



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 30, 2016 – 10:46 AM EDT

PDB ID : 5SZQ
Title : Protocadherin Gamma A4 extracellular cadherin domains 3-6
Authors : Goodman, K.M.; Mannepalli, S.; Bahna, F.; Honig, B.; Shapiro, L.
Deposited on : 2016-08-14
Resolution : 2.61 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 : 1.7.1 (RC1), CSD as537be (2016)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20027939
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) : rb-20027939

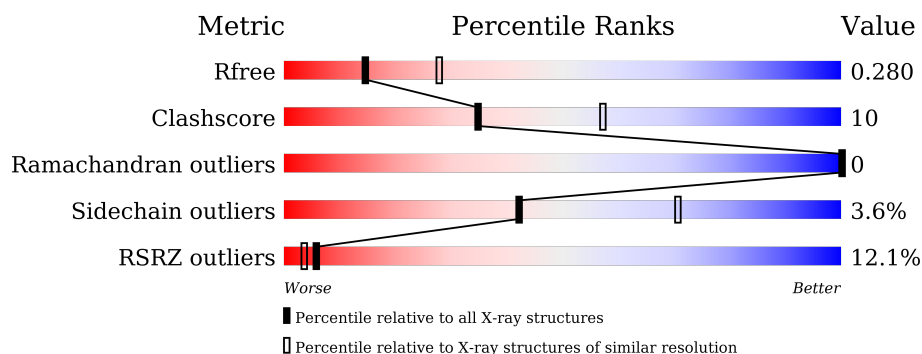
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.61 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	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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	441	<div> <div>12%</div> <div>71%</div> <div>23%</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
2	MAN	A	701	-	-	-	X
2	MAN	A	706	-	-	-	X

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	CA	A	710	-	-	-	X
4	CA	A	716	-	-	-	X
4	CA	A	718	-	-	-	X

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 3306 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.

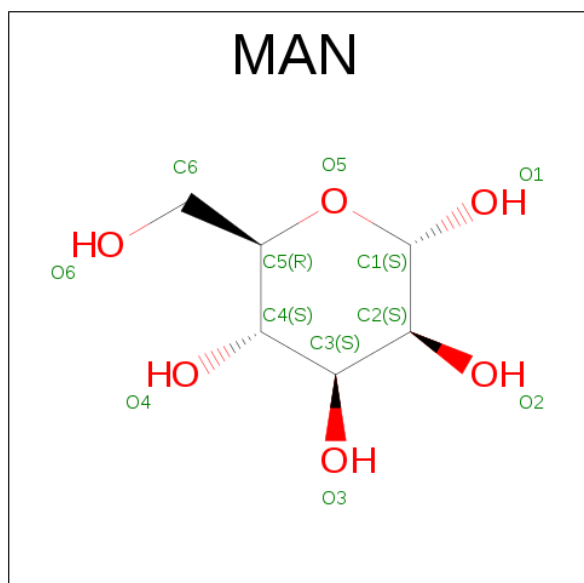
- Molecule 1 is a protein called Protocadherin gamma-A4.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	422	3189	1991	530	666	2	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

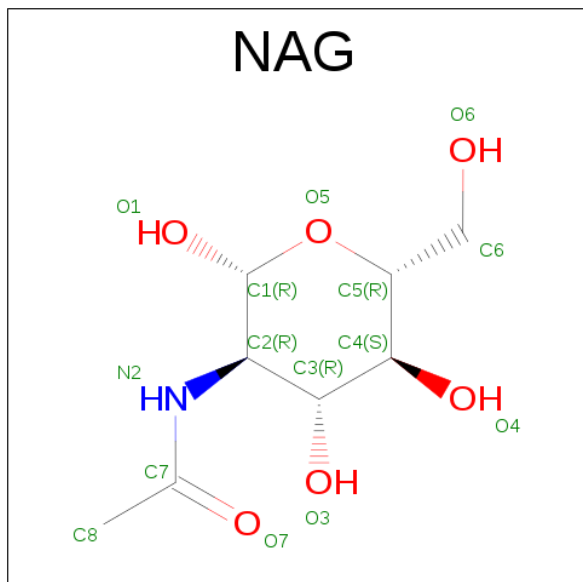
Chain	Residue	Modelled	Actual	Comment	Reference
A	643	HIS	-	expression tag	UNP Q91XY4
A	644	HIS	-	expression tag	UNP Q91XY4
A	645	HIS	-	expression tag	UNP Q91XY4
A	646	HIS	-	expression tag	UNP Q91XY4
A	647	HIS	-	expression tag	UNP Q91XY4
A	648	HIS	-	expression tag	UNP Q91XY4
A	649	HIS	-	expression tag	UNP Q91XY4
A	650	HIS	-	expression tag	UNP Q91XY4

