



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 5, 2024 – 05:58 PM EDT

PDB ID : 5VCR
Title : Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
with bound uranium dioxide
Authors : Sanders, J.H.; Kadirvelraj, R.; Wood, Z.A.
Deposited on : 2017-03-31
Resolution : 1.99 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

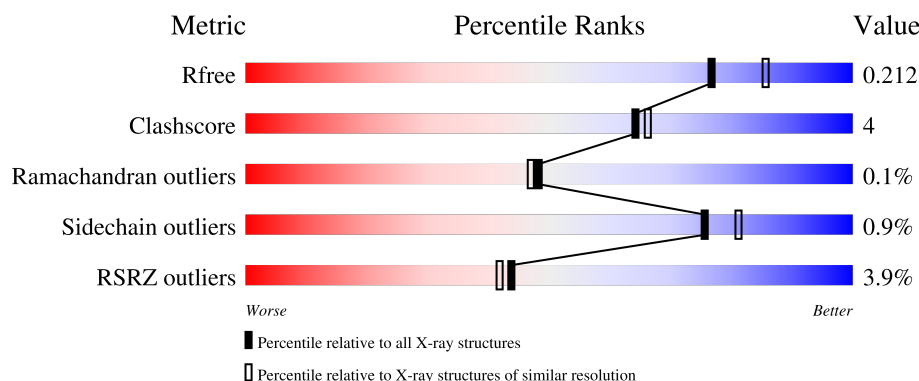
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.99 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}	164625	9409 (2.00-2.00)
Clashscore	180529	10737 (2.00-2.00)
Ramachandran outliers	177936	10628 (2.00-2.00)
Sidechain outliers	177891	10627 (2.00-2.00)
RSRZ outliers	164620	9409 (2.00-2.00)

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 of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. 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	419	 4% 75% 8% 16%
1	B	419	 3% 73% 9% 18%

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	IUM	A	501	-	-	X	-
2	IUM	A	502	-	-	X	-
2	IUM	B	502	-	-	X	-
2	IUM	B	503	-	-	X	-
4	CL	B	504	-	-	-	X

2 Entry composition [i](#)

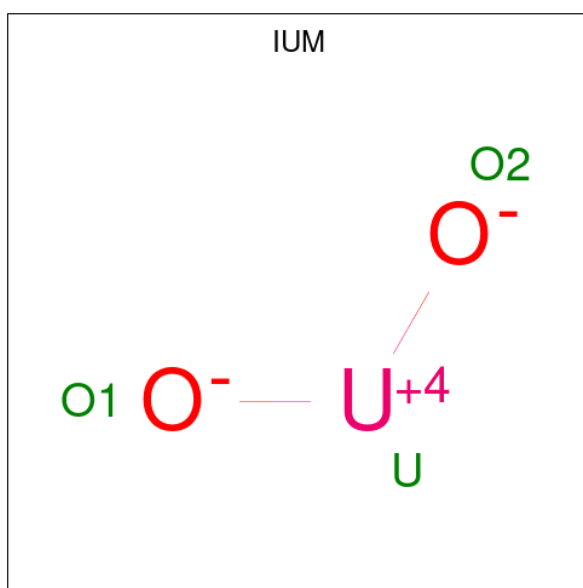
There are 6 unique types of molecules in this entry. The entry contains 6108 atoms, of which 0 are hydrogens and 0 are deuteriums.

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-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	350	Total	C	N	O	S	0	2	0
			2920	1895	496	516	13			
1	B	343	Total	C	N	O	S	0	1	0
			2862	1858	484	506	14			

- Molecule 2 is URANYL (VI) ION (three-letter code: IUM) (formula: O₂U).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	U	0	0
			3	2	1		
2	A	1	Total	O	U	0	0
			3	2	1		
2	B	1	Total	O	U	0	0
			3	2	1		
2	B	1	Total	O	U	0	0
			3	2	1		

- Molecule 3 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 4 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Cl	0	0
			1	1		
4	B	1	Total	Cl	0	0
			1	1		

- Molecule 5 is DIMETHYL SULFOXIDE (three-letter code: DMS) (formula: C_2H_6OS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	B	1	Total	C	O	S	0	0
			4	2	1	1		

