



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 14, 2017 – 08:12 am GMT

PDB ID : 4K24
Title : Structure of anti-uPAR Fab ATN-658 in complex with uPAR
Authors : Huang, M.D.; Xu, X.; Yuan, C.
Deposited on : 2013-04-08
Resolution : 4.50 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : trunk28620
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : recalc28949

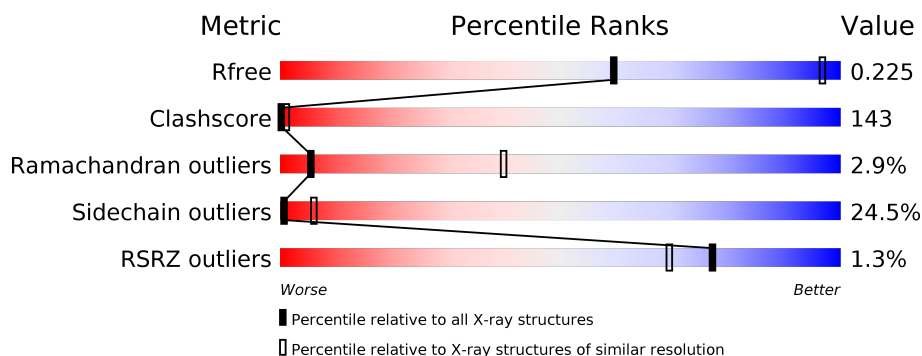
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 4.50 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}	100719	1007 (5.30-3.64)
Clashscore	112137	1029 (5.30-3.70)
Ramachandran outliers	110173	1025 (5.30-3.66)
Sidechain outliers	110143	1006 (5.30-3.66)
RSRZ outliers	101464	1015 (5.30-3.64)

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	135	<div> <div>9%</div> <div>55%</div> <div>25%</div> <div>7%</div> </div>
2	B	40	<div> <div>10%</div> <div>55%</div> <div>33%</div> </div>
3	H	228	<div> <div>14%</div> <div>59%</div> <div>20%</div> <div>7%</div> </div>
4	L	219	<div> <div>15%</div> <div>68%</div> <div>16%</div> </div>
5	U	283	<div> <div>15%</div> <div>61%</div> <div>19%</div> </div>

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

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
6	NAG	U	305	-	-	X	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 6771 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 Urokinase-type plasminogen activator.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	125	Total	C	N	O	S	0	0	0
			987	608	187	178	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-1	ARG	-	EXPRESSION TAG	UNP P00749
A	0	SER	-	EXPRESSION TAG	UNP P00749

- Molecule 2 is a protein called Vitronectin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	40	Total	C	N	O	S	0	0	0
			312	185	51	68	8			

- Molecule 3 is a protein called anti-uPAR antibody, heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	H	212	Total	C	N	O	S	0	0	0
			1606	1019	263	317	7			

- Molecule 4 is a protein called anti-uPAR antibody, light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	L	218	Total	C	N	O	S	0	0	0
			1690	1059	284	341	6			

- Molecule 5 is a protein called Urokinase plasminogen activator surface receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
5	U	273	Total	C	N	O	S	0	0	0
			2095	1253	388	420	34			

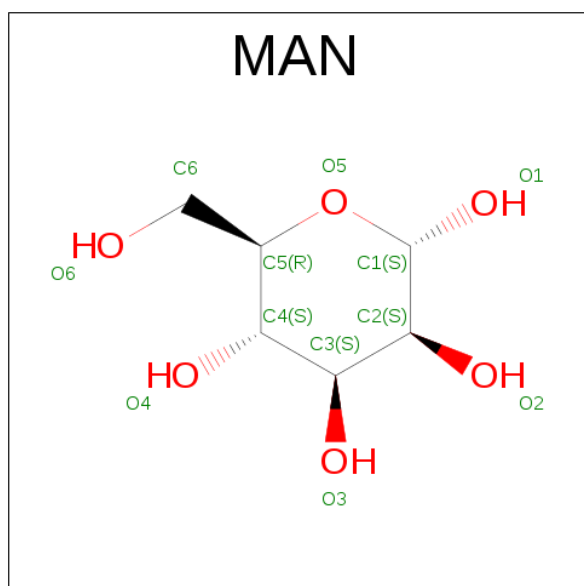
There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
U	-1	ARG	-	EXPRESSION TAG	UNP Q03405
U	0	SER	-	EXPRESSION TAG	UNP Q03405

- Molecule 6 is a polymer of unknown type called SUGAR (2-MER).

