



Full wwPDB X-ray Structure Validation Report ⓘ

Jan 30, 2019 – 12:10 PM EST

PDB ID : 6F5G
Title : Complete PCSK9 C-ter domain in complex with VHH P.140
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Deposited on : 2017-12-01
Resolution : 2.20 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.7.3 (157068), CSD as539be (2018)
Xtriage (Phenix) : 1.13
EDS : rb-20031633
Percentile statistics : 20171227.v01 (using entries in the PDB archive December 27th 2017)
Refmac : 5.8.0158
CCP4 : 7.0 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : rb-20031633

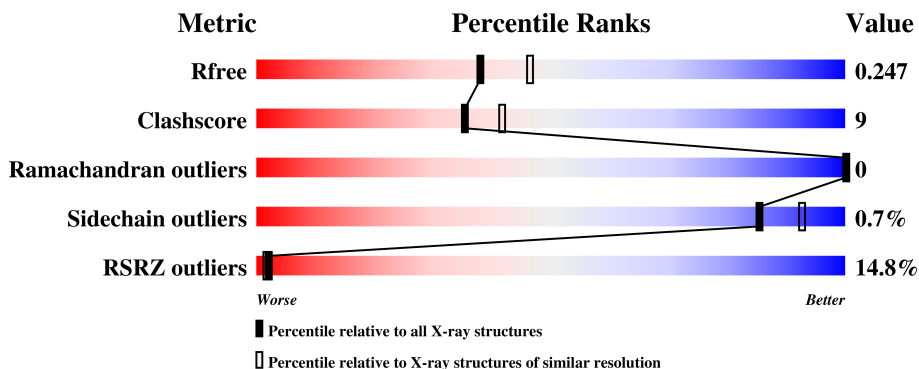
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	111664	4343 (2.20-2.20)
Clashscore	122126	5027 (2.20-2.20)
Ramachandran outliers	120053	4952 (2.20-2.20)
Sidechain outliers	120020	4953 (2.20-2.20)
RSRZ outliers	108989	4245 (2.20-2.20)

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	703	
2	B	128	

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	NAG	A	902	-	-	-	X
4	BMA	A	903	-	-	-	X
5	MAN	A	904	-	-	-	X
5	MAN	A	906	-	-	-	X
6	FUC	A	905	-	-	-	X

2 Entry composition

There are 8 unique types of molecules in this entry. The entry contains 2995 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 Proprotein convertase subtilisin/kexin type 9.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	231	Total	C	N	O	S	0	1	0
			1712	1037	331	323	21			

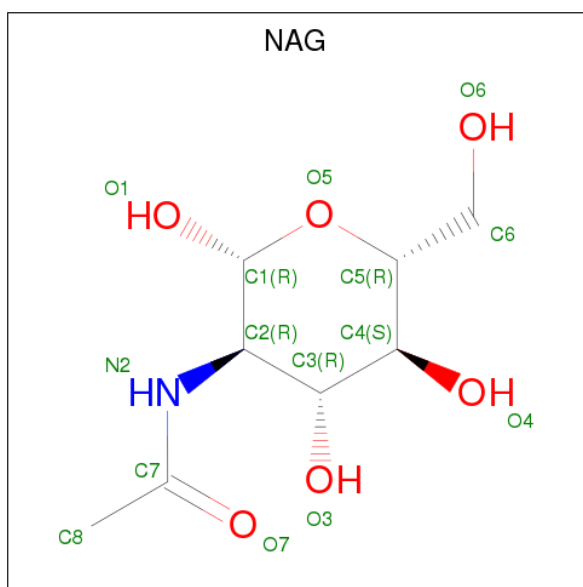
There are 11 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	693	THR	-	expression tag	UNP Q8NBP7
A	694	GLY	-	expression tag	UNP Q8NBP7
A	695	HIS	-	expression tag	UNP Q8NBP7
A	696	HIS	-	expression tag	UNP Q8NBP7
A	697	HIS	-	expression tag	UNP Q8NBP7
A	698	HIS	-	expression tag	UNP Q8NBP7
A	699	HIS	-	expression tag	UNP Q8NBP7
A	700	HIS	-	expression tag	UNP Q8NBP7
A	701	GLY	-	expression tag	UNP Q8NBP7
A	702	GLY	-	expression tag	UNP Q8NBP7
A	703	GLN	-	expression tag	UNP Q8NBP7

- Molecule 2 is a protein called VHH minibody anti-Cter PCSK9.

