Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 10:27 AM GMT

PDB ID	:	3LXA
Title	:	Interconversion of Human Lysosomal Enzyme Specificities
Authors	:	Tomasic, I.B.; Metcalf, M.C.; Guce, A.I.; Clark, N.E.; Garman, S.C.
Deposited on	:	2010-02-25
Resolution	:	3.04 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 (i) symbol.

The following versions of software and data (see references (1)) were used in the production of this report:

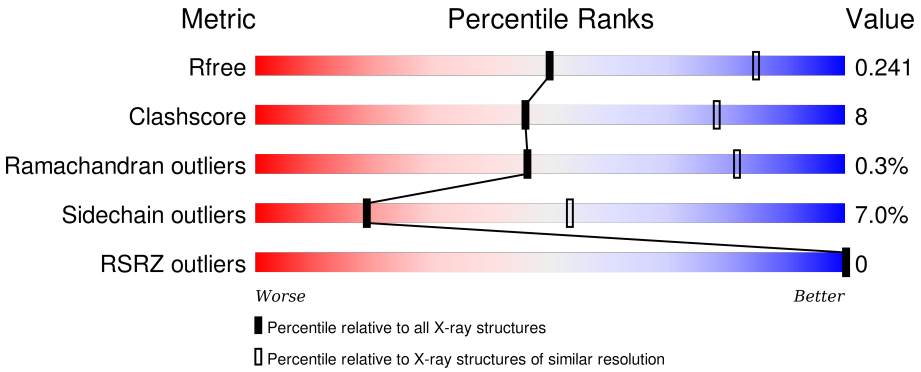
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	trunk26865

1 Overall quality at a glance (i)

The following experimental techniques were used to determine the structure:
X-RAY DIFFRACTION

The reported resolution of this entry is 3.04 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	1995 (3.08-3.00)
Clashscore	102246	2351 (3.08-3.00)
Ramachandran outliers	100387	2272 (3.08-3.00)
Sidechain outliers	100360	2275 (3.08-3.00)
RSRZ outliers	91569	2013 (3.08-3.00)

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 <=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	404	74% 21%
1	B	404	78% 17%

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
5	GLA	A	803	-	-	-	X
5	GLA	B	804	-	-	-	X

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 6557 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.

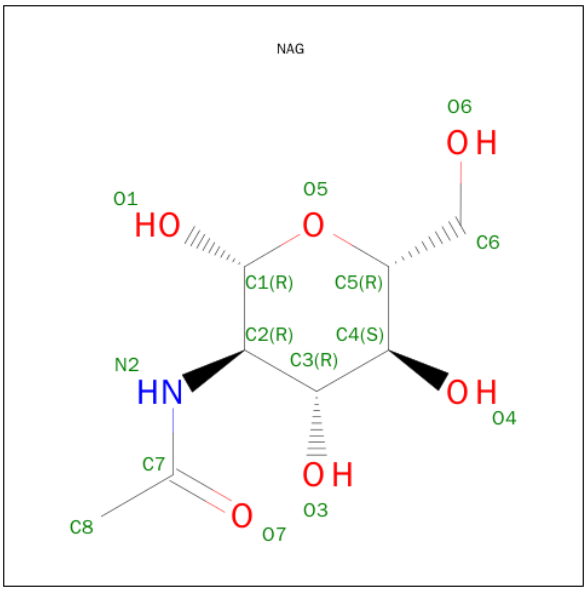
- Molecule 1 is a protein called Alpha-galactosidase A.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	395	Total	C	N	O	S	0	0	0
			3156	2008	541	580	27			
1	B	394	Total	C	N	O	S	0	0	0
			3147	2002	539	579	27			

There are 16 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	203	SER	GLU	ENGINEERED	UNP P06280
A	206	ALA	LEU	ENGINEERED	UNP P06280
A	430	HIS	-	EXPRESSION TAG	UNP P06280
A	431	HIS	-	EXPRESSION TAG	UNP P06280
A	432	HIS	-	EXPRESSION TAG	UNP P06280
A	433	HIS	-	EXPRESSION TAG	UNP P06280
A	434	HIS	-	EXPRESSION TAG	UNP P06280
A	435	HIS	-	EXPRESSION TAG	UNP P06280
B	203	SER	GLU	ENGINEERED	UNP P06280
B	206	ALA	LEU	ENGINEERED	UNP P06280
B	430	HIS	-	EXPRESSION TAG	UNP P06280
B	431	HIS	-	EXPRESSION TAG	UNP P06280
B	432	HIS	-	EXPRESSION TAG	UNP P06280
B	433	HIS	-	EXPRESSION TAG	UNP P06280
B	434	HIS	-	EXPRESSION TAG	UNP P06280
B	435	HIS	-	EXPRESSION TAG	UNP P06280

