Full wwPDB X-ray Structure Validation Report (i)

Feb 1, 2016 – 02:00 AM GMT

PDB ID	:	2F7Q
Title	:	Golgi alpha-mannosidase II complex with aminocyclopentitetrol
Authors	:	Kuntz, D.A.; Rose, D.R.
Deposited on	:	2005-12-01
Resolution	:	1.85 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:

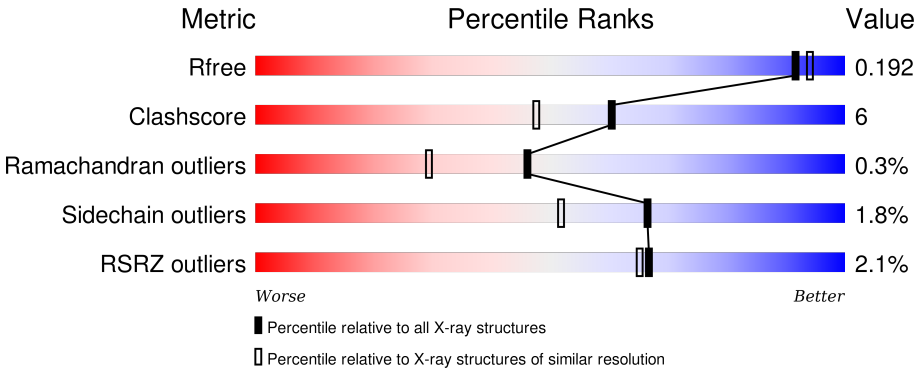
MolProbity	:	4.02b-467
Mogul	:	1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20026688
Percentile statistics	:	20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac	:	5.8.0135
CCP4	:	6.5.0
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)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

1 Overall quality at a glance

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

The reported resolution of this entry is 1.85 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	1745 (1.86-1.86)
Clashscore	102246	1898 (1.86-1.86)
Ramachandran outliers	100387	1875 (1.86-1.86)
Sidechain outliers	100360	1875 (1.86-1.86)
RSRZ outliers	91569	1747 (1.86-1.86)

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	1045	2% 84% 12%

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	MPD	A	5003	X	-	-	-

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 9434 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.

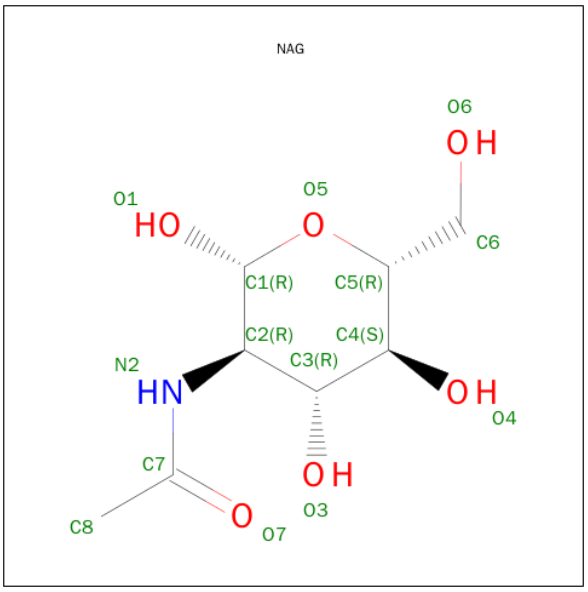
- Molecule 1 is a protein called alpha-mannosidase II.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1014	Total	C	N	O	S	0	19	0
			8256	5241	1444	1529	42			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ARG	-	CLONING ARTIFACT	GB 517481
A	2	SER	-	CLONING ARTIFACT	GB 517481
A	3	SER	-	CLONING ARTIFACT	GB 517481
A	4	HIS	-	EXPRESSION TAG	GB 517481
A	5	HIS	-	EXPRESSION TAG	GB 517481
A	6	HIS	-	EXPRESSION TAG	GB 517481
A	7	HIS	-	EXPRESSION TAG	GB 517481
A	8	HIS	-	EXPRESSION TAG	GB 517481
A	9	HIS	-	EXPRESSION TAG	GB 517481
A	10	GLY	-	CLONING ARTIFACT	GB 517481
A	11	GLU	-	CLONING ARTIFACT	GB 517481
A	12	PHE	-	CLONING ARTIFACT	GB 517481