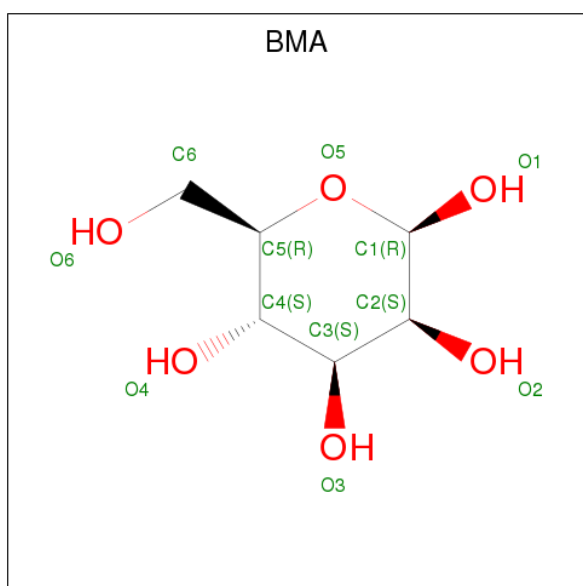
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	127	Total	C	N	O	S	0	0	0
			1009	630	175	200	4			

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (three-letter code: NAG) (formula: C₈H₁₅NO₆).



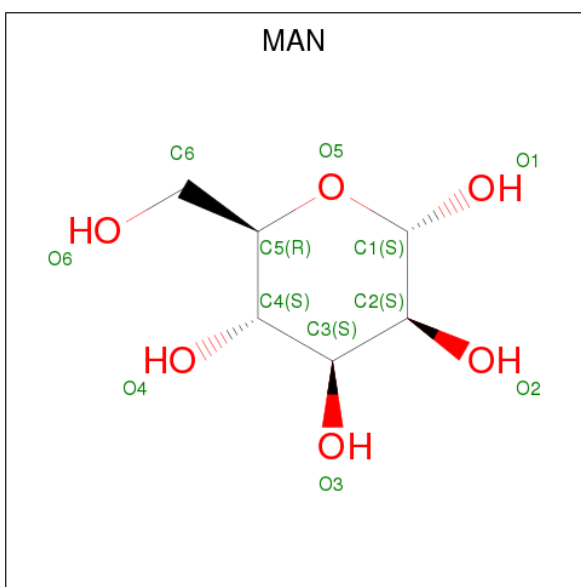
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
3	A	1	Total	C	N	O	0	0
			14	8	1	5		
3	A	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 4 is BETA-D-MANNOSE (three-letter code: BMA) (formula: $C_6H_{12}O_6$).



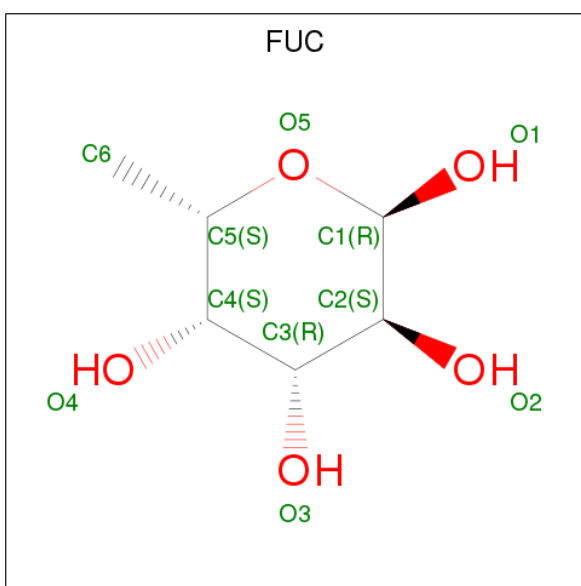
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			11	6	5		

