.58
1:A:452:PHE:CG	1:A:453:PRO:HD2	2.38	0.58
1:B:81:THR:HG23	1:B:299:ILE:HB	1.86	0.58
1:B:483:GLN:NE2	1:B:617:SER:O	2.32	0.57
1:A:151:SER:HB3	1:A:154:MET:HB2	1.86	0.57
1:A:81:THR:HG23	1:A:299:ILE:HB	1.86	0.57
1:A:80:THR:OG1	1:A:81:THR:N	2.38	0.56
1:A:581:ARG:HH12	2:U:194:ASP:H	1.54	0.56
2:U:60:ALA:CB	2:U:120:ILE:HD13	2.36	0.56
1:B:543:GLN:HG3	4:B:1004:NAG:C7	2.35	0.56
2:U:184:TRP:HE1	2:U:204:GLN:HE22	1.52	0.55
1:A:519:LEU:HD13	1:A:520:LEU:H	1.71	0.55
2:U:21:PHE:CE1	2:U:56:ASP:HB2	2.42	0.54
1:B:360:SER:O	1:B:364:GLN:HG3	2.09	0.53
1:B:409:ARG:NH1	1:B:465:ASP:OD1	2.35	0.53
2:U:43:TRP:CE2	2:U:132:LYS:HE3	2.44	0.52
1:A:107:GLN:HB2	1:A:543:GLN:HE22	1.75	0.52
2:U:58:THR:C	2:U:60:ALA:H	2.14	0.52
2:U:21:PHE:CZ	2:U:56:ASP:HB2	2.46	0.51
1:A:166:MET:HB3	1:A:600:MET:CE	2.42	0.51
1:A:377:ASP:OD1	7:A:2087:HOH:O	2.19	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:U:135:GLU:O	2:U:139:GLU:HG2	2.12	0.50
1:A:422:ALA:HB3	1:A:460:ARG:NH2	2.26	0.50
2:U:187:ASP:OD2	2:U:281:ARG:NH2	2.39	0.49
2:U:58:THR:O	2:U:60:ALA:N	2.45	0.49
1:B:253:LYS:HE3	1:B:259:ASP:OD1	2.12	0.49
1:B:374:LEU:HD22	1:B:405:ILE:HD12	1.95	0.49
1:B:113:ARG:HG3	1:B:114:GLU:N	2.28	0.49
1:A:486:PRO:HA	1:A:490:SER:HB2	1.95	0.49
1:B:526:GLU:O	1:B:530:VAL:HG23	2.14	0.48
1:B:83:TYR:CG	1:B:84:PRO:HD2	2.49	0.48
1:A:253:LYS:HE2	1:A:259:ASP:OD1	2.13	0.48
1:A:83:TYR:HH	1:A:93:SER:HG	1.44	0.48
1:B:187:PRO:HB2	1:B:188:PHE:CD2	2.49	0.48
1:B:375:GLU:O	1:B:379:ARG:HG2	2.14	0.48
1:B:56:GLN:HG2	4:B:1001:NAG:HN2	1.78	0.47
1:A:374:LEU:HD22	1:A:405:ILE:HD12	1.97	0.47
1:A:108:THR:HG23	1:A:538:ARG:HD3	1.97	0.46
1:A:417:ASP:OD1	1:A:460:ARG:NH1	2.48	0.46
1:A:452:PHE:CD1	1:A:453:PRO:HD2	2.50	0.46
1:B:495:LEU:HD23	1:B:495:LEU:HA	1.78	0.46
1:B:158:CYS:O	1:B:495:LEU:HD11	2.16	0.46
1:A:166:MET:O	1:A:600:MET:HE1	2.16	0.46
1:A:417:ASP:HA	1:A:460:ARG:HH12	1.80	0.45
1:A:51:ASN:OD1	1:A:51:ASN:N	2.50	0.45
1:B:502:ALA:HB3	1:B:522:TRP:CD1	2.51	0.45
1:A:424:ASP:HA	7:A:2096:HOH:O	2.17	0.45
1:B:264:PRO:HG3	1:B:271:TRP:CZ2	2.52	0.45
1:B:168:ARG:HD3	7:B:2024:HOH:O	2.16	0.45
2:U:197:ASN:HB2	2:U:304:THR:HB	1.97	0.45
1:B:298:GLU:OE1	1:B:329:ARG:NE	2.46	0.45
1:B:552:ARG:HG2	1:B:579:THR:OG1	2.16	0.45