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

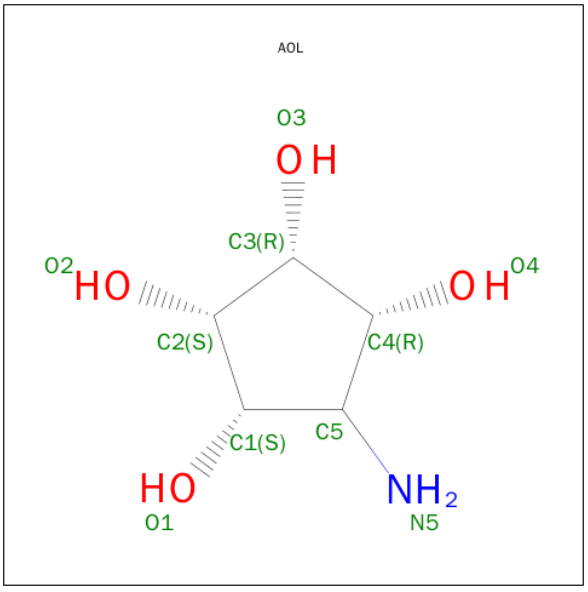


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

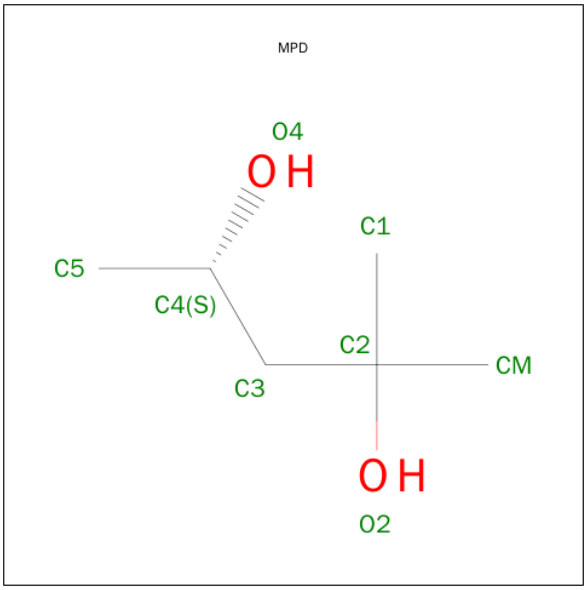
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	1	Total	Zn	0	0
			1	1		

- Molecule 4 is (1R,2R,3S,4S,5R)-5-AMINOCYCLOPENTANE-1,2,3,4-TETROL (three-letter code: AOL) (formula: $C_5H_{11}NO_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
4	A	1	Total	C	N	O	0	0
			10	5	1	4		

- Molecule 5 is (4S)-2-METHYL-2,4-PENTANEDIOL (three-letter code: MPD) (formula: $C_6H_{14}O_2$).



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

- Molecule 6 is water.

