



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 04:57 AM GMT

PDB ID : 2OW7
Title : Golgi alpha-mannosidase II complex with (1R,6S,7R,8S)-1-thioniabicyclo[4.3.0]nonan-7,8-diol chloride
Authors : Kuntz, D.A.
Deposited on : 2007-02-15
Resolution : 1.77 Å(reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.
We welcome your comments at validation@mail.wwpdb.org
A user guide is available at
<http://wwpdb.org/validation/2016/XrayValidationReportHelp>
with specific help available everywhere you see the ⓘ symbol.

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

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

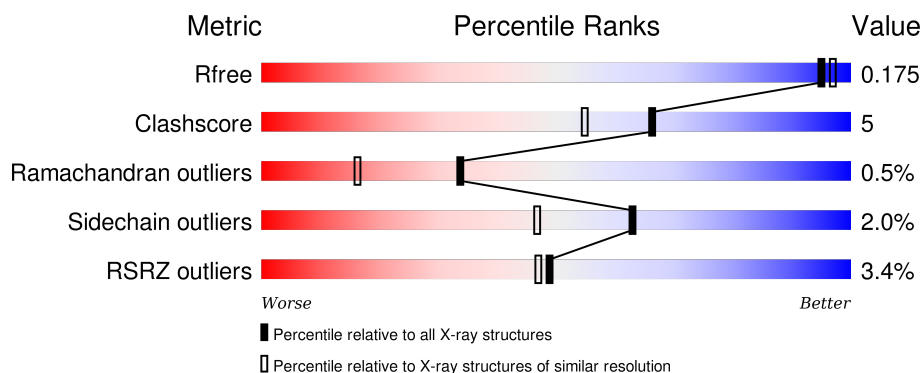
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.77 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	6655 (1.80-1.76)
Clashscore	102246	7658 (1.80-1.76)
Ramachandran outliers	100387	7570 (1.80-1.76)
Sidechain outliers	100360	7569 (1.80-1.76)
RSRZ outliers	91569	6671 (1.80-1.76)

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	1045	<div> <div>3%</div> <div>85%</div> <div>11%</div> <div>..</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
3	SO4	A	4001	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
3	SO4	A	4003	-	-	-	X
3	SO4	A	4005	-	-	-	X

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 9465 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-mannosidase 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	1016	8281	5259	1453	1528	41	0	13	0

There are 13 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ARG	-	EXPRESSION TAG	UNP Q24451
A	2	SER	-	EXPRESSION TAG	UNP Q24451
A	3	SER	-	EXPRESSION TAG	UNP Q24451
A	4	HIS	-	EXPRESSION TAG	UNP Q24451
A	5	HIS	-	EXPRESSION TAG	UNP Q24451
A	6	HIS	-	EXPRESSION TAG	UNP Q24451
A	7	HIS	-	EXPRESSION TAG	UNP Q24451
A	8	HIS	-	EXPRESSION TAG	UNP Q24451
A	9	HIS	-	EXPRESSION TAG	UNP Q24451
A	10	GLY	-	EXPRESSION TAG	UNP Q24451
A	11	GLU	-	EXPRESSION TAG	UNP Q24451
A	12	PHE	-	EXPRESSION TAG	UNP Q24451
A	907	LYS	GLU	CONFLICT	UNP Q24451

- 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	0	0
			14	8	1	5		

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



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

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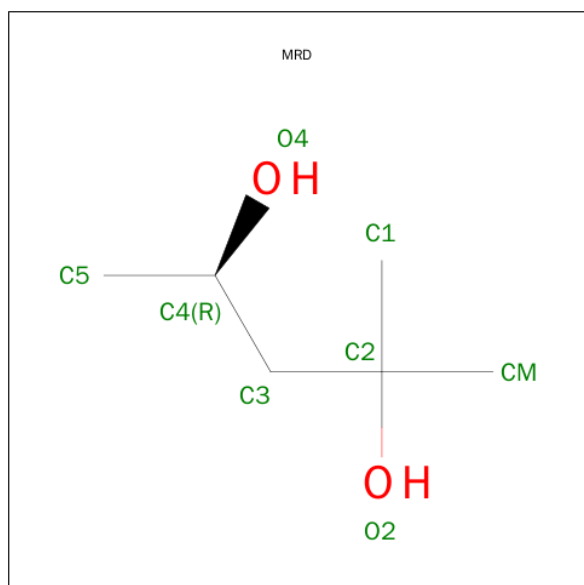
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Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	O	S	0	0
			5	4	1		
3	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 4 is ZINC ION (three-letter code: ZN) (formula: Zn).