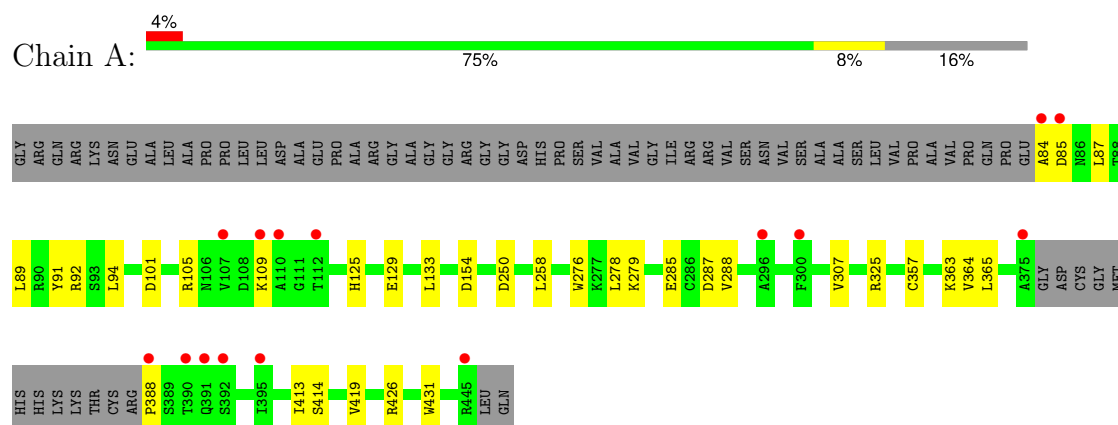
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	154	Total	O	0	0
			154	154		
6	B	140	Total	O	0	0
			140	140		

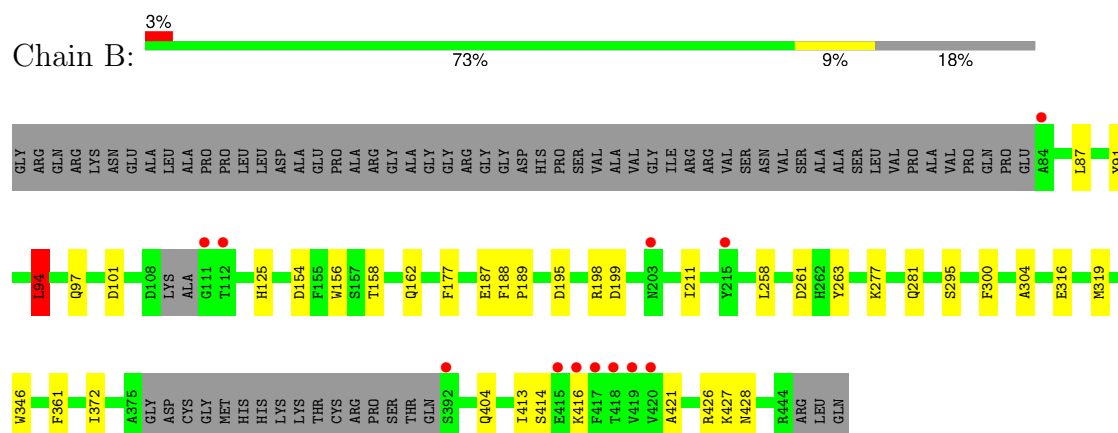
3 Residue-property plots

These plots are drawn for all protein, RNA, DNA and oligosaccharide 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: Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase



- Molecule 1: Alpha-1,6-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase



4 Data and refinement statistics

Property	Value	Source
Space group	P 43 21 2	Depositor
Cell constants a, b, c, α , β , γ	105.67Å 105.67Å 171.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	56.40 – 1.99 56.40 – 1.99	Depositor EDS
% Data completeness (in resolution range)	99.0 (56.40-1.99) 99.0 (56.40-1.99)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.17 (at 2.00Å)	Xtriage
Refinement program	PHENIX (1.10.1_2155: ???)	Depositor
R, R_{free}	0.177 , 0.208 0.180 , 0.212	Depositor DCC
R_{free} test set	63229 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	32.1	Xtriage
Anisotropy	0.528	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 46.3	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	6108	wwPDB-VP
Average B, all atoms (Å ²)	44.0	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.*

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, CL, IUM, DMS

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	0.81	1/3015 (0.0%)	0.80	4/4099 (0.1%)
1	B	0.81	4/2952 (0.1%)	0.78	4/4012 (0.1%)
All	All	0.81	5/5967 (0.1%)	0.79	8/8111 (0.1%)