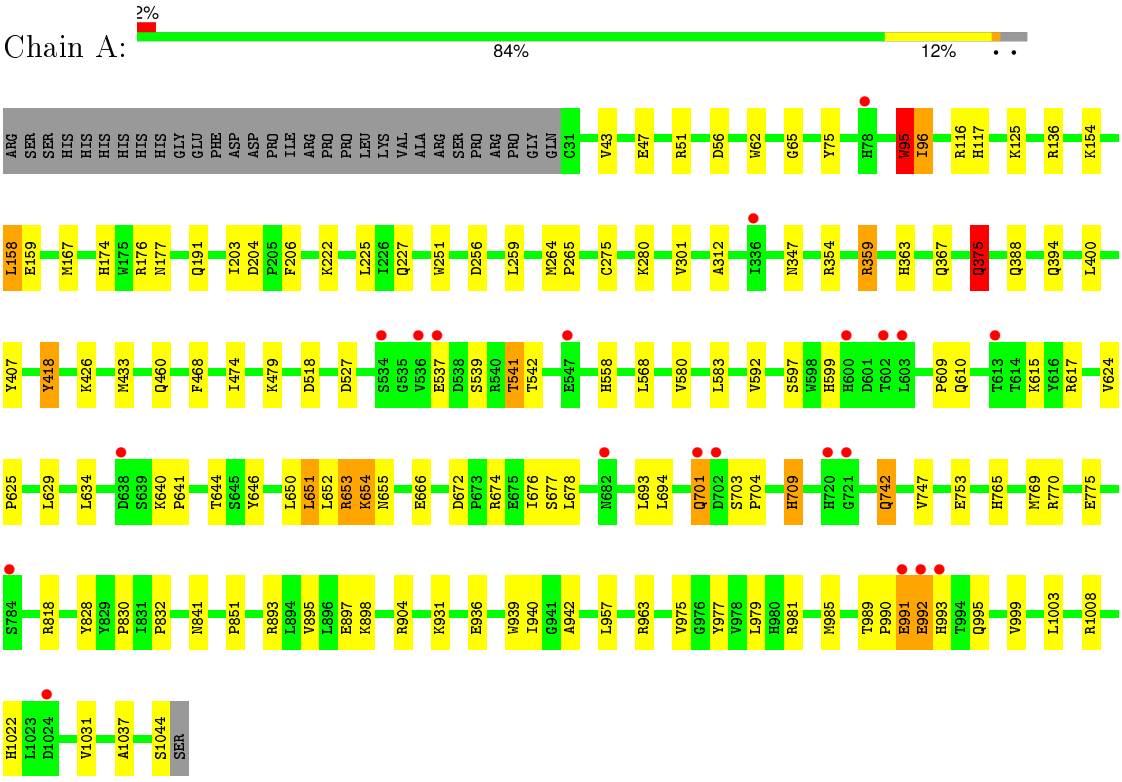
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1145	Total	O	0	0
			1145	1145		

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 II

Chain A:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α, β, γ	68.81Å 109.67Å 137.67Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.64 – 1.85 29.64 – 1.84	Depositor EDS
% Data completeness (in resolution range)	96.2 (29.64-1.85) 95.8 (29.64-1.84)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	5.16 (at 1.84Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.150 , 0.190 0.154 , 0.192	Depositor DCC
R_{free} test set	2143 reflections (2.49%)	DCC
Wilson B-factor (Å^2)	18.0	Xtriage
Anisotropy	0.378	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 51.4	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning[2]	$< \|L\| > = 0.50$, $< L^2 > = 0.33$	Xtriage
Outliers	0 of 90155 reflections	Xtriage
F_o,F_c correlation	0.97	EDS
Total number of atoms	9434	wwPDB-VP
Average B, all atoms (Å^2)	20.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.58% 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: MPD, AOL, ZN, 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	1.12	12/8557 (0.1%)	1.01	10/11618 (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	6

All (12) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	312	ALA	CA-CB	6.24	1.65	1.52
1	A	742	GLN	CD-OE1	5.78	1.36	1.24
1	A	977	TYR	CD1-CE1	5.64	1.47	1.39
1	A	655	ASN	CG-OD1	5.63	1.36	1.24
1	A	460	GLN	CD-NE2	-5.58	1.18	1.32
1	A	418	TYR	CD1-CE1	5.50	1.47	1.39
1	A	95	TRP	CB-CG	5.32	1.59	1.50
1	A	347	ASN	CG-OD1	5.31	1.35	1.24
1	A	388	GLN	CD-OE1	5.29	1.35	1.24
1	A	191	GLN	CD-OE1	5.26	1.35	1.24
1	A	936	GLU	CG-CD	5.25	1.59	1.51
1	A	701	GLN	CD-OE1	5.17	1.35	1.24

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	56	ASP	CB-CG-OD1	5.95	123.65	118.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	A	167	MET	N-CA-C	-5.78	95.39	111.00
1	A	818	ARG	NE-CZ-NH2	-5.77	117.41	120.30
1	A	518	ASP	N-CA-C	-5.53	96.07	111.00
1	A	963	ARG	NE-CZ-NH2	-5.46	117.57	120.30
1	A	136	ARG	NE-CZ-NH1	-5.24	117.68	120.30
1	A	991	GLU	N-CA-C	5.20	125.04	111.00
1	A	265	PRO	N-CA-C	5.14	125.47	112.10
1	A	359	ARG	NE-CZ-NH2	-5.11	117.75	120.30
1	A	674	ARG	NE-CZ-NH2	-5.06	117.77	120.30

There are no chirality outliers.