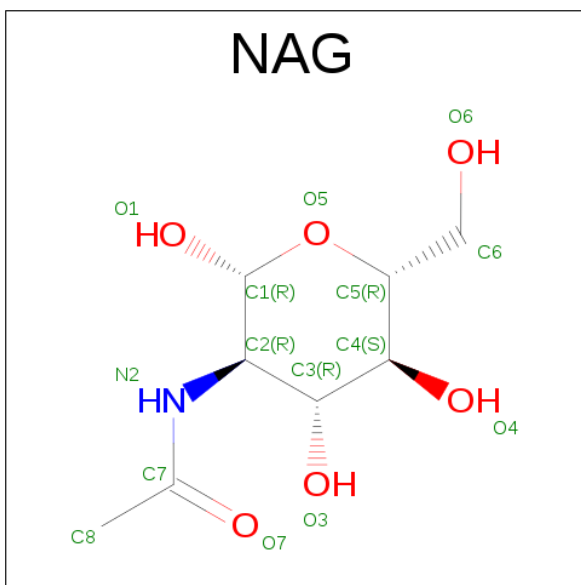
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	U	2	Total	C	N	O	0	0
			28	16	2	10		
6	U	2	Total	C	N	O	0	0
			28	16	2	10		

- Molecule 7 is SUGAR (ALPHA-D-MANNOSE) (three-letter code: MAN) (formula: $C_6H_{12}O_6$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
7	U	1	Total	C	O	0	0
			11	6	5		

- Molecule 8 is SUGAR (N-ACETYL-D-GLUCOSAMINE) (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).

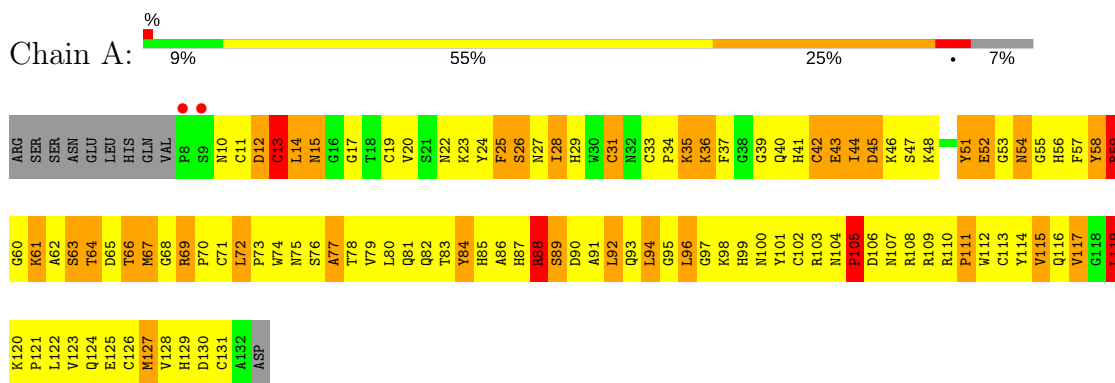


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
8	U	1	Total	C	N	O	0	0
			14	8	1	5		

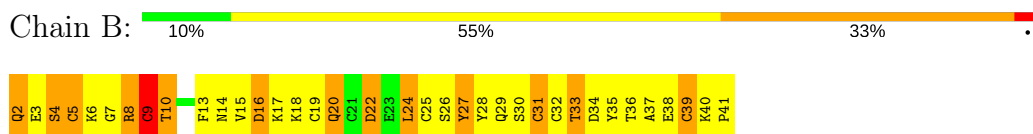
3 Residue-property plots [i](#)

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

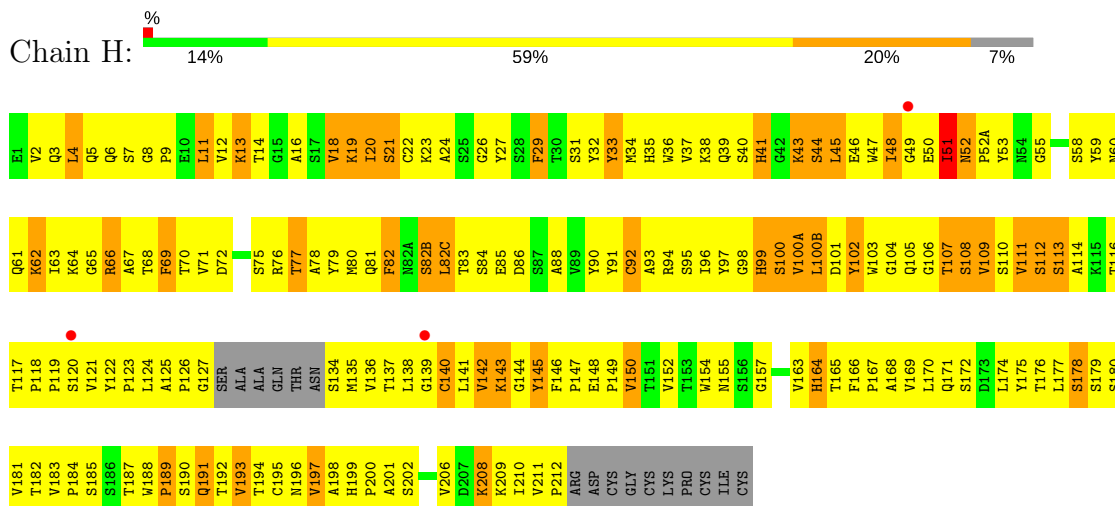
- Molecule 1: Urokinase-type plasminogen activator