1:B:572:ASN:O	1:B:576:VAL:HG23	2.17	0.44
1:A:550:THR:HG22	1:A:552:ARG:H	1.83	0.44
1:A:81:THR:HB	1:A:295:THR:HB	1.99	0.44
1:A:436:LEU:HD12	1:A:439:TRP:HE3	1.82	0.44
1:B:177:LYS:HE2	1:B:381:ARG:HG2	1.99	0.44
1:A:396:PRO:HG2	1:A:600:MET:CE	2.45	0.44
2:U:198:ILE:HB	2:U:270:PHE:HB2	2.00	0.44
1:A:479:HIS:CD2	1:A:612:ASN:HB3	2.53	0.44
1:B:355:ILE:HD13	1:B:355:ILE:HA	1.86	0.44
2:U:182:VAL:CG2	2:U:288:LEU:HD11	2.48	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:232:ALA:HA	1:A:256:VAL:HG21	1.99	0.44
1:B:294:HIS:CE1	1:B:328:ILE:HG12	2.53	0.44
1:B:478:HIS:CE1	1:B:482:ASN:HB3	2.53	0.44
1:B:201:THR:OG1	1:B:202:THR:N	2.51	0.43
1:A:91:ASN:HD22	6:A:1006:NAG:H83	1.82	0.43
1:B:417:ASP:HA	1:B:460:ARG:HH12	1.81	0.43
2:U:143:PRO:HA	2:U:144:GLY:HA2	1.75	0.43
2:U:57:GLU:HG3	2:U:57:GLU:H	1.66	0.43
2:U:64:THR:HA	2:U:111:PHE:O	2.19	0.43
2:U:123:LEU:HD23	2:U:123:LEU:HA	1.93	0.43
1:B:122:ILE:HD11	1:B:137:LEU:HA	1.99	0.43
1:B:173:PRO:HG3	1:B:397:PHE:CG	2.54	0.43
2:U:194:ASP:OD1	2:U:194:ASP:O	2.37	0.43
1:B:48:THR:O	1:B:59:ARG:NH2	2.46	0.42
2:U:30:SER:HB2	2:U:38:ALA:HB2	2.00	0.42
2:U:302:ASP:HB3	2:U:313:LEU:HD21	2.00	0.42
2:U:257:GLU:CD	2:U:271:ALA:HB2	2.40	0.42
1:A:409:ARG:NH1	1:A:465:ASP:OD1	2.47	0.42
1:B:48:THR:HG22	1:B:59:ARG:HH12	1.85	0.42
2:U:118:GLN:NE2	2:U:339:VAL:O	2.53	0.42
1:A:194:VAL:HG13	1:A:265:LEU:HD12	2.02	0.42
1:B:479:HIS:CD2	1:B:612:ASN:HB3	2.55	0.42
1:B:140:GLY:CA	1:B:143:LYS:HZ1	2.32	0.42
1:A:170:SER:HB3	1:A:600:MET:HE3	2.02	0.41
1:B:338:ASN:N	1:B:338:ASN:OD1	2.49	0.41
1:A:284:PHE:CE2	1:A:349:LEU:HD12	2.55	0.41
1:B:140:GLY:HA2	1:B:143:LYS:HZ1	1.86	0.41
1:B:226:GLN:NE2	1:B:347:PHE:O	2.54	0.41
2:U:116:PRO:O	2:U:117:GLY:C	2.59	0.41
1:B:273:LEU:O	1:B:277:MET:HG3	2.21	0.40
1:B:166:MET:O	1:B:600:MET:HE3	2.21	0.40
2:U:20:ALA:N	2:U:154:ASP:OD1	2.53	0.40
1:A:167:GLU:OE1	1:A:168:ARG:NH2	2.54	0.40
1:A:531:GLU:OE2	7:A:2112:HOH:O	2.22	0.40
1:A:391:ARG:NH1	7:A:2090:HOH:O	2.23	0.40
2:U:148:PHE:O	2:U:158:SER:HA	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	557/618 (90%)	533 (96%)	22 (4%)	2 (0%)	39	65
1	B	550/618 (89%)	523 (95%)	26 (5%)	1 (0%)	52	77
2	U	303/320 (95%)	282 (93%)	13 (4%)	8 (3%)	7	11
All	All	1410/1556 (91%)	1338 (95%)	61 (4%)	11 (1%)	24	46