All (6) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	375[B]	GLN	Mainchain
1	A	407	TYR	Sidechain
1	A	597[B]	SER	Mainchain
1	A	677[B]	SER	Mainchain
1	A	709[B]	HIS	Mainchain
1	A	75	TYR	Sidechain

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	8256	0	8029	89	0
2	A	14	0	13	2	0
3	A	1	0	0	0	0
4	A	10	0	9	1	0
5	A	8	0	14	0	0
6	A	1145	0	0	16	0
All	All	9434	0	8065	91	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 (91) 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:117[B]:HIS:CE1	1:A:354:ARG:HE	1.83	0.95
1:A:117[B]:HIS:HE1	1:A:354:ARG:HE	1.14	0.91
1:A:256:ASP:HB2	6:A:5763:HOH:O	1.74	0.86
1:A:47:GLU:OE2	1:A:51:ARG:HD3	1.75	0.86
1:A:742:GLN:HG3	6:A:5546:HOH:O	1.76	0.83
1:A:568:LEU:HD12	1:A:770[A]:ARG:HD3	1.64	0.78
1:A:227:GLN:HB2	1:A:264[B]:MET:CE	2.16	0.75
1:A:753:GLU:OE2	1:A:770[B]:ARG:NH1	2.19	0.75
1:A:537:GLU:HG2	1:A:539:SER:HB3	1.69	0.74
1:A:678:LEU:HD12	1:A:769[A]:MET:HE1	1.70	0.71
1:A:701:GLN:HG2	6:A:5409:HOH:O	1.91	0.70
1:A:117[B]:HIS:HE1	1:A:354:ARG:NE	1.90	0.68
1:A:654:LYS:NZ	1:A:672:ASP:OD1	2.30	0.64
1:A:227:GLN:HB2	1:A:264[B]:MET:HE3	1.79	0.63
1:A:96:ILE:CG2	6:A:5838:HOH:O	2.46	0.63
1:A:96:ILE:HG23	6:A:5838:HOH:O	2.02	0.59
1:A:651:LEU:CD1	1:A:653:ARG:HG2	2.33	0.59
1:A:904:ARG:HG2	1:A:985:MET:SD	2.45	0.57
2:A:5002:NAG:H3	2:A:5002:NAG:H82	1.86	0.57
1:A:678:LEU:HD12	1:A:769[A]:MET:CE	2.33	0.57
1:A:701:GLN:OE1	1:A:701:GLN:HA	2.05	0.56
1:A:895:VAL:HG12	1:A:897:GLU:HG3	1.88	0.56
1:A:580:VAL:HG22	1:A:634:LEU:HD22	1.88	0.55
1:A:359:ARG:NE	6:A:5182:HOH:O	2.38	0.55
1:A:541:THR:CG2	6:A:5458:HOH:O	2.53	0.55
1:A:841:ASN:O	1:A:898:LYS:HE2	2.07	0.55
1:A:280:LYS:HE2	1:A:301:VAL:CG2	2.36	0.55
1:A:375[B]:GLN:NE2	6:A:5884:HOH:O	2.39	0.55
1:A:47:GLU:OE1	1:A:51:ARG:NH1	2.40	0.54
1:A:651:LEU:HD13	1:A:653:ARG:HG2	1.90	0.54
1:A:979[B]:LEU:HD21	1:A:999:VAL:HG11	1.90	0.53
1:A:227:GLN:HB2	1:A:264[B]:MET:HE2	1.88	0.52
2:A:5002:NAG:C3	2:A:5002:NAG:H82	2.40	0.52
1:A:62:TRP:CD2	1:A:65:GLY:HA3	2.46	0.51
1:A:694:LEU:O	1:A:709[B]:HIS:HD2	1.93	0.51
1:A:158:LEU:HD23	1:A:158:LEU:C	2.31	0.51
1:A:981:ARG:HD2	1:A:1031:VAL:O	2.11	0.50
1:A:96:ILE:HD12	1:A:479:LYS:HE2	1.93	0.49
1:A:653:ARG:NH1	6:A:5537:HOH:O	2.41	0.49
1:A:957:LEU:HD11	1:A:979[A]:LEU:HG	1.95	0.49
1:A:541:THR:HG23	6:A:5458:HOH:O	2.11	0.48