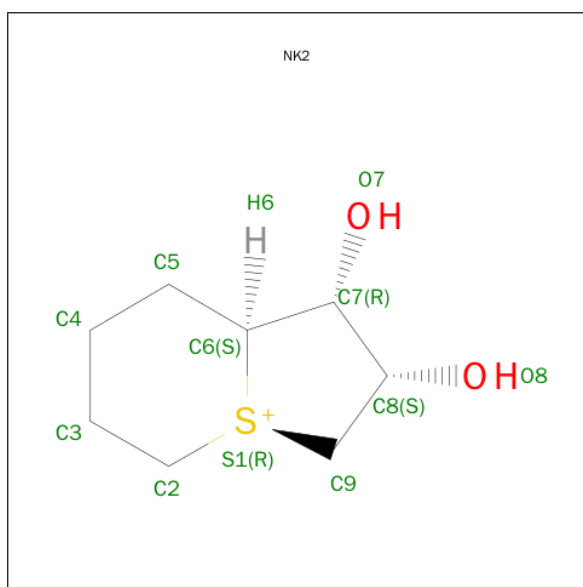
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Zn	0	0
			1	1		

- Molecule 5 is (4R)-2-METHYLPENTANE-2,4-DIOL (three-letter code: MRD) (formula: C₆H₁₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			8	6	2		

- Molecule 6 is (1R,6S,7R,8S)-1-THIONIABICYCLO[4.3.0]NONAN-7,8-DIOL (three-letter code: NK2) (formula: C₈H₁₅O₂S).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	O	S	0	0
			11	8	2	1		

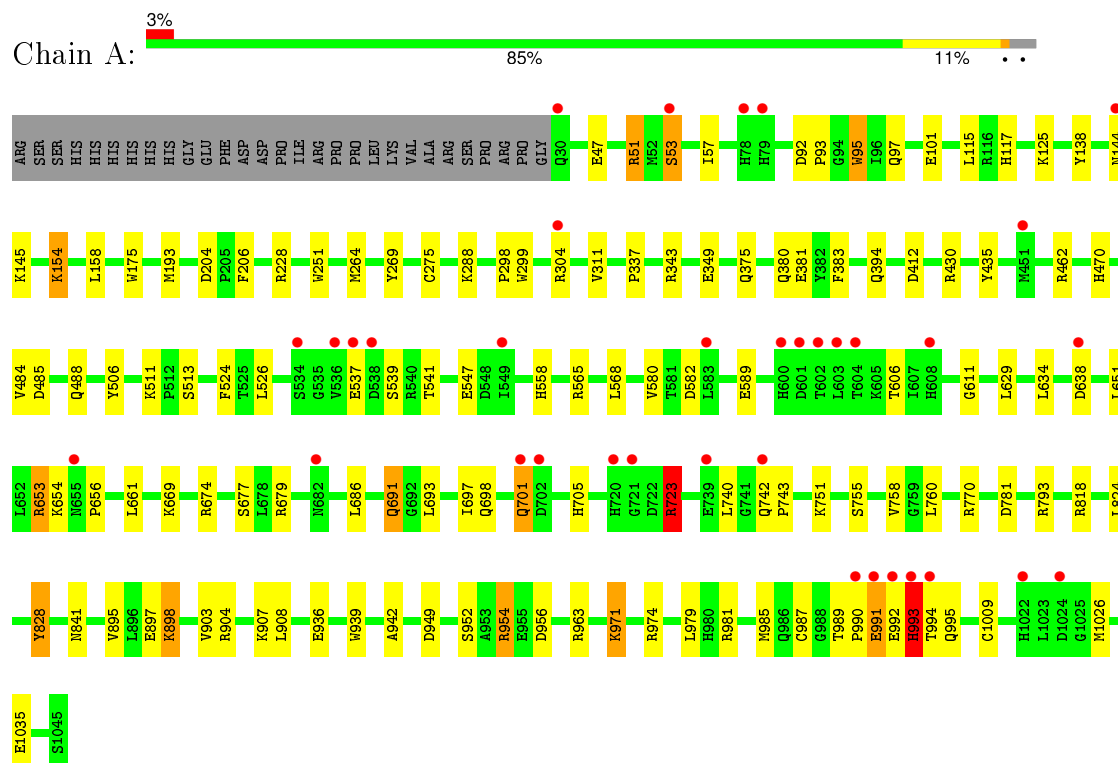
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	1115	Total	O	0	10
			1125	1125		