- Molecule 2 is ALPHA-D-MANNOSE (three-letter code: MAN) (formula: C₆H₁₂O₆).



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

- Molecule 3 is N-ACETYL-D-GLUCOSAMINE (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		
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		

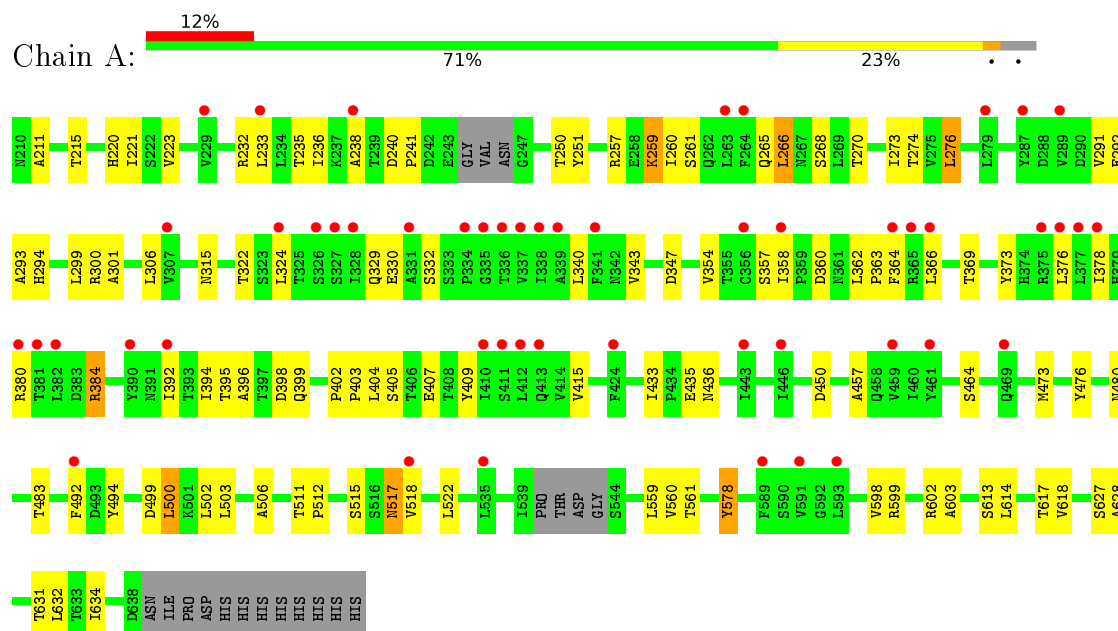
- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	9	Total	Ca	0	0
			9	9		

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 ($\text{RSRZ} > 2$). 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: Protocadherin gamma-A4



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	31.89Å 63.64Å 344.31Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	19.96 – 2.61 46.74 – 2.61	Depositor EDS
% Data completeness (in resolution range)	51.7 (19.96-2.61) 52.1 (46.74-2.61)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.27 (at 2.61Å)	Xtriage
Refinement program	PHENIX (1.10.1 _2155: ???)	Depositor
R, R_{free}	0.251 , 0.282 0.255 , 0.280	Depositor DCC
R_{free} test set	555 reflections (4.73%)	DCC
Wilson B-factor (Å ²)	48.7	Xtriage
Anisotropy	1.776	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 47.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.46$, $\langle L^2 \rangle = 0.30$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	3306	wwPDB-VP
Average B, all atoms (Å ²)	98.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.43% 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: CA, 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	0.27	0/3248	0.49	0/4450

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	3189	0	3065	61	1
2	A	66	0	60	2	0
3	A	42	0	38	2	0
4	A	9	0	0	0	0
All	All	3306	0	3163	64	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 10.