- Molecule 2 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

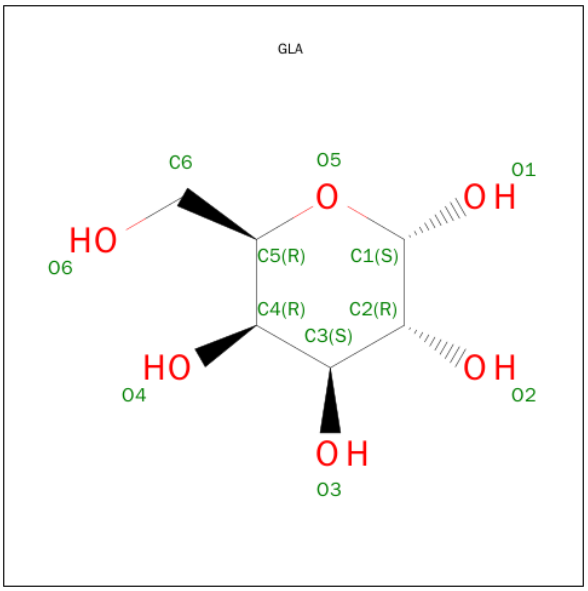
- Molecule 3 is a polymer of unknown type called SUGAR (4-MER).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	4	Total C N O 50 28 2 20	0	0
3	B	4	Total C N O 50 28 2 20	0	0

- 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 28 16 2 10	0	0

- Molecule 5 is SUGAR (ALPHA D-GALACTOSE) (three-letter code: GLA) (formula: $C_6H_{12}O_6$).



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

- Molecule 6 is water.

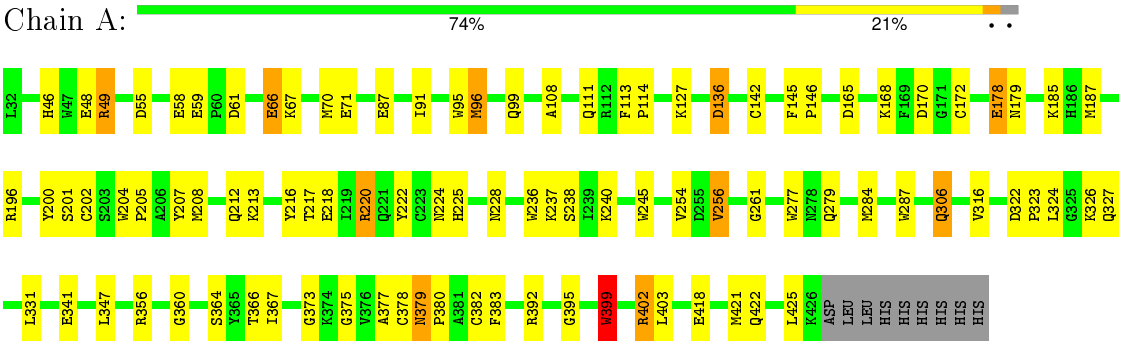
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	19	Total O 19 19	0	0
6	B	17	Total O 17 17	0	0

3 Residue-property plots (i)

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of 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.