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-mannosidase 2



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	68.90Å 108.58Å 137.78Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	10.54 – 1.77 10.54 – 1.77	Depositor EDS
% Data completeness (in resolution range)	99.6 (10.54-1.77) 99.6 (10.54-1.77)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	3.15 (at 1.77Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.162 , 0.203 0.165 , 0.175	Depositor DCC
R_{free} test set	1470 reflections (1.49%)	DCC
Wilson B-factor (Å ²)	13.8	Xtriage
Anisotropy	0.053	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.45 , 69.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Outliers	0 of 100293 reflections	Xtriage
F_o, F_c correlation	0.96	EDS
Total number of atoms	9465	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.30% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

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

5 Model quality

5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: MRD, ZN, NAG, NK2, SO4

The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 5$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Chain	Bond lengths		Bond angles	
		RMSZ	$\# Z > 5$	RMSZ	$\# Z > 5$
1	A	1.22	17/8516 (0.2%)	1.03	21/11559 (0.2%)

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	2

All (17) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	381	GLU	CD-OE1	-7.77	1.17	1.25
1	A	53[A]	SER	C-O	7.75	1.38	1.23
1	A	53[B]	SER	C-O	7.75	1.38	1.23
1	A	506	TYR	CD1-CE1	6.48	1.49	1.39
1	A	1035	GLU	CG-CD	6.26	1.61	1.51
1	A	547	GLU	CB-CG	6.01	1.63	1.52
1	A	311	VAL	CB-CG2	5.88	1.65	1.52
1	A	524	PHE	CG-CD1	5.53	1.47	1.38
1	A	175	TRP	CG-CD1	5.45	1.44	1.36
1	A	206	PHE	CD1-CE1	5.23	1.49	1.39
1	A	565	ARG	CZ-NH1	5.19	1.39	1.33
1	A	987	CYS	CB-SG	-5.17	1.73	1.81
1	A	95	TRP	CE3-CZ3	5.15	1.47	1.38
1	A	269	TYR	CD2-CE2	5.12	1.47	1.39
1	A	206	PHE	CG-CD2	5.09	1.46	1.38
1	A	383	PHE	CE2-CZ	5.09	1.47	1.37
1	A	828	TYR	CD1-CE1	5.08	1.47	1.39

All (21) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	565	ARG	NE-CZ-NH2	-9.47	115.56	120.30
1	A	818	ARG	NE-CZ-NH2	-8.44	116.08	120.30
1	A	462	ARG	NE-CZ-NH1	8.01	124.31	120.30
1	A	818	ARG	NE-CZ-NH1	7.75	124.18	120.30
1	A	228	ARG	NE-CZ-NH2	-7.64	116.48	120.30
1	A	51	ARG	NE-CZ-NH2	-6.94	116.83	120.30
1	A	781	ASP	CB-CG-OD1	6.85	124.46	118.30
1	A	963	ARG	NE-CZ-NH1	6.71	123.66	120.30
1	A	92	ASP	CB-CG-OD1	-6.53	112.43	118.30
1	A	51	ARG	NE-CZ-NH1	6.48	123.54	120.30
1	A	343	ARG	NE-CZ-NH1	6.43	123.52	120.30
1	A	723	ARG	NE-CZ-NH1	6.19	123.39	120.30
1	A	979	LEU	CB-CG-CD1	-6.14	100.56	111.00
1	A	430	ARG	NE-CZ-NH2	-5.68	117.46	120.30
1	A	793	ARG	NE-CZ-NH1	-5.59	117.50	120.30
1	A	963	ARG	NE-CZ-NH2	-5.50	117.55	120.30
1	A	674	ARG	NE-CZ-NH2	-5.26	117.67	120.30
1	A	949	ASP	CB-CG-OD1	5.21	122.99	118.30
1	A	485	ASP	CB-CG-OD2	5.16	122.94	118.30
1	A	412	ASP	CB-CG-OD2	-5.06	113.74	118.30
1	A	824	LEU	CB-CG-CD1	-5.06	102.39	111.00