All (5) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	316	GLU	CB-CG	-5.99	1.40	1.52
1	B	346	TRP	CE3-CZ3	5.89	1.48	1.38
1	B	263	TYR	CD1-CE1	5.36	1.47	1.39
1	A	431	TRP	CB-CG	5.11	1.59	1.50
1	B	177	PHE	CD2-CE2	5.05	1.49	1.39

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	94	LEU	CA-CB-CG	9.72	137.66	115.30
1	B	94	LEU	CB-CG-CD2	-8.48	96.59	111.00
1	A	105	ARG	NE-CZ-NH1	7.91	124.25	120.30
1	A	278	LEU	CA-CB-CG	7.20	131.86	115.30
1	A	105	ARG	NE-CZ-NH2	-5.98	117.31	120.30
1	A	426	ARG	NE-CZ-NH2	-5.70	117.45	120.30
1	B	195	ASP	CB-CG-OD1	5.53	123.28	118.30
1	B	101	ASP	CB-CG-OD1	5.14	122.93	118.30

There are no chirality outliers.

There are no planarity outliers.

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	2920	0	2854	19	1
1	B	2862	0	2784	20	1
2	A	6	0	0	4	0
2	B	6	0	0	5	0
3	A	14	0	13	0	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
5	B	4	0	6	0	0
6	A	154	0	0	3	0
6	B	140	0	0	4	0
All	All	6108	0	5657	44	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 4.

All (44) 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:B:502:IUM:O1	2:B:502:IUM:U	1.71	0.71
1:B:426:ARG:NH1	1:B:428:ASN:OD1	2.25	0.68
2:B:502:IUM:U	2:B:502:IUM:O2	1.74	0.68
1:A:84:ALA:HB1	1:A:89:LEU:HB3	1.76	0.67
2:B:503:IUM:O2	2:B:503:IUM:U	1.76	0.66
1:A:363:LYS:NZ	6:A:601:HOH:O	2.08	0.66
2:B:503:IUM:U	2:B:503:IUM:O1	1.76	0.65
1:B:427:LYS:NZ	6:B:603:HOH:O	2.29	0.65
2:A:501:IUM:U	2:A:501:IUM:O1	1.80	0.62
1:B:94:LEU:HD11	1:B:156:TRP:CH2	2.34	0.62
2:A:501:IUM:U	2:A:501:IUM:O2	1.80	0.62
2:A:502:IUM:O1	2:A:502:IUM:U	1.80	0.62
2:A:502:IUM:U	2:A:502:IUM:O2	1.81	0.61
1:A:363:LYS:HE2	1:A:419:VAL:CG2	2.35	0.57
1:B:198:ARG:NH1	1:B:199:ASP:OD1	2.39	0.56
1:A:133:LEU:HD11	1:A:388:PRO:HB2	1.87	0.55
1:A:89:LEU:HD23	1:A:92:ARG:HD2	1.89	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:101:ASP:OD1	1:B:158:THR:HG22	2.08	0.53
1:A:276:TRP:CZ3	1:A:279:LYS:HD2	2.44	0.53
1:B:361:PHE:CD2	1:B:421:ALA:HB2	2.45	0.52
1:A:287:ASP:OD2	6:A:602:HOH:O	2.18	0.51
1:A:363:LYS:HE2	1:A:419:VAL:HG21	1.93	0.50
1:B:87:LEU:HD11	1:B:91:TYR:CZ	2.47	0.49
1:B:404:GLN:HG2	6:B:701:HOH:O	2.14	0.48
1:B:413:ILE:HG22	1:B:414:SER:O	2.14	0.47
1:B:261:ASP:OD2	2:B:502:IUM:O2	2.33	0.47
1:A:307[B]:VAL:HG21	1:A:365:LEU:HG	1.96	0.46
1:A:325:ARG:NH2	6:A:603:HOH:O	2.29	0.46
1:A:109:LYS:HD3	1:B:162:GLN:HG2	1.97	0.46
1:B:188:PHE:CD1	1:B:189:PRO:HA	2.51	0.45
1:A:129:GLU:CD	1:A:388:PRO:HD2	2.38	0.44
1:A:413:ILE:HG22	1:A:414:SER:O	2.17	0.44
1:B:187:GLU:OE1	6:B:601:HOH:O	2.21	0.44
1:A:125:HIS:ND1	1:A:154:ASP:OD1	2.48	0.43
1:B:277:LYS:HE2	1:B:281:GLN:NE2	2.34	0.43
1:A:87:LEU:HD11	1:A:91:TYR:CZ	2.53	0.43
1:A:288:VAL:HG23	1:A:364:VAL:HG23	2.00	0.43
1:A:285:GLU:HG3	1:A:363:LYS:NZ	2.34	0.43
1:B:319:MET:HB3	6:B:658:HOH:O	2.18	0.43
1:B:319:MET:HG2	1:B:372:ILE:CG2	2.49	0.42
1:A:94:LEU:HD11	1:B:97:GLN:HB3	2.01	0.42
1:B:125:HIS:ND1	1:B:154:ASP:OD1	2.52	0.41
1:B:300:PHE:HB3	1:B:304:ALA:HB2	2.03	0.41
1:B:211:ILE:HG21	1:B:211:ILE:HD13	1.84	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:363:LYS:NZ	1:B:295:SER:OG[7_456]	2.02	0.18