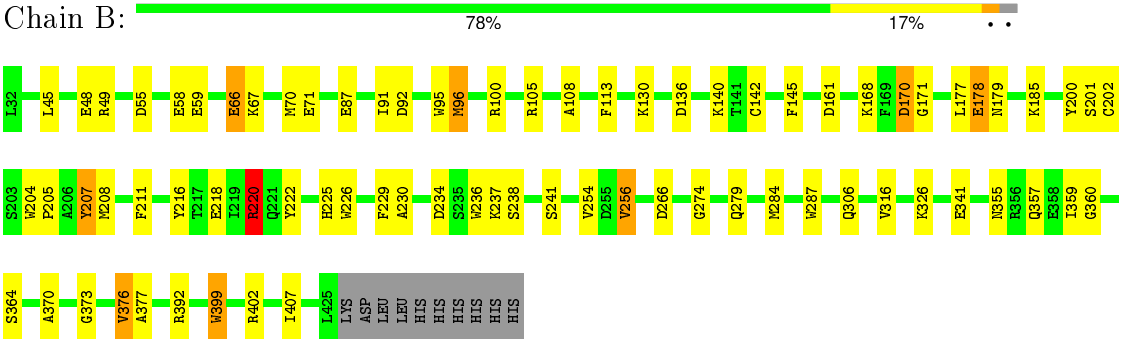
- Molecule 1: Alpha-galactosidase A

Chain A:



- Molecule 1: Alpha-galactosidase A

Chain B:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	59.24Å 104.96Å 181.04Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.63 – 3.04 49.62 – 3.04	Depositor EDS
% Data completeness (in resolution range)	99.5 (49.63-3.04) 99.5 (49.62-3.04)	Depositor EDS
R_{merge}	0.27	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	3.01 (at 3.07Å)	Xtriage
Refinement program	REFMAC 5.5.0070	Depositor
R, R_{free}	0.214 , 0.244 0.213 , 0.241	Depositor DCC
R_{free} test set	1128 reflections (5.30%)	DCC
Wilson B-factor (Å^2)	42.0	Xtriage
Anisotropy	0.148	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.35 , 42.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.32$	Xtriage
Outliers	1 of 22400 reflections (0.004%)	Xtriage
F_o,F_c correlation	0.90	EDS
Total number of atoms	6557	wwPDB-VP
Average B, all atoms (Å^2)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.21% of the height of the origin peak. No significant pseudotranslation is detected.*

[1] Intensities estimated from amplitudes.

[2] Theoretical values of $< |L| >$, $< L^2 >$ 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: GLA, BMA, NAG, MAN

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	0.70	7/3243 (0.2%)	0.70	4/4402 (0.1%)
1	B	0.75	8/3234 (0.2%)	0.70	7/4391 (0.2%)
All	All	0.72	15/6477 (0.2%)	0.70	11/8793 (0.1%)

All (15) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	178	GLU	CD-OE2	24.13	1.52	1.25
1	A	178	GLU	CD-OE2	21.75	1.49	1.25
1	B	399	TRP	CG-CD1	-8.01	1.25	1.36
1	B	207	TYR	CE1-CZ	-7.16	1.29	1.38
1	A	399	TRP	CG-CD1	-7.00	1.26	1.36
1	A	207	TYR	CE1-CZ	-6.67	1.29	1.38
1	A	207	TYR	CE2-CZ	-6.63	1.29	1.38
1	B	207	TYR	CE2-CZ	-6.55	1.30	1.38
1	B	207	TYR	CG-CD2	-6.39	1.30	1.39
1	B	207	TYR	CG-CD1	-6.25	1.31	1.39
1	A	207	TYR	CG-CD2	-5.80	1.31	1.39
1	A	207	TYR	CG-CD1	-5.50	1.31	1.39
1	A	399	TRP	CB-CG	-5.45	1.40	1.50
1	B	399	TRP	CB-CG	-5.44	1.40	1.50
1	B	220	ARG	CZ-NH1	5.40	1.40	1.33

All (11) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	170	ASP	CB-CG-OD1	7.26	124.83	118.30
1	B	399	TRP	CA-CB-CG	-6.78	100.81	113.70
1	A	220	ARG	CG-CD-NE	-6.70	97.72	111.80
1	A	218	GLU	OE1-CD-OE2	-6.11	115.96	123.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	399	TRP	CB-CG-CD1	-5.86	119.39	127.00
1	A	66	GLU	OE1-CD-OE2	-5.77	116.38	123.30
1	B	399	TRP	CB-CG-CD2	5.72	134.03	126.60
1	B	218	GLU	OE1-CD-OE2	-5.61	116.57	123.30
1	B	220	ARG	NE-CZ-NH2	-5.58	117.51	120.30
1	A	136	ASP	CB-CG-OD2	5.55	123.30	118.30
1	B	66	GLU	OE1-CD-OE2	-5.04	117.25	123.30

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	3156	0	3020	58	0
1	B	3147	0	3007	41	0
2	A	14	0	13	0	0
2	B	28	0	26	0	0
3	A	50	0	43	0	0
3	B	50	0	43	1	0
4	A	28	0	25	3	0
5	A	24	0	24	2	0
5	B	24	0	24	1	0
6	A	19	0	0	1	0
6	B	17	0	0	1	0
All	All	6557	0	6225	98	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 8.