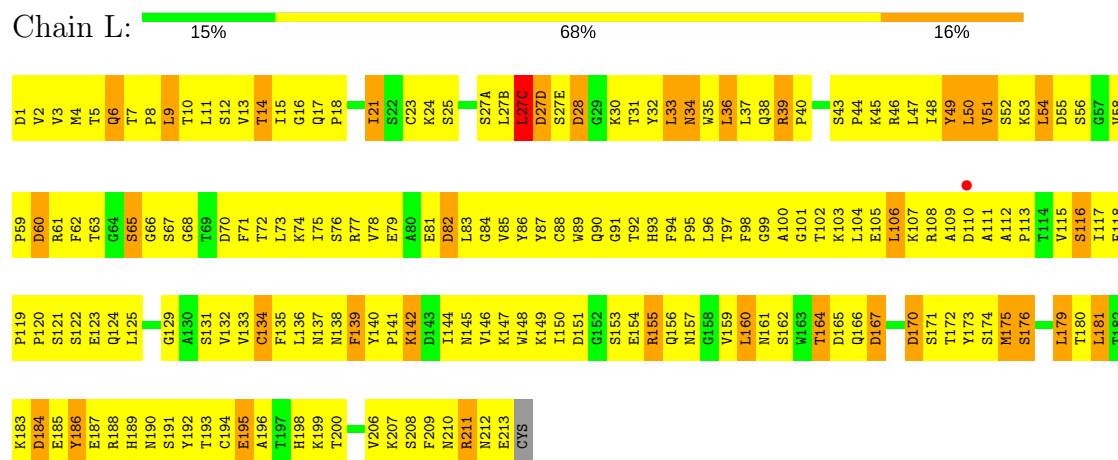
- Molecule 2: Vitronectin



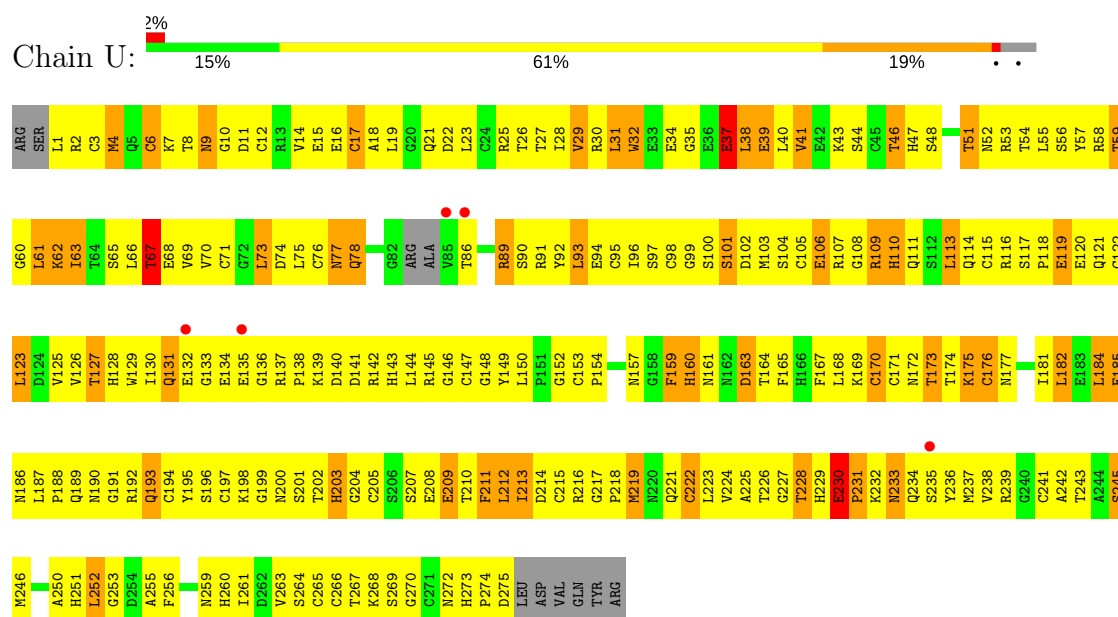
- Molecule 3: anti-uPAR antibody, heavy chain