All (64) 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:363:PRO:HB2	1:A:380:ARG:HG3	1.70	0.74
1:A:366:LEU:HD12	1:A:376:LEU:HD13	1.73	0.70
1:A:473:MET:HG2	1:A:502:LEU:HD21	1.74	0.69
1:A:517:ASN:OD1	1:A:517:ASN:N	2.26	0.69
1:A:259:LYS:HD2	1:A:259:LYS:H	1.59	0.67
1:A:435:GLU:HG3	1:A:494:TYR:H	1.59	0.67
1:A:369:THR:N	1:A:373:TYR:O	2.31	0.64
1:A:476:TYR:HB3	1:A:492:PHE:HE1	1.62	0.64
1:A:343:VAL:HG21	1:A:354:VAL:HG21	1.83	0.61
1:A:329:GLN:HB3	1:A:332:SER:HB2	1.83	0.61
1:A:450:ASP:OD2	1:A:457:ALA:HA	2.02	0.59
1:A:211:ALA:HB2	1:A:299:LEU:HB3	1.85	0.58
1:A:292:GLU:HA	1:A:301:ALA:O	2.04	0.58
1:A:266:LEU:HB3	1:A:273:ILE:HD13	1.85	0.57
1:A:464:SER:HB3	1:A:503:LEU:HB3	1.86	0.57
1:A:503:LEU:HD11	1:A:517:ASN:HB2	1.87	0.56
1:A:329:GLN:HA	1:A:415:VAL:HB	1.86	0.56
1:A:232:ARG:HA	1:A:274:THR:HG22	1.88	0.56
1:A:330:GLU:HG3	1:A:384:ARG:H	1.71	0.54
1:A:476:TYR:HB3	1:A:492:PHE:CE1	2.43	0.53
1:A:250:THR:HB	1:A:294:HIS:HB2	1.90	0.53
1:A:560:VAL:HG11	1:A:634:ILE:HD13	1.91	0.52
1:A:293:ALA:O	1:A:300:ARG:HA	2.10	0.52
1:A:480:ASN:HB3	1:A:483:THR:O	2.09	0.52
1:A:433:ILE:HD12	1:A:522:LEU:HD11	1.92	0.51
1:A:559:LEU:HA	1:A:599:ARG:HG2	1.91	0.51
1:A:618:VAL:O	1:A:627:SER:HA	2.10	0.51
1:A:238:ALA:N	1:A:251:TYR:OH	2.39	0.51
1:A:257:ARG:HB2	1:A:260:ILE:HB	1.93	0.50
1:A:473:MET:SD	1:A:500:LEU:HD12	2.52	0.50
1:A:236:ILE:HD12	1:A:291:VAL:HG11	1.92	0.50
1:A:358:ILE:HG13	1:A:392:ILE:HD11	1.94	0.49
1:A:613:SER:HA	1:A:632:LEU:O	2.12	0.49
1:A:257:ARG:O	1:A:261:SER:N	2.35	0.49
1:A:396:ALA:O	1:A:405:SER:HA	2.12	0.49
3:A:707:NAG:H62	3:A:708:NAG:N2	2.28	0.49
1:A:617:THR:HA	1:A:628:ALA:O	2.13	0.49
1:A:398:ASP:HB3	1:A:404:LEU:H	1.78	0.48
1:A:220:HIS:CE1	1:A:306:LEU:HD12	2.48	0.48
1:A:233:LEU:HB2	1:A:273:ILE:HG22	1.97	0.47
1:A:499:ASP:N	1:A:499:ASP:OD1	2.48	0.47
1:A:561:THR:HG22	1:A:598:VAL:HB	1.97	0.46