All (98) 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:A:379:ASN:HB2	1:A:399:TRP:HE3	1.40	0.85
1:A:399:TRP:C	1:A:399:TRP:CD1	2.50	0.81

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:379:ASN:HB2	1:A:399:TRP:CE3	2.17	0.80
1:B:370:ALA:HA	1:B:399:TRP:HE1	1.46	0.79
1:A:378:CYS:O	1:A:399:TRP:HB2	1.83	0.78
1:A:67:LYS:HE3	1:A:71:GLU:OE2	1.85	0.76
1:B:67:LYS:HE3	1:B:71:GLU:OE2	1.86	0.75
1:A:375:GLY:O	1:A:399:TRP:HZ3	1.73	0.71
1:A:379:ASN:HD22	1:A:380:PRO:HA	1.56	0.71
1:B:177:LEU:HD11	1:B:211:PHE:HB3	1.74	0.70
1:B:177:LEU:HD11	1:B:211:PHE:CB	2.22	0.69
1:B:399:TRP:CD1	1:B:399:TRP:O	2.49	0.66
1:B:136:ASP:OD1	1:B:140:LYS:O	2.15	0.64
1:A:220:ARG:NH1	1:A:256:VAL:O	2.30	0.64
1:B:177:LEU:HD11	1:B:211:PHE:CG	2.33	0.63
1:B:399:TRP:C	1:B:399:TRP:CD1	2.68	0.62
1:B:67:LYS:O	1:B:71:GLU:HG3	1.98	0.62
1:A:331:LEU:HD22	1:A:341:GLU:OE2	2.01	0.61
1:A:67:LYS:O	1:A:71:GLU:HG3	2.01	0.61
1:A:375:GLY:O	1:A:399:TRP:CZ3	2.52	0.61
3:B:694:BMA:H2	3:B:695:MAN:H3	1.83	0.59
1:A:399:TRP:C	1:A:399:TRP:HD1	2.05	0.59
1:A:217:THR:CG2	4:A:715:NAG:H5	2.32	0.59
1:A:204:TRP:HB3	1:A:205:PRO:HD3	1.85	0.59
1:A:367:ILE:HG13	6:A:19:HOH:O	2.04	0.57
1:B:204:TRP:HB3	1:B:205:PRO:HD3	1.88	0.55
1:A:66:GLU:OE2	1:A:114:PRO:HG2	2.07	0.55
1:A:216:TYR:HB3	1:A:256:VAL:HG21	1.89	0.54
1:A:142:CYS:HB2	5:A:801:GLA:O6	2.07	0.54
1:B:236:TRP:CE3	1:B:279:GLN:HG2	2.43	0.54
1:A:379:ASN:CB	1:A:399:TRP:CE3	2.91	0.53
1:A:378:CYS:HA	1:A:382:CYS:HB3	1.89	0.53
1:B:168:LYS:HA	1:B:201:SER:HB3	1.90	0.53
1:B:96:MET:HG3	1:B:145:PHE:HB3	1.92	0.52
1:B:100:ARG:HA	1:B:105:ARG:O	2.10	0.52
1:A:108:ALA:HB1	1:A:113:PHE:HB2	1.92	0.51
1:B:357:GLN:HE21	1:B:359:ILE:HG23	1.75	0.51
1:B:108:ALA:HB1	1:B:113:PHE:HB2	1.92	0.51
1:B:142:CYS:SG	1:B:170:ASP:OD2	2.70	0.50
1:A:228:ASN:HB3	1:A:245:TRP:CH2	2.47	0.49
1:B:161:ASP:HB2	6:B:9:HOH:O	2.11	0.49
1:A:96:MET:HG3	1:A:145:PHE:HB3	1.94	0.49
1:A:208:MET:O	1:A:212:GLN:HB2	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:217:THR:HG22	4:A:715:NAG:H5	1.95	0.48
1:A:224:ASN:O	1:A:261:GLY:HA2	2.14	0.48
1:A:168:LYS:HA	1:A:201:SER:HB3	1.94	0.48
1:A:55:ASP:OD2	1:A:58:GLU:HB2	2.14	0.48
1:B:58:GLU:C	1:B:59:GLU:HG2	2.34	0.47
1:B:216:TYR:HB3	1:B:256:VAL:HG21	1.96	0.47
1:A:216:TYR:O	1:A:220:ARG:HB2	2.14	0.47