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	348/419 (83%)	342 (98%)	5 (1%)	1 (0%)	37	35
1	B	338/419 (81%)	328 (97%)	10 (3%)	0	100	100
All	All	686/838 (82%)	670 (98%)	15 (2%)	1 (0%)	48	47

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	357	CYS

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	321/370 (87%)	318 (99%)	3 (1%)	75	81
1	B	314/370 (85%)	311 (99%)	3 (1%)	73	78
All	All	635/740 (86%)	629 (99%)	6 (1%)	75	81

All (6) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	85	ASP
1	A	250	ASP
1	A	258	LEU
1	B	94	LEU
1	B	258	LEU
1	B	416	LYS

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 8 ligands modelled in this entry, 2 are monoatomic - leaving 6 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	$\# Z > 2$
3	NAG	A	503	1	14,14,15	0.36	0	17,19,21	0.65	0
2	IUM	B	502	1	0,2,2	-	-	-		
2	IUM	A	502	6,1	0,2,2	-	-	-		
2	IUM	B	503	1	0,2,2	-	-	-		
2	IUM	A	501	1	0,2,2	-	-	-		
5	DMS	B	501	-	3,3,3	0.65	0	3,3,3	0.54	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
3	NAG	A	503	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	503	NAG	O5-C5-C6-O6
3	A	503	NAG	C4-C5-C6-O6

There are no ring outliers.

4 monomers are involved in 9 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	502	IUM	3	0
2	A	502	IUM	2	0
2	B	503	IUM	2	0
2	A	501	IUM	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	350/419 (83%)	0.22	15 (4%) 40 38	18, 40, 88, 114	2 (0%)
1	B	343/419 (81%)	0.15	12 (3%) 47 45	26, 41, 64, 95	1 (0%)
All	All	693/838 (82%)	0.19	27 (3%) 44 42	18, 40, 76, 114	3 (0%)

All (27) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	84	ALA	6.5
1	B	84	ALA	4.2
1	B	417	PHE	4.1
1	B	416	LYS	4.1
1	A	445	ARG	3.9
1	B	418	THR	3.5
1	A	395	ILE	3.4
1	B	419	VAL	3.2
1	A	296	ALA	3.1
1	A	375	ALA	3.1
1	A	112	THR	3.1
1	A	300	PHE	3.0
1	A	110	ALA	2.9
1	B	392	SER	2.9
1	A	85	ASP	2.7
1	A	391	GLN	2.5
1	A	390	THR	2.5
1	B	112	THR	2.5
1	A	109	LYS	2.4
1	B	203	ASN	2.4
1	B	415	GLU	2.4
1	A	388	PRO	2.4
1	B	215	TYR	2.3
1	A	107	VAL	2.3

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Mol	Chain	Res	Type	RSRZ
1	B	420	VAL	2.2
1	B	111	GLY	2.1
1	A	392	SER	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 monosaccharides 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. 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	B-factors(Å ²)	Q<0.9
4	CL	B	504	1/1	0.63	0.53	60,60,60,60	1
5	DMS	B	501	4/4	0.76	0.26	89,91,96,149	0
3	NAG	A	503	14/15	0.80	0.23	48,59,67,69	14
4	CL	A	504	1/1	0.89	0.50	51,51,51,51	1
2	IUM	B	503	3/3	0.92	0.28	23,23,29,44	3
2	IUM	A	502	3/3	0.96	0.15	58,58,65,70	3
2	IUM	B	502	3/3	0.98	0.32	25,25,40,48	3
2	IUM	A	501	3/3	0.99	0.15	46,46,106,148	3

6.5 Other polymers [i](#)

There are no such residues in this entry.