1:A:542:THR:OG1	1:A:615:LYS:HD2	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:479:LYS:HD3	6:A:5836:HOH:O	2.13	0.48
1:A:703:SER:HB2	1:A:704:PRO:HD2	1.96	0.47
1:A:174:HIS:CE1	1:A:176:ARG:HD3	2.49	0.47
1:A:251:TRP:C	1:A:251:TRP:CD1	2.87	0.47
1:A:280:LYS:HE2	1:A:301:VAL:HG21	1.96	0.47
1:A:641:PRO:HG2	1:A:644:THR:HB	1.97	0.47
1:A:117[B]:HIS:CE1	1:A:354:ARG:NE	2.66	0.46
1:A:992:GLU:HB3	1:A:993:HIS:H	1.40	0.46
1:A:125:LYS:HE2	6:A:5172:HOH:O	2.14	0.46
1:A:940:ILE:HD12	6:A:6074:HOH:O	2.16	0.46
1:A:939:TRP:CD2	1:A:942:ALA:HB2	2.50	0.46
1:A:830:PRO:HB2	1:A:832:PRO:HD3	1.97	0.45
1:A:599:HIS:HD2	1:A:610:GLN:CG	2.30	0.45
1:A:203:ILE:HG22	1:A:264[B]:MET:HE1	1.98	0.44
1:A:468:PHE:CZ	1:A:474:ILE:HA	2.52	0.44
1:A:177:ASN:HD21	1:A:433:MET:HB2	1.82	0.44
1:A:770[B]:ARG:NH2	1:A:775:GLU:OE1	2.47	0.44
1:A:939:TRP:CG	1:A:942:ALA:HB2	2.53	0.44
1:A:640:LYS:HD2	1:A:646:TYR:CE2	2.54	0.43
1:A:280:LYS:HE2	1:A:301:VAL:HG23	2.00	0.43
1:A:154:LYS:HE2	6:A:6043:HOH:O	2.19	0.43
1:A:989:THR:HA	1:A:990:PRO:HD3	1.79	0.43
1:A:975:VAL:HG21	1:A:1003:LEU:CD1	2.48	0.43
1:A:363:HIS:O	1:A:367:GLN:HG2	2.18	0.43
1:A:225:LEU:HD21	1:A:264[A]:MET:SD	2.59	0.42
1:A:975:VAL:HG21	1:A:1003:LEU:HD13	2.01	0.42
1:A:426:LYS:HD3	1:A:851:PRO:O	2.19	0.42
1:A:1031:VAL:HG11	1:A:1037:ALA:HB3	2.02	0.42
1:A:43:VAL:O	1:A:400:LEU:HA	2.19	0.42
1:A:650:LEU:HD21	1:A:652:LEU:HD21	2.02	0.42
1:A:599:HIS:CD2	1:A:610:GLN:HG3	2.55	0.41
1:A:558:HIS:HA	1:A:629:LEU:HD23	2.02	0.41
1:A:583:LEU:HD12	1:A:583:LEU:HA	1.89	0.41
1:A:527:ASP:O	1:A:931:LYS:HE3	2.21	0.41
1:A:568:LEU:HD12	1:A:770[A]:ARG:CD	2.44	0.41
1:A:222:LYS:NZ	6:A:5151:HOH:O	2.51	0.41
1:A:1008:ARG:CZ	1:A:1022:HIS:CD2	3.03	0.41
1:A:624:VAL:HA	1:A:625:PRO:HD3	1.94	0.41
1:A:206:PHE:HB2	1:A:418:TYR:CE1	2.55	0.41
1:A:227:GLN:OE1	1:A:264[A]:MET:HB2	2.21	0.41
1:A:259:LEU:HA	1:A:259:LEU:HD12	1.92	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:158:LEU:HD23	1:A:159:GLU:N	2.36	0.41
1:A:775:GLU:HA	1:A:893:ARG:HD2	2.03	0.40
1:A:95:TRP:CZ2	4:A:5009:AOL:H2	2.56	0.40
1:A:693:LEU:HD23	1:A:765:HIS:CD2	2.56	0.40
1:A:51:ARG:HG3	6:A:5369:HOH:O	2.20	0.40
1:A:981:ARG:HB2	1:A:1031:VAL:HG23	2.04	0.40
1:A:676:ILE:HD13	1:A:747:VAL:HG21	2.03	0.40
1:A:592:VAL:HA	1:A:617:ARG:O	2.22	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	1031/1045 (99%)	1004 (97%)	24 (2%)	3 (0%)	46 29