1:B:229:PHE:CG	1:B:230:ALA:N	2.83	0.47
1:A:200:TYR:CE2	1:A:202:CYS:SG	3.08	0.46
1:B:216:TYR:O	1:B:220:ARG:HB3	2.16	0.46
1:A:236:TRP:CE3	1:A:279:GLN:HG2	2.51	0.46
1:A:379:ASN:CB	1:A:399:TRP:HE3	2.19	0.46
1:A:136:ASP:OD1	1:A:172:CYS:HB2	2.16	0.45
1:A:185:LYS:HG2	1:A:222:TYR:CZ	2.51	0.45
1:B:66:GLU:O	1:B:70:MET:HG3	2.17	0.45
1:B:341:GLU:OE1	1:B:373:GLY:N	2.44	0.45
1:A:324:LEU:HD22	1:A:326:LYS:HB2	1.99	0.45
1:A:49:ARG:HD2	1:A:49:ARG:HA	1.51	0.45
1:A:324:LEU:CD2	1:A:326:LYS:HB2	2.47	0.45
1:A:284:MET:HG3	1:A:316:VAL:HG11	1.99	0.44
1:B:185:LYS:HG2	1:B:222:TYR:CZ	2.52	0.44
1:A:48:GLU:O	1:B:360:GLY:HA2	2.17	0.44
1:B:202:CYS:O	1:B:226:TRP:HA	2.18	0.44
1:B:200:TYR:CE2	1:B:202:CYS:SG	3.10	0.44
1:A:402:ARG:HB3	1:A:402:ARG:HE	1.61	0.43
1:A:58:GLU:C	1:A:59:GLU:HG2	2.37	0.43
1:B:55:ASP:OD2	1:B:58:GLU:HB2	2.19	0.43
1:B:171:GLY:HA3	1:B:207:TYR:CD2	2.54	0.43
1:A:165:ASP:OD1	1:A:196:ARG:NH2	2.51	0.43
1:A:366:THR:HG22	1:A:402:ARG:HH21	1.84	0.43
1:A:66:GLU:O	1:A:70:MET:HG3	2.19	0.42
1:B:236:TRP:CD2	1:B:279:GLN:HG2	2.55	0.42
1:B:373:GLY:O	1:B:376:VAL:HG23	2.19	0.42
1:A:217:THR:HG21	4:A:715:NAG:H5	2.02	0.42
1:B:91:ILE:HG21	1:B:95:TRP:HB3	2.00	0.42
1:A:383:PHE:CE1	1:A:395:GLY:HA2	2.54	0.42
1:A:403:LEU:HD23	1:A:403:LEU:C	2.40	0.42
1:A:360:GLY:HA2	1:B:48:GLU:O	2.20	0.42
1:B:284:MET:HG3	1:B:316:VAL:HG11	2.02	0.42
1:B:234:ASP:O	1:B:274:GLY:HA3	2.20	0.41
1:A:145:PHE:HB3	1:A:146:PRO:HD2	2.01	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:91:ILE:HG21	1:A:95:TRP:HB3	2.01	0.41
1:A:254:VAL:HG13	1:A:327:GLN:HG2	2.02	0.41
1:A:277:TRP:CZ3	1:A:306:GLN:HB3	2.55	0.41
1:A:236:TRP:CD2	1:A:279:GLN:HG2	2.56	0.41
1:B:254:VAL:HB	5:B:804:GLA:O4	2.21	0.41
1:B:45:LEU:HD11	1:B:92:ASP:OD2	2.21	0.41
1:A:378:CYS:O	1:A:399:TRP:CB	2.63	0.41
1:A:373:GLY:HA3	1:A:377:ALA:HB2	2.03	0.41
1:A:322:ASP:HA	1:A:323:PRO:HD3	1.98	0.40
1:B:205:PRO:CG	1:B:226:TRP:HB2	2.51	0.40
1:A:170:ASP:OD1	5:A:801:GLA:H2	2.21	0.40
1:B:355:ASN:HB2	1:B:407:ILE:HB	2.02	0.40
1:B:373:GLY:HA3	1:B:377:ALA:HB2	2.03	0.40
1:A:240:LYS:HD2	1:A:356:ARG:NH2	2.37	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	393/404 (97%)	372 (95%)	20 (5%)	1 (0%)	46 82
1	B	392/404 (97%)	375 (96%)	16 (4%)	1 (0%)	46 82
All	All	785/808 (97%)	747 (95%)	36 (5%)	2 (0%)	46 82