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



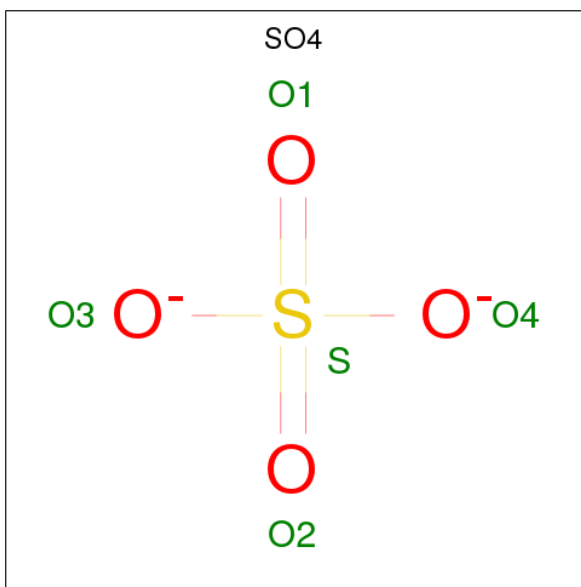
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
5	A	1	Total	C	O	0	0
			11	6	5		
5	A	1	Total	C	O	0	0
			11	6	5		

- Molecule 6 is ALPHA-L-FUCOSE (three-letter code: FUC) (formula: $C_6H_{12}O_5$).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
6	A	1	Total	C	O	0	0
			10	6	4		

- Molecule 7 is SULFATE ION (three-letter code: SO4) (formula: O_4S).



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

- Molecule 8 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	A	115	Total	O	0	0
			115	115		
8	B	83	Total	O	0	0
			83	83		



4 Data and refinement statistics

Property	Value	Source
Space group	P 41 21 2	Depositor
Cell constants a, b, c, α , β , γ	52.43Å 52.43Å 263.41Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	45.02 – 2.20 48.71 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.7 (45.02-2.20) 99.7 (48.71-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	0.24	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.11 (at 2.20Å)	Xtriage
Refinement program	PHENIX (1.12_2829: ???)	Depositor
R, R_{free}	0.195 , 0.249 0.202 , 0.247	Depositor DCC
R_{free} test set	991 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	44.6	Xtriage
Anisotropy	0.238	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 56.9	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	2995	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.93% 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: MAN, SO4, BMA, NAG, FUC

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	0.43	0/1750	0.68	0/2376
2	B	0.44	0/1031	0.67	0/1395
All	All	0.43	0/2781	0.68	0/3771

There are no bond length outliers.

There are no bond angle outliers.

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	1712	0	1630	34	0
2	B	1009	0	953	15	0
3	A	28	0	23	1	0
4	A	11	0	8	0	0
5	A	22	0	20	0	0
6	A	10	0	10	1	0
7	A	5	0	0	0	0
8	A	115	0	0	4	0
8	B	83	0	0	2	0
All	All	2995	0	2644	48	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 9.