- Molecule 4: anti-uPAR antibody, light chain



● Molecule 5: Urokinase plasminogen activator surface receptor



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	164.66Å 164.66Å 391.58Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	26.90 – 4.50 26.90 – 4.49	Depositor EDS
% Data completeness (in resolution range)	99.3 (26.90-4.50) 90.6 (26.90-4.49)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.65 (at 4.41Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.8.1_1168)	Depositor
R, R_{free}	0.217 , 0.275 0.218 , 0.225	Depositor DCC
R_{free} test set	618 reflections (5.01%)	DCC
Wilson B-factor (Å ²)	175.6	Xtriage
Anisotropy	0.376	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 371.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.43$, $\langle L^2 \rangle = 0.25$	Xtriage
Estimated twinning fraction	0.043 for -h,1/3*h-1/3*k-1/3*l,-4/3*h-8/3*k +1/3*l 0.035 for -1/3*h+1/3*k+1/3*l,-k,8/3*h+4/ 3*k+1/3*l 0.048 for -2/3*h-1/3*k-1/3*l,-1/3*h-2/3*k+ 1/3*l,-4/3*h+4/3*k+1/3*l	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	6771	wwPDB-VP
Average B, all atoms (Å ²)	308.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.46% 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

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: 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	0.73	0/1015	1.08	5/1372 (0.4%)
2	B	0.63	0/316	0.87	0/421
3	H	0.68	0/1650	0.96	4/2253 (0.2%)
4	L	0.54	0/1727	0.85	3/2346 (0.1%)
5	U	0.63	0/2129	0.91	1/2867 (0.0%)
All	All	0.64	0/6837	0.93	13/9259 (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	1
2	B	0	1
3	H	0	1
5	U	0	2
All	All	0	5

There are no bond length outliers.

The worst 5 of 13 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	L	27(C)	LEU	CA-CB-CG	-6.89	99.45	115.30
3	H	33	TYR	CA-CB-CG	6.79	126.31	113.40
1	A	94	LEU	CA-CB-CG	-6.65	100.00	115.30
1	A	59	ARG	N-CA-C	-6.36	93.84	111.00
5	U	41	VAL	CB-CA-C	-6.28	99.47	111.40

There are no chirality outliers.

All (5) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	88	ARG	Peptide
2	B	10	THR	Peptide
3	H	51	ILE	Peptide
5	U	230	GLU	Peptide
5	U	37	GLU	Peptide

5.2 Too-close contacts ⓘ

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	987	0	919	329	1
2	B	312	0	272	99	0
3	H	1606	0	1560	600	1
4	L	1690	0	1649	463	0
5	U	2095	0	1946	537	0
6	U	56	0	49	15	0
7	U	11	0	10	3	0
8	U	14	0	13	1	0
All	All	6771	0	6418	1891	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 143.

The worst 5 of 1891 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)
3:H:154:TRP:CZ3	3:H:195:CYS:HB3	1.36	1.60
4:L:35:TRP:CZ3	4:L:88:CYS:HB3	1.53	1.44
3:H:145:TYR:CE2	3:H:175:TYR:HB2	1.53	1.43
3:H:188:TRP:CD1	3:H:189:PRO:HA	1.52	1.43
5:U:38:LEU:HD12	5:U:39:GLU:N	1.42	1.35

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:93:GLN:OE1	3:H:55:GLY:O[3_555]	2.11	0.09

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	123/135 (91%)	86 (70%)	26 (21%)	11 (9%)	1	15
2	B	38/40 (95%)	27 (71%)	9 (24%)	2 (5%)	2	27
3	H	208/228 (91%)	176 (85%)	27 (13%)	5 (2%)	7	44
4	L	216/219 (99%)	201 (93%)	13 (6%)	2 (1%)	20	63
5	U	269/283 (95%)	218 (81%)	46 (17%)	5 (2%)	9	49
All	All	854/905 (94%)	708 (83%)	121 (14%)	25 (3%)	5	40

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
3	H	52(A)	PRO
3	H	82(B)	SER
4	L	51	VAL
5	U	185	GLU
1	A	36	LYS