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	954	ARG	Sidechain
1	A	993	HIS	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	8281	0	8058	79	0
2	A	14	0	13	0	0
3	A	25	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	A	1	0	0	0	0
5	A	8	0	14	2	0
6	A	11	0	14	0	0
7	A	1125	0	0	22	0
All	All	9465	0	8099	81	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 5.

All (81) 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:936:GLU:HG2	7:A:6881:HOH:O	1.47	1.14
1:A:144:ASN:HB2	7:A:6738:HOH:O	1.68	0.92
1:A:954:ARG:NH2	1:A:981[A]:ARG:HH21	1.67	0.90
1:A:435:TYR:HE2	1:A:526:LEU:HD13	1.41	0.85
1:A:952:SER:H	1:A:995:GLN:NE2	1.76	0.84
5:A:2001:MRD:H1C1	7:A:6596:HOH:O	1.80	0.81
1:A:723:ARG:HH11	1:A:723:ARG:HG2	1.46	0.80
1:A:952:SER:H	1:A:995:GLN:HE21	1.28	0.80
1:A:154:LYS:HE2	7:A:6731:HOH:O	1.82	0.78
1:A:992:GLU:O	1:A:993:HIS:HB2	1.92	0.69
1:A:435:TYR:CE2	1:A:526:LEU:HD13	2.27	0.67
1:A:47:GLU:OE2	1:A:51:ARG:HD3	1.94	0.67
1:A:971:LYS:NZ	1:A:971:LYS:HB2	2.11	0.66
1:A:723:ARG:HH11	1:A:723:ARG:CG	2.09	0.65
1:A:125:LYS:HE2	7:A:6755:HOH:O	1.99	0.63
1:A:435:TYR:HE2	1:A:526:LEU:CD1	2.10	0.62
1:A:989:THR:CG2	1:A:991:GLU:HG3	2.30	0.62
1:A:541:THR:HG23	7:A:6148:HOH:O	2.00	0.61
1:A:679:ARG:HH12	1:A:701:GLN:HG2	1.65	0.60
5:A:2001:MRD:H1C3	7:A:6429:HOH:O	2.03	0.58
1:A:742:GLN:HG3	7:A:6196:HOH:O	2.03	0.58
1:A:47:GLU:OE2	1:A:51:ARG:CD	2.50	0.58
1:A:541:THR:HG21	7:A:6162:HOH:O	2.03	0.58
1:A:537:GLU:HG2	1:A:539:SER:HB3	1.86	0.57
1:A:47:GLU:CD	1:A:51:ARG:HD3	2.25	0.57
1:A:990:PRO:O	1:A:991:GLU:C	2.43	0.57
1:A:679:ARG:NH1	1:A:701:GLN:HG2	2.20	0.57
1:A:989:THR:HG22	1:A:991:GLU:HG3	1.86	0.56
1:A:755[B]:SER:HB3	7:A:6308:HOH:O	2.07	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:154:LYS:CE	7:A:6731:HOH:O	2.45	0.54
1:A:679:ARG:HH12	1:A:701:GLN:CG	2.19	0.54
1:A:907:LYS:HG3	7:A:7111:HOH:O	2.05	0.54
1:A:651:LEU:CD1	1:A:653:ARG:HG2	2.38	0.54
1:A:904:ARG:HG2	1:A:985[A]:MET:SD	2.48	0.54
1:A:954:ARG:NH2	1:A:956:ASP:OD2	2.40	0.53
1:A:125:LYS:CE	7:A:6755:HOH:O	2.56	0.53
1:A:117:HIS:ND1	7:A:6776:HOH:O	2.23	0.53
1:A:484:VAL:O	1:A:488:GLN:HG3	2.09	0.53
1:A:511:LYS:HE2	1:A:513:SER:OG	2.10	0.52