All (48) 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:643:HIS:HB2	1:A:659:ARG:HB2	1.60	0.82
1:A:619:GLN:HB3	8:A:1049:HOH:O	1.89	0.70
1:A:643:HIS:CE1	1:A:661:VAL:HB	2.33	0.64
1:A:460:VAL:HG13	1:A:524:ALA:HB3	1.79	0.64
1:A:584:GLN:HB2	1:A:587:GLN:OE1	1.98	0.63
2:B:39:GLN:HB2	2:B:45:ARG:HG2	1.82	0.62
2:B:83:MET:HE2	2:B:86:LEU:HD21	1.82	0.61
1:A:477:CYS:HB3	1:A:481:GLU:HG3	1.82	0.61
1:A:582:ARG:O	1:A:582:ARG:HG3	2.02	0.60
1:A:584:GLN:OE1	1:A:585:PRO:HD2	2.05	0.57
1:A:662:SER:H	2:B:75:ALA:HB2	1.68	0.56
1:A:506:LYS:NZ	8:A:1005:HOH:O	2.39	0.55
1:A:660:ASP:HB2	2:B:74:ASN:OD1	2.08	0.53
3:A:902:NAG:HO6	6:A:905:FUC:HO2	1.56	0.53
1:A:659:ARG:HB3	1:A:661:VAL:HG23	1.91	0.53
1:A:551:HIS:HB2	1:A:586:ASN:O	2.09	0.52
1:A:618:PRO:HB3	1:A:672:VAL:HG21	1.93	0.51
1:A:477:CYS:HB3	1:A:481:GLU:CG	2.42	0.49
1:A:580:ARG:HB3	1:A:581:PRO:HD2	1.94	0.48
2:B:25:SER:HB2	8:B:231:HOH:O	2.13	0.47
2:B:7:SER:HB2	2:B:21:SER:HB3	1.97	0.47
2:B:106:VAL:HG23	2:B:107:TYR:CD2	2.50	0.47
1:A:552:CYS:HB3	1:A:557:HIS:HB3	1.98	0.46
2:B:64:VAL:HG13	2:B:68:PHE:CG	2.51	0.46
1:A:565:HIS:CE1	1:A:597:HIS:HE2	2.35	0.45
2:B:106:VAL:HG22	8:B:236:HOH:O	2.15	0.45
2:B:9:GLY:HA2	2:B:18:LEU:HD21	1.98	0.45
1:A:660:ASP:HB3	8:A:1075:HOH:O	2.16	0.45
1:A:493:GLY:HA3	1:A:659:ARG:NH2	2.30	0.45
2:B:44:GLU:O	2:B:46:GLU:HG3	2.17	0.45
1:A:554:GLN:HB2	1:A:557:HIS:ND1	2.32	0.45
1:A:546:MET:CE	1:A:577:PRO:HG2	2.47	0.44
1:A:496:ARG:HA	1:A:566:TRP:CE2	2.52	0.44
1:A:581:PRO:HB3	1:A:612:GLU:OE1	2.17	0.44
1:A:498:GLU:HG2	1:A:563:SER:HB3	1.98	0.44
1:A:523:ILE:HD13	1:A:648:TYR:HB3	2.00	0.44
1:A:554:GLN:O	1:A:557:HIS:HB2	2.17	0.44
1:A:495:ARG:HB2	8:A:1042:HOH:O	2.16	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:644:VAL:HG23	1:A:644:VAL:O	2.19	0.43
1:A:643:HIS:CB	1:A:659:ARG:HB2	2.39	0.43
2:B:5:GLU:O	2:B:22:CYS:HA	2.18	0.43
1:A:566:TRP:CE2	1:A:571:LEU:HD21	2.54	0.42
1:A:496:ARG:NE	1:A:513:ASN:O	2.50	0.42
2:B:62:ASP:C	2:B:64:VAL:H	2.24	0.41
2:B:33:ALA:HB3	2:B:99:ARG:HB3	2.02	0.41
1:A:557:HIS:CD2	1:A:602:HIS:NE2	2.88	0.40
1:A:566:TRP:CD2	1:A:571:LEU:HD21	2.57	0.40
2:B:83:MET:HB3	2:B:86:LEU:HD21	2.03	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	230/703 (33%)	221 (96%)	9 (4%)	0	100	100
2	B	125/128 (98%)	121 (97%)	4 (3%)	0	100	100
All	All	355/831 (43%)	342 (96%)	13 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	184/565 (33%)	182 (99%)	2 (1%)	76	87
2	B	107/107 (100%)	107 (100%)	0	100	100
All	All	291/672 (43%)	289 (99%)	2 (1%)	85	93

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	579	LEU
1	A	619	GLN

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	643	HIS
2	B	1	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](#)

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
3	NAG	A	901	1,3,6	14,14,15	0.49	0	17,19,21	2.05	5 (29%)
3	NAG	A	902	3,4	14,14,15	0.33	0	17,19,21	1.26	2 (11%)
4	BMA	A	903	3,5	11,11,12	0.54	0	15,15,17	1.46	3 (20%)
5	MAN	A	904	4	11,11,12	0.28	0	15,15,17	0.81	0
6	FUC	A	905	3	9,10,11	0.42	0	13,14,16	1.88	4 (30%)
5	MAN	A	906	4	11,11,12	1.16	1 (9%)	15,15,17	3.21	6 (40%)
7	SO4	A	907	-	4,4,4	0.14	0	6,6,6	0.07	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	901	1,3,6	-	0/6/23/26	0/1/1/1
3	NAG	A	902	3,4	-	0/6/23/26	0/1/1/1
4	BMA	A	903	3,5	-	0/2/19/22	0/1/1/1
5	MAN	A	904	4	-	0/2/19/22	0/1/1/1
6	FUC	A	905	3	-	0/0/17/20	0/1/1/1
5	MAN	A	906	4	-	0/2/19/22	0/1/1/1
7	SO4	A	907	-	-	0/0/0/0	0/0/0/0

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	906	MAN	C1-C2	3.24	1.59	1.52