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	U	58	THR
2	U	62	ASP
2	U	61	GLY
2	U	117	GLY
1	A	476	GLY
2	U	179	THR
1	A	422	ALA
1	B	476	GLY
2	U	222	LEU
2	U	181	GLY
2	U	59	ILE

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	451/491 (92%)	445 (99%)	6 (1%)	76	91

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	448/491 (91%)	437 (98%)	11 (2%)	55	81
2	U	265/277 (96%)	258 (97%)	7 (3%)	54	80
All	All	1164/1259 (92%)	1140 (98%)	24 (2%)	61	85

All (24) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	51	ASN
1	A	168	ARG
1	A	391	ARG
1	A	395	PHE
1	A	531	GLU
1	A	550	THR
1	B	48	THR
1	B	98	LEU
1	B	113	ARG
1	B	148	GLU
1	B	290	HIS
1	B	379	ARG
1	B	395	PHE
1	B	482	ASN
1	B	574	ARG
1	B	600	MET
1	B	617	SER
2	U	56	ASP
2	U	57	GLU
2	U	115	ASP
2	U	123	LEU
2	U	160	SER
2	U	166	LEU
2	U	204	GLN

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

Mol	Chain	Res	Type
2	U	204	GLN

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 ⓘ

11 carbohydrates 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	$\# Z > 2$
4	NAG	A	1001	1,4	14,14,15	0.58	0	15,19,21	0.29	0
4	NAG	A	1002	4	14,14,15	0.38	0	15,19,21	0.62	0
5	NAG	A	1003	1,5	14,14,15	0.58	0	15,19,21	0.51	0
5	NAG	A	1004	5	14,14,15	0.56	0	15,19,21	0.98	1 (6%)
5	NAG	A	1005	5	14,14,15	1.28	1 (7%)	15,19,21	2.11	4 (26%)
4	NAG	A	1007	1,4	14,14,15	0.20	0	15,19,21	0.49	0
4	NAG	A	1008	4	14,14,15	0.27	0	15,19,21	0.46	0
4	NAG	B	1001	1,4	14,14,15	0.96	1 (7%)	15,19,21	1.97	2 (13%)
4	NAG	B	1002	4	14,14,15	1.43	1 (7%)	15,19,21	0.72	0
4	NAG	B	1004	1,4	14,14,15	0.54	0	15,19,21	1.40	1 (6%)
4	NAG	B	1005	4	14,14,15	0.30	0	15,19,21	0.65	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	NAG	A	1001	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1002	4	-	0/6/23/26	0/1/1/1
5	NAG	A	1003	1,5	-	0/6/23/26	0/1/1/1
5	NAG	A	1004	5	-	0/6/23/26	0/1/1/1
5	NAG	A	1005	5	-	0/6/23/26	0/1/1/1
4	NAG	A	1007	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	1008	4	-	0/6/23/26	0/1/1/1
4	NAG	B	1001	1,4	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	NAG	B	1002	4	-	0/6/23/26	0/1/1/1
4	NAG	B	1004	1,4	-	0/6/23/26	0/1/1/1
4	NAG	B	1005	4	-	0/6/23/26	0/1/1/1

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1002	NAG	O5-C1	-4.90	1.35	1.43
4	B	1001	NAG	O5-C1	2.98	1.48	1.43
5	A	1005	NAG	O5-C1	4.49	1.51	1.43

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	1005	NAG	C4-C3-C2	-2.05	108.15	111.34
5	A	1004	NAG	C1-O5-C5	2.33	115.57	112.14
5	A	1005	NAG	O3-C3-C4	2.35	115.66	110.36
4	B	1004	NAG	C2-N2-C7	4.45	128.90	123.11
5	A	1005	NAG	C2-N2-C7	4.48	128.93	123.11
4	B	1001	NAG	O4-C4-C5	4.86	122.03	109.23
4	B	1001	NAG	C1-O5-C5	5.08	119.61	112.14
5	A	1005	NAG	C1-O5-C5	5.52	120.25	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