1:A:939:TRP:CD2	1:A:942:ALA:HB2	2.46	0.51
1:A:974:ARG:NH1	7:A:6661:HOH:O	2.40	0.51
1:A:971:LYS:HZ3	1:A:971:LYS:HB2	1.77	0.49
1:A:990:PRO:O	1:A:991:GLU:O	2.30	0.49
1:A:264[B]:MET:SD	1:A:337:PRO:HG2	2.52	0.49
1:A:723:ARG:NH1	1:A:723:ARG:HG2	2.21	0.48
1:A:651:LEU:HD11	1:A:653:ARG:HD2	1.95	0.47
1:A:740:LEU:HD22	1:A:760:LEU:HD22	1.96	0.47
1:A:611:GLY:HA3	1:A:661:LEU:CD2	2.45	0.47
1:A:743:PRO:HB2	1:A:758:VAL:CG2	2.44	0.46
1:A:606:THR:HG21	1:A:653:ARG:NH2	2.30	0.46
1:A:580:VAL:HG22	1:A:634:LEU:HD22	1.97	0.46
1:A:568:LEU:HD12	1:A:770:ARG:HD3	1.97	0.45
1:A:115:LEU:HD23	1:A:145:LYS:HD3	1.99	0.45
1:A:954:ARG:NH2	1:A:981[A]:ARG:NH2	2.49	0.45
1:A:656:PRO:HB3	7:A:6930:HOH:O	2.16	0.45
1:A:138:TYR:CE1	1:A:193:MET:HE3	2.52	0.45
1:A:51:ARG:HG3	7:A:6409:HOH:O	2.16	0.44
1:A:582:ASP:C	1:A:582:ASP:OD1	2.56	0.44
1:A:558:HIS:HA	1:A:629:LEU:HD23	1.99	0.44
1:A:691:GLN:NE2	7:A:6208:HOH:O	2.48	0.44
1:A:589:GLU:OE2	1:A:751:LYS:HD3	2.18	0.43
1:A:693:LEU:HD13	7:A:6381:HOH:O	2.19	0.43
1:A:653:ARG:HD3	1:A:656:PRO:HA	2.01	0.43
1:A:686:LEU:HD22	1:A:697:ILE:HG12	2.00	0.42
1:A:903:VAL:O	1:A:985[B]:MET:HE1	2.19	0.42
1:A:251:TRP:C	1:A:251:TRP:CD1	2.92	0.42
1:A:954:ARG:CZ	1:A:981[A]:ARG:HH21	2.32	0.42
1:A:895:VAL:HG12	1:A:897:GLU:HG3	2.01	0.42
1:A:954:ARG:HH22	1:A:981[A]:ARG:HH21	1.57	0.41
1:A:53[A]:SER:HB2	7:A:6420:HOH:O	2.19	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:288:LYS:HD2	1:A:349:GLU:CD	2.40	0.41
1:A:298:PRO:HD2	1:A:299:TRP:CZ3	2.55	0.41
1:A:841:ASN:HB3	1:A:898:LYS:NZ	2.35	0.41
1:A:1009:CYS:HB3	1:A:1026:MET:HA	2.03	0.41
1:A:908:LEU:HG	7:A:7110:HOH:O	2.19	0.41
1:A:93:PRO:HD2	1:A:470:HIS:CE1	2.56	0.41
1:A:606:THR:HG21	1:A:653:ARG:HH21	1.86	0.40
1:A:138:TYR:CE1	1:A:193:MET:CE	3.04	0.40
1:A:698:GLN:HB2	1:A:705:HIS:ND1	2.37	0.40
1:A:97:GLN:HB3	1:A:101:GLU:HB2	2.03	0.40
1:A:380[A]:GLN:OE1	7:A:6044:HOH:O	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	1027/1045 (98%)	998 (97%)	24 (2%)	5 (0%)	34 16

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	991	GLU
1	A	993	HIS
1	A	95	TRP
1	A	994	THR
1	A	204	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	914/929 (98%)	896 (98%)	18 (2%)	63	47