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	425	LEU
1	B	266	ASP

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	335/344 (97%)	308 (92%)	27 (8%)	15 45
1	B	334/344 (97%)	314 (94%)	20 (6%)	24 60
All	All	669/688 (97%)	622 (93%)	47 (7%)	19 53

All (47) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	46	HIS
1	A	49	ARG
1	A	61	ASP
1	A	87	GLU
1	A	96	MET
1	A	99	GLN
1	A	111	GLN
1	A	127	LYS
1	A	178	GLU
1	A	179	ASN
1	A	187	MET
1	A	213	LYS
1	A	225	HIS
1	A	237	LYS
1	A	238	SER
1	A	256	VAL
1	A	287	TRP
1	A	306	GLN
1	A	347	LEU
1	A	364	SER
1	A	379	ASN
1	A	392	ARG
1	A	399	TRP
1	A	402	ARG
1	A	418	GLU
1	A	421	MET
1	A	422	GLN

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Mol	Chain	Res	Type
1	B	49	ARG
1	B	87	GLU
1	B	96	MET
1	B	130	LYS
1	B	178	GLU
1	B	179	ASN
1	B	208	MET
1	B	220	ARG
1	B	225	HIS
1	B	237	LYS
1	B	238	SER
1	B	241	SER
1	B	256	VAL
1	B	287	TRP
1	B	306	GLN
1	B	326	LYS
1	B	364	SER
1	B	376	VAL
1	B	392	ARG
1	B	402	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	111	GLN
1	A	122	ASN
1	A	336	ASN
1	A	379	ASN
1	B	111	GLN
1	B	122	ASN
1	B	157	GLN
1	B	228	ASN
1	B	357	GLN

5.3.3 RNA

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)

10 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	$\#\|Z\| > 2$
3	NAG	A	692	1,3	14,14,15	0.50	0	15,19,21	0.81	0
3	NAG	A	693	3	14,14,15	0.48	0	15,19,21	0.81	0
3	BMA	A	694	3	11,11,12	0.42	0	14,15,17	0.93	1 (7%)
3	MAN	A	695	3	11,11,12	0.59	0	14,15,17	1.01	1 (7%)
4	NAG	A	715	1,4	14,14,15	0.53	0	15,19,21	0.89	1 (6%)
4	NAG	A	716	4	14,14,15	0.54	0	15,19,21	0.83	0
3	NAG	B	692	1,3	14,14,15	0.50	0	15,19,21	0.74	0
3	NAG	B	693	3	14,14,15	0.58	0	15,19,21	0.96	1 (6%)
3	BMA	B	694	3	11,11,12	0.51	0	14,15,17	1.56	2 (14%)
3	MAN	B	695	3	11,11,12	0.58	0	14,15,17	2.40	2 (14%)

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	NAG	A	692	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	693	3	-	0/6/23/26	0/1/1/1
3	BMA	A	694	3	-	0/2/19/22	0/1/1/1
3	MAN	A	695	3	-	0/2/19/22	0/1/1/1
4	NAG	A	715	1,4	-	0/6/23/26	0/1/1/1
4	NAG	A	716	4	-	0/6/23/26	0/1/1/1
3	NAG	B	692	1,3	-	0/6/23/26	0/1/1/1
3	NAG	B	693	3	-	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	BMA	B	694	3	-	0/2/19/22	0/1/1/1
3	MAN	B	695	3	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
3	A	694	BMA	O5-C5-C6	2.03	111.73	107.35
3	A	695	MAN	C1-C2-C3	2.08	112.00	109.54
4	A	715	NAG	C1-O5-C5	2.10	114.91	112.25
3	B	693	NAG	C4-C3-C2	2.11	114.51	111.23
3	B	694	BMA	C3-C4-C5	2.39	114.37	110.20
3	B	695	MAN	O5-C1-C2	2.85	115.47	110.86
3	B	694	BMA	C1-C2-C3	4.50	114.86	109.54
3	B	695	MAN	C1-O5-C5	7.84	122.20	112.25