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	109/119 (92%)	78 (72%)	31 (28%)	0	3
2	B	37/37 (100%)	25 (68%)	12 (32%)	0	2
3	H	184/197 (93%)	139 (76%)	45 (24%)	1	6
4	L	195/196 (100%)	156 (80%)	39 (20%)	1	10
5	U	242/251 (96%)	181 (75%)	61 (25%)	0	6
All	All	767/800 (96%)	579 (76%)	188 (24%)	1	6

5 of 188 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
3	H	197	VAL
4	L	82	ASP
5	U	193	GLN
3	H	211	VAL
4	L	28	ASP

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 17 such sidechains are listed below:

Mol	Chain	Res	Type
3	H	105	GLN
3	H	155	ASN
5	U	190	ASN
3	H	99	HIS
5	U	260	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates ⓘ

4 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
6	NAG	U	301	6	14,14,15	0.72	0	15,19,21	2.95	7 (46%)
6	NAG	U	302	7,6	14,14,15	1.00	1 (7%)	15,19,21	2.24	4 (26%)
6	NAG	U	305	5,6	14,14,15	0.84	0	15,19,21	2.21	4 (26%)
6	NAG	U	306	6	14,14,15	0.51	0	15,19,21	1.40	2 (13%)

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	U	301	6	-	0/6/23/26	0/1/1/1
6	NAG	U	302	7,6	-	0/6/23/26	0/1/1/1
6	NAG	U	305	5,6	-	0/6/23/26	0/1/1/1
6	NAG	U	306	6	-	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	U	302	NAG	O7-C7	2.55	1.29	1.23

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	U	302	NAG	C1-O5-C5	-6.68	102.96	112.17
6	U	301	NAG	C1-C2-N2	-4.42	102.94	110.49
6	U	305	NAG	C1-O5-C5	-4.16	106.43	112.17
6	U	301	NAG	C8-C7-N2	-3.88	109.10	116.11
6	U	302	NAG	O5-C1-C2	-2.94	107.39	111.47

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	U	302	NAG	3	0
6	U	305	NAG	12	0

5.6 Ligand geometry

2 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
7	MAN	U	303	6	11,11,12	2.30	2 (18%)	13,15,17	2.77	6 (46%)
8	NAG	U	304	5	14,14,15	0.62	0	15,19,21	1.32	2 (13%)

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
7	MAN	U	303	6	-	0/2/19/22	0/1/1/1
8	NAG	U	304	5	-	0/6/23/26	0/1/1/1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	U	303	MAN	C4-C3	-5.06	1.39	1.52
7	U	303	MAN	O5-C5	4.83	1.53	1.43

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	U	303	MAN	O3-C3-C4	-3.74	102.21	110.36
7	U	303	MAN	O2-C2-C3	-2.89	104.50	110.17
7	U	303	MAN	C6-C5-C4	-2.34	107.54	113.00
8	U	304	NAG	C4-C3-C2	2.53	114.73	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	U	303	MAN	O6-C6-C5	2.81	120.81	111.34

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
7	U	303	MAN	3	0
8	U	304	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 [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	125/135 (92%)	-0.37	2 (1%) 72 64	171, 240, 348, 489	0
2	B	40/40 (100%)	-0.33	0 100 100	226, 301, 419, 468	0
3	H	212/228 (92%)	-0.26	3 (1%) 75 67	187, 291, 431, 531	0
4	L	218/219 (99%)	-0.20	1 (0%) 90 86	220, 335, 449, 596	0
5	U	273/283 (96%)	-0.24	5 (1%) 69 61	192, 290, 443, 635	0
All	All	868/905 (95%)	-0.26	11 (1%) 77 69	171, 296, 440, 635	0

The worst 5 of 11 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
5	U	85	VAL	5.1
1	A	9	SER	4.7
1	A	8	PRO	4.4
5	U	235	SER	3.7
5	U	135	GLU	3.6

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](#)

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
6	NAG	U	305	14/15	0.77	0.41	-0.25	444,446,448,449	0
6	NAG	U	301	14/15	0.88	0.17	-	281,296,310,313	0
6	NAG	U	306	14/15	0.77	0.43	-	449,453,455,456	0
6	NAG	U	302	14/15	0.90	0.23	-	443,452,459,461	0

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
8	NAG	U	304	14/15	0.78	0.41	-	492,494,498,498	0
7	MAN	U	303	11/12	0.71	0.28	-	404,442,450,450	0

6.5 Other polymers [i](#)

There are no such residues in this entry.