All (18) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	57	ILE
1	A	154	LYS
1	A	158	LEU
1	A	275	CYS
1	A	304	ARG
1	A	375	GLN
1	A	394	GLN
1	A	638	ASP
1	A	653	ARG
1	A	654	LYS
1	A	669	LYS
1	A	677	SER
1	A	691	GLN
1	A	701	GLN
1	A	723	ARG
1	A	828	TYR
1	A	898	LYS
1	A	971	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	701	GLN
1	A	995	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 9 ligands modelled in this entry, 1 is monoatomic - leaving 8 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	$\# Z > 2$
5	MRD	A	2001	-	6,7,7	0.86	0	7,10,10	0.76	0
2	NAG	A	3001	1	14,14,15	0.64	0	15,19,21	2.86	2 (13%)
3	SO4	A	4001	-	4,4,4	1.23	1 (25%)	6,6,6	0.36	0
3	SO4	A	4002	-	4,4,4	0.52	0	6,6,6	0.34	0
3	SO4	A	4003	-	4,4,4	0.31	0	6,6,6	0.64	0
3	SO4	A	4004	-	4,4,4	0.38	0	6,6,6	0.72	0
3	SO4	A	4005	-	4,4,4	0.23	0	6,6,6	0.08	0
6	NK2	A	6001	4	10,12,12	0.57	0	8,17,17	1.16	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
5	MRD	A	2001	-	-	0/5/5/5	0/0/0/0
2	NAG	A	3001	1	-	0/6/23/26	0/1/1/1
3	SO4	A	4001	-	-	0/0/0/0	0/0/0/0
3	SO4	A	4002	-	-	0/0/0/0	0/0/0/0
3	SO4	A	4003	-	-	0/0/0/0	0/0/0/0
3	SO4	A	4004	-	-	0/0/0/0	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	SO4	A	4005	-	-	0/0/0/0	0/0/0/0
6	NK2	A	6001	4	-	0/0/23/23	0/2/2/2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	4001	SO4	O3-S	2.17	1.55	1.47

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	3001	NAG	C4-C3-C2	-2.61	107.18	111.23
2	A	3001	NAG	C1-O5-C5	9.98	124.91	112.25

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 2 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	2001	MRD	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	1016/1045 (97%)	-0.21	35 (3%)	49 47	6, 14, 28, 51	0

All (35) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	993	HIS	9.5
1	A	992	GLU	8.2
1	A	991	GLU	7.3
1	A	994	THR	6.3
1	A	603	LEU	5.6
1	A	602	THR	5.0
1	A	702	ASP	4.9
1	A	534	SER	4.9
1	A	600	HIS	4.1
1	A	583	LEU	4.0
1	A	721	GLY	4.0
1	A	990	PRO	3.8
1	A	701	GLN	3.8
1	A	604	THR	3.7
1	A	30	GLN	3.7
1	A	78	HIS	3.6
1	A	537	GLU	3.5
1	A	304	ARG	3.5
1	A	601	ASP	3.4
1	A	549	ILE	3.3
1	A	638	ASP	3.2
1	A	720	HIS	3.1
1	A	538	ASP	3.1
1	A	682	ASN	3.0
1	A	1024	ASP	2.7
1	A	451	MET	2.6
1	A	739	GLU	2.6

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Mol	Chain	Res	Type	RSRZ
1	A	53[A]	SER	2.3
1	A	536	VAL	2.2
1	A	655	ASN	2.2
1	A	144	ASN	2.2
1	A	1022	HIS	2.1
1	A	742	GLN	2.0
1	A	79	HIS	2.0
1	A	608	HIS	2.0

6.2 Non-standard residues in protein, DNA, RNA chains [i](#)

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

6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(Å ²)	Q<0.9
3	SO4	A	4001	5/5	0.95	0.20	10.67	21,23,29,38	0
3	SO4	A	4005	5/5	0.80	0.47	6.03	20,20,20,20	0
3	SO4	A	4003	5/5	0.93	0.17	5.48	48,49,54,54	0
6	NK2	A	6001	11/11	0.98	0.07	1.73	7,9,12,13	0
3	SO4	A	4004	5/5	0.86	0.21	1.29	51,53,58,58	0
3	SO4	A	4002	5/5	0.91	0.20	0.86	41,45,48,48	0
5	MRD	A	2001	8/8	0.96	0.08	0.15	13,19,24,25	0
4	ZN	A	5001	1/1	1.00	0.02	-5.28	11,11,11,11	0
2	NAG	A	3001	14/15	0.61	0.38	-	48,58,62,63	0

6.5 Other polymers [i](#)

There are no such residues in this entry.