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	991	GLU
1	A	95	TRP
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	920/929 (99%)	902 (98%)	18 (2%)	63 47

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

Mol	Chain	Res	Type
1	A	96	ILE
1	A	116	ARG
1	A	158	LEU
1	A	275	CYS
1	A	375[A]	GLN
1	A	375[B]	GLN
1	A	394	GLN
1	A	541	THR
1	A	609	PRO
1	A	651	LEU
1	A	653	ARG
1	A	654	LYS
1	A	666[A]	GLU
1	A	666[B]	GLU
1	A	828	TYR
1	A	992	GLU
1	A	995	GLN
1	A	1044	SER

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	119	HIS
1	A	919	HIS

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 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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	$\#\|Z\| > 2$
2	NAG	A	5002	1	14,14,15	0.85	0	15,19,21	0.93	0
5	MPD	A	5003	-	6,7,7	0.63	0	7,10,10	0.43	0
4	AOL	A	5009	3	10,10,10	0.32	0	10,15,15	1.73	4 (40%)

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	5002	1	-	1/6/23/26	0/1/1/1
5	MPD	A	5003	-	1/1/2/2	0/5/5/5	0/0/0/0
4	AOL	A	5009	3	-	0/0/20/20	0/1/1/1

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
4	A	5009	AOL	C2-C3-C4	2.09	105.99	102.72
4	A	5009	AOL	O4-C4-C3	2.13	118.76	111.83
4	A	5009	AOL	O3-C3-C2	2.20	118.97	111.83
4	A	5009	AOL	O1-C1-C5	2.74	118.10	111.26

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
5	A	5003	MPD	C4

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	5002	NAG	O7-C7-N2-C2

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	5002	NAG	2	0
4	A	5009	AOL	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, 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	1014/1045 (97%)	-0.14	21 (2%) 67 65	9, 17, 30, 64	0

All (21) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	993	HIS	5.9
1	A	1024	ASP	4.5
1	A	638	ASP	4.1
1	A	701	GLN	4.0
1	A	721	GLY	4.0
1	A	78	HIS	3.9
1	A	702	ASP	3.9
1	A	536	VAL	3.7
1	A	991	GLU	3.6
1	A	602	THR	3.6
1	A	720	HIS	3.5
1	A	537	GLU	3.4
1	A	600	HIS	3.1
1	A	547	GLU	2.9
1	A	682	ASN	2.9
1	A	992	GLU	2.6
1	A	534	SER	2.5
1	A	613	THR	2.3
1	A	784	SER	2.2
1	A	336	ILE	2.1
1	A	603	LEU	2.1

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 (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, 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	MPD	A	5003	8/8	0.90	0.15	1.49	18,21,24,25	0
4	AOL	A	5009	10/10	0.98	0.08	-0.20	11,14,17,18	0
3	ZN	A	5001	1/1	1.00	0.03	-6.08	15,15,15,15	0
2	NAG	A	5002	14/15	0.76	0.36	-	39,45,49,49	0

6.5 Other polymers (i)

There are no such residues in this entry.