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:578:TYR:HD1	1:A:618:VAL:HG22	1.80	0.46
1:A:221:ILE:HG13	1:A:223:VAL:HG13	1.98	0.46
3:A:707:NAG:H62	3:A:708:NAG:C7	2.45	0.46
1:A:511:THR:HA	1:A:512:PRO:HA	1.74	0.44
1:A:357:SER:HB2	1:A:395:THR:OG1	2.18	0.44
1:A:395:THR:HG22	1:A:407:GLU:HB3	2.00	0.43
1:A:315:ASN:HB2	1:A:347:ASP:OD2	2.18	0.43
1:A:251:TYR:HB2	1:A:268:SER:HA	2.00	0.43
2:A:702:MAN:O3	2:A:704:MAN:O5	2.32	0.43
1:A:402:PRO:HA	1:A:403:PRO:HD3	1.90	0.43
1:A:265:GLN:HB2	1:A:276:LEU:HD23	2.01	0.42
1:A:233:LEU:N	1:A:273:ILE:O	2.43	0.42
1:A:614:LEU:O	1:A:631:THR:HA	2.19	0.42
1:A:506:ALA:O	1:A:515:SER:HA	2.19	0.42
1:A:364:PHE:HD1	1:A:378:ILE:HA	1.83	0.41
1:A:602:ARG:NH2	1:A:603:ALA:O	2.53	0.41
1:A:627:SER:HB2	2:A:701:MAN:H2	1.53	0.41
1:A:357:SER:O	1:A:394:ILE:HA	2.21	0.41
1:A:398:ASP:OD1	1:A:399:GLN:N	2.53	0.41
1:A:322:THR:HB	1:A:340:LEU:O	2.20	0.41
1:A:503:LEU:HD12	1:A:518:VAL:O	2.21	0.41
1:A:240:ASP:HA	1:A:241:PRO:HD3	1.89	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:215:THR:OG1	1:A:436:ASN:O[3_244]	2.07	0.13

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	416/441 (94%)	398 (96%)	18 (4%)	0	100	100

There are no Ramachandran outliers to report.

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	363/390 (93%)	350 (96%)	13 (4%)	42	71

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	235	THR
1	A	259	LYS
1	A	266	LEU
1	A	270	THR
1	A	276	LEU
1	A	324	LEU
1	A	360	ASP
1	A	362	LEU
1	A	384	ARG
1	A	409	TYR
1	A	500	LEU
1	A	517	ASN
1	A	578	TYR

Some 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 carbohydrates in this entry.

5.6 Ligand geometry ⓘ

Of 18 ligands modelled in this entry, 9 are monoatomic - leaving 9 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	MAN	A	701	1	11,11,12	0.87	0	15,15,17	1.07	1 (6%)
2	MAN	A	702	1	11,11,12	0.48	0	15,15,17	1.20	3 (20%)
2	MAN	A	703	1	11,11,12	0.69	0	15,15,17	0.87	1 (6%)
2	MAN	A	704	1	11,11,12	0.99	0	15,15,17	1.19	1 (6%)
2	MAN	A	705	1	11,11,12	0.68	0	15,15,17	1.34	3 (20%)
2	MAN	A	706	1	11,11,12	0.93	0	15,15,17	0.90	0
3	NAG	A	707	1,3	14,14,15	0.41	0	15,19,21	0.56	0
3	NAG	A	708	3	14,14,15	0.90	1 (7%)	15,19,21	0.61	0
3	NAG	A	709	1	14,14,15	0.31	0	15,19,21	0.30	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
2	MAN	A	701	1	-	0/2/19/22	0/1/1/1
2	MAN	A	702	1	-	0/2/19/22	0/1/1/1
2	MAN	A	703	1	-	0/2/19/22	0/1/1/1
2	MAN	A	704	1	-	0/2/19/22	0/1/1/1
2	MAN	A	705	1	-	0/2/19/22	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	MAN	A	706	1	-	0/2/19/22	0/1/1/1
3	NAG	A	707	1,3	-	0/6/23/26	0/1/1/1
3	NAG	A	708	3	-	0/6/23/26	0/1/1/1
3	NAG	A	709	1	-	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)
3	A	708	NAG	C1-C2	2.60	1.56	1.52