3 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1005	NAG	1	0
4	B	1001	NAG	1	0
4	B	1004	NAG	2	0

5.6 Ligand geometry

Of 7 ligands modelled in this entry, 2 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
6	NAG	A	1006	1	14,14,15	0.44	0	15,19,21	0.54	0
6	NAG	A	1009	1	14,14,15	0.74	1 (7%)	15,19,21	0.71	0
6	NAG	B	1003	1	14,14,15	0.24	0	15,19,21	0.65	1 (6%)
6	NAG	B	1006	1	14,14,15	0.49	0	15,19,21	0.88	1 (6%)
6	NAG	B	1007	1	14,14,15	0.39	0	15,19,21	0.29	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
6	NAG	A	1006	1	-	0/6/23/26	0/1/1/1
6	NAG	A	1009	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1003	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1006	1	-	0/6/23/26	0/1/1/1
6	NAG	B	1007	1	-	0/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	A	1009	NAG	O5-C1	-2.17	1.40	1.43

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	B	1003	NAG	C1-O5-C5	2.15	115.31	112.14
6	B	1006	NAG	C1-O5-C5	2.61	115.98	112.14

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
6	A	1006	NAG	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	563/618 (91%)	-0.54	2 (0%) 93 91	6, 14, 31, 69	0
1	B	556/618 (89%)	-0.37	2 (0%) 93 91	11, 23, 42, 73	0
2	U	309/320 (96%)	-0.03	14 (4%) 37 29	15, 29, 74, 105	0
All	All	1428/1556 (91%)	-0.36	18 (1%) 79 75	6, 21, 43, 105	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	U	59	ILE	4.7
2	U	62	ASP	3.8
2	U	118	GLN	3.5
2	U	117	GLY	3.4
2	U	241	SER	3.4
2	U	60	ALA	3.1
1	B	386	GLU	3.1
1	A	388	SER	2.7
2	U	57	GLU	2.7
2	U	115	ASP	2.6
2	U	116	PRO	2.5
2	U	61	GLY	2.3
2	U	263	ASP	2.3
2	U	194	ASP	2.3
2	U	193	GLY	2.3
2	U	232	ASP	2.2
1	B	459	ARG	2.1
1	A	423	ASP	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 ⓘ

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
4	NAG	B	1002	14/15	0.87	0.24	6.48	43,48,55,62	0
4	NAG	B	1001	14/15	0.93	0.17	3.20	28,34,41,42	0
5	NAG	A	1005	14/15	0.85	0.20	2.31	24,27,39,40	0
5	NAG	A	1004	14/15	0.97	0.13	0.30	15,19,23,24	0
4	NAG	A	1001	14/15	0.95	0.12	-0.49	18,26,32,35	0
5	NAG	A	1003	14/15	0.97	0.11	-0.60	11,12,15,18	0
4	NAG	A	1007	14/15	0.92	0.15	-	24,31,35,42	0
4	NAG	B	1005	14/15	0.85	0.26	-	49,52,56,57	0
4	NAG	B	1004	14/15	0.84	0.32	-	41,47,52,63	0
4	NAG	A	1002	14/15	0.86	0.27	-	40,48,54,55	0
4	NAG	A	1008	14/15	0.91	0.24	-	32,38,48,58	0

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(Å ²)	Q<0.9
6	NAG	B	1006	14/15	0.76	0.31	8.57	47,59,66,73	0
3	MN	B	1000	1/1	0.95	0.28	2.87	56,56,56,56	0
6	NAG	B	1003	14/15	0.86	0.36	1.55	45,63,71,76	0
6	NAG	A	1009	14/15	0.97	0.15	0.26	14,17,21,24	0
6	NAG	B	1007	14/15	0.90	0.15	-0.65	32,35,39,40	0
3	MN	A	1000	1/1	0.99	0.12	-1.51	8,8,8,8	0
6	NAG	A	1006	14/15	0.83	0.35	-	32,46,59,63	0

6.5 Other polymers ⓘ

There are no such residues in this entry.