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
4	A	715	NAG	3	0
3	B	694	BMA	1	0
3	B	695	MAN	1	0

5.6 Ligand geometry

7 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
2	NAG	A	639	1	14,14,15	0.67	1 (7%)	15,19,21	2.00	3 (20%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\|>2$	Counts	RMSZ	$\#\|Z\|>2$
5	GLA	A	801	-	12,12,12	0.36	0	17,17,17	1.05	1 (5%)
5	GLA	A	803	-	12,12,12	0.82	0	17,17,17	1.23	1 (5%)
2	NAG	B	639	1	14,14,15	0.56	0	15,19,21	1.21	1 (6%)
2	NAG	B	715	1	14,14,15	0.56	0	15,19,21	0.87	1 (6%)
5	GLA	B	802	-	12,12,12	0.60	0	17,17,17	0.91	0
5	GLA	B	804	-	12,12,12	0.59	0	17,17,17	1.00	1 (5%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	639	1	-	0/6/23/26	0/1/1/1
5	GLA	A	801	-	-	0/2/22/22	0/1/1/1
5	GLA	A	803	-	-	0/2/22/22	0/1/1/1
2	NAG	B	639	1	-	0/6/23/26	0/1/1/1
2	NAG	B	715	1	-	0/6/23/26	0/1/1/1
5	GLA	B	802	-	-	0/2/22/22	0/1/1/1
5	GLA	B	804	-	-	0/2/22/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	A	639	NAG	C1-C2	2.06	1.55	1.52

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
2	A	639	NAG	C3-C4-C5	-2.57	105.72	110.20
2	A	639	NAG	O7-C7-C8	-2.21	118.00	122.06
2	B	715	NAG	C1-O5-C5	2.02	114.81	112.25
2	B	639	NAG	C2-N2-C7	2.10	125.74	123.04
5	B	804	GLA	C1-O5-C5	2.39	117.90	113.47
5	A	801	GLA	C1-O5-C5	2.99	119.00	113.47
5	A	803	GLA	C1-O5-C5	3.01	119.04	113.47
2	A	639	NAG	C1-O5-C5	5.77	119.57	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	801	GLA	2	0
5	B	804	GLA	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

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, 95^{th} 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	395/404 (97%)	-0.26	0	100	100	13, 32, 56, 79	0
1	B	394/404 (97%)	-0.27	0	100	100	12, 31, 53, 75	0
All	All	789/808 (97%)	-0.27	0	100	100	12, 31, 55, 79	0

There are no RSRZ outliers to report.

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, 95^{th} 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
3	NAG	A	692	14/15	0.95	0.22	-0.05	32,35,40,43	0
3	NAG	B	692	14/15	0.94	0.18	-1.30	35,39,46,48	0
4	NAG	A	715	14/15	0.84	0.26	-	53,60,66,72	0
3	MAN	A	695	11/12	0.72	0.30	-	78,79,81,83	0
3	MAN	B	695	11/12	0.72	0.26	-	68,71,73,74	0
4	NAG	A	716	14/15	0.80	0.35	-	76,79,85,87	0
3	NAG	A	693	14/15	0.92	0.30	-	43,50,54,55	0
3	BMA	B	694	11/12	0.87	0.34	-	61,64,67,68	0
3	NAG	B	693	14/15	0.92	0.20	-	43,52,56,57	0
3	BMA	A	694	11/12	0.83	0.24	-	63,67,72,74	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, 95^{th} 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	GLA	B	804	12/12	0.85	0.51	10.03	52,54,55,58	0
5	GLA	A	803	12/12	0.81	0.39	3.20	46,51,53,54	0
5	GLA	B	802	12/12	0.93	0.18	0.86	25,32,36,38	0
2	NAG	A	639	14/15	0.80	0.24	-0.12	51,55,58,60	0
5	GLA	A	801	12/12	0.96	0.17	-0.20	16,19,22,23	0
2	NAG	B	639	14/15	0.84	0.21	-0.58	47,54,56,58	0
2	NAG	B	715	14/15	0.75	0.34	-	59,68,71,74	0

6.5 Other polymers

There are no such residues in this entry.