All (20) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	A	906	MAN	O5-C1-C2	-7.59	98.94	110.78
5	A	906	MAN	C2-C3-C4	-5.44	101.42	110.87
5	A	906	MAN	C3-C4-C5	-3.82	103.41	110.24
3	A	902	NAG	O5-C1-C2	-3.08	107.27	111.52
5	A	906	MAN	C1-O5-C5	-3.05	107.99	112.19
6	A	905	FUC	C6-C5-C4	-3.05	107.83	113.06
3	A	901	NAG	O5-C5-C6	-2.76	102.78	107.15
6	A	905	FUC	O5-C1-C2	-2.64	106.67	110.78
6	A	905	FUC	C2-C3-C4	-2.61	106.34	110.87
3	A	901	NAG	C2-N2-C7	-2.51	119.27	122.94
3	A	901	NAG	C4-C3-C2	-2.28	107.67	111.02

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	903	BMA	C1-O5-C5	-2.25	109.09	112.19
4	A	903	BMA	C3-C4-C5	2.50	114.71	110.24
5	A	906	MAN	O5-C5-C4	3.17	118.53	110.83
4	A	903	BMA	C1-C2-C3	3.26	113.78	109.66
3	A	902	NAG	C1-O5-C5	3.32	116.76	112.19
6	A	905	FUC	O5-C5-C4	3.68	115.60	109.62
3	A	901	NAG	C1-O5-C5	4.34	118.16	112.19
3	A	901	NAG	O4-C4-C5	5.14	122.19	109.31
5	A	906	MAN	C1-C2-C3	5.43	116.53	109.66

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	902	NAG	1	0
6	A	905	FUC	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, 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	231/703 (32%)	1.56	49 (21%) 1 0	29, 48, 144, 188	0
2	B	127/128 (99%)	0.54	4 (3%) 49 46	29, 42, 74, 98	0
All	All	358/831 (43%)	1.20	53 (14%) 2 2	29, 45, 135, 188	0

All (53) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	577	PRO	15.2
1	A	576	PRO	12.8
1	A	664	THR	12.0
1	A	665	GLY	10.9
1	A	662	SER	10.3
1	A	666	SER	9.4
1	A	640	GLY	8.6
1	A	575	LYS	8.6
1	A	667	THR	8.1
1	A	663	THR	8.1
1	A	578	VAL	7.7
1	A	579	LEU	7.4
1	A	574	HIS	7.4
1	A	580	ARG	7.1
1	A	583	GLY	5.7
1	A	493	GLY	5.6
1	A	668	SER	5.5
1	A	581	PRO	5.4
1	A	641	THR	5.4
1	A	582	ARG	5.2
1	A	463	ALA	5.0
1	A	639	PRO	4.8
1	A	620	GLU	4.6
1	A	659	ARG	4.2

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Mol	Chain	Res	Type	RSRZ
1	A	546	MET	4.2
2	B	27	ARG	4.2
1	A	661	VAL	4.1
1	A	573	THR	4.0
1	A	453	TRP	4.0
1	A	544	ALA	3.9
1	A	682	ARG	3.9
2	B	26	ASP	3.9
1	A	452	GLY	3.5
2	B	127	SER	3.1
1	A	670	GLY	3.0
1	A	660	ASP	3.0
1	A	542	ALA	2.9
1	A	642	SER	2.9
1	A	669	GLU	2.9
1	A	468	THR	2.7
2	B	1	GLN	2.7
1	A	681	SER	2.6
1	A	677	ILE	2.5
1	A	618	PRO	2.5
1	A	638	LEU	2.5
1	A	472	THR	2.5
1	A	658	SER	2.4
1	A	628[A]	GLU	2.3
1	A	571	LEU	2.2
1	A	643	HIS	2.2
1	A	460	VAL	2.2
1	A	455	LEU	2.1
1	A	633	THR	2.0

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 ⓘ

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. 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	BMA	A	903	11/12	0.02	0.53	147,154,158,162	0
5	MAN	A	904	11/12	0.16	0.59	110,136,146,151	0
3	NAG	A	902	14/15	0.23	0.44	98,123,139,146	0
5	MAN	A	906	11/12	0.28	0.58	166,169,174,178	0
6	FUC	A	905	10/11	0.62	0.49	152,166,172,174	0
3	NAG	A	901	14/15	0.66	0.34	82,100,119,134	0
7	SO4	A	907	5/5	0.86	0.19	107,112,113,119	0

6.5 Other polymers [i](#)

There are no such residues in this entry.