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	A	703	MAN	O2-C2-C3	-2.18	105.80	110.19
2	A	705	MAN	O2-C2-C3	-2.08	106.00	110.19
2	A	702	MAN	O2-C2-C3	-2.03	106.09	110.19
2	A	702	MAN	O5-C1-C2	2.01	114.10	110.89
2	A	701	MAN	C1-O5-C5	2.33	115.56	112.14
2	A	704	MAN	C1-O5-C5	2.36	115.61	112.14
2	A	705	MAN	O5-C1-C2	2.55	114.97	110.89
2	A	702	MAN	C1-O5-C5	2.93	116.44	112.14
2	A	705	MAN	C1-O5-C5	3.08	116.67	112.14

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

5 monomers are involved in 4 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	701	MAN	1	0
2	A	702	MAN	1	0
2	A	704	MAN	1	0
3	A	707	NAG	2	0
3	A	708	NAG	2	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	422/441 (95%)	0.38	51 (12%) 6 3	29, 101, 147, 177	0

All (51) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	328	ILE	7.3
1	A	365	ARG	7.0
1	A	287	TYR	5.6
1	A	376	LEU	5.6
1	A	335	GLY	5.4
1	A	337	VAL	5.2
1	A	336	THR	5.1
1	A	412	LEU	4.9
1	A	229	VAL	4.2
1	A	338	ILE	4.2
1	A	382	LEU	4.2
1	A	356	CYS	4.1
1	A	334	PRO	4.0
1	A	446	ILE	3.9
1	A	233	LEU	3.8
1	A	459	VAL	3.6
1	A	424	PHE	3.6
1	A	324	LEU	3.6
1	A	411	SER	3.6
1	A	413	GLN	3.6
1	A	366	LEU	3.5
1	A	364	PHE	3.3
1	A	279	LEU	3.3
1	A	390	TYR	3.2
1	A	377	LEU	3.2
1	A	327	SER	3.2
1	A	264	PHE	3.1

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	380	ARG	3.0
1	A	331	ALA	2.9
1	A	307	VAL	2.9
1	A	518	VAL	2.8
1	A	469	GLN	2.8
1	A	358	ILE	2.8
1	A	378	ILE	2.7
1	A	410	ILE	2.5
1	A	289	VAL	2.5
1	A	341	PHE	2.5
1	A	589	PHE	2.5
1	A	461	TYR	2.5
1	A	392	ILE	2.5
1	A	492	PHE	2.4
1	A	263	LEU	2.4
1	A	326	SER	2.4
1	A	443	ILE	2.3
1	A	535	LEU	2.3
1	A	593	LEU	2.3
1	A	375	ARG	2.2
1	A	381	THR	2.2
1	A	591	VAL	2.1
1	A	238	ALA	2.1
1	A	339	ALA	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 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(\AA^2)	Q<0.9
2	MAN	A	701	11/12	0.88	0.33	5.08	100,112,120,127	0
4	CA	A	718	1/1	0.93	0.32	4.84	86,86,86,86	0
4	CA	A	710	1/1	0.93	0.19	3.80	88,88,88,88	0
2	MAN	A	706	11/12	0.88	0.46	2.26	102,128,133,136	0
4	CA	A	716	1/1	0.95	0.28	2.03	74,74,74,74	0
4	CA	A	711	1/1	0.98	0.23	1.82	65,65,65,65	0
4	CA	A	717	1/1	0.92	0.26	1.15	41,41,41,41	0
4	CA	A	712	1/1	0.97	0.15	0.19	60,60,60,60	0
4	CA	A	715	1/1	0.63	0.11	-0.54	72,72,72,72	0
4	CA	A	714	1/1	0.99	0.10	-0.56	62,62,62,62	0
2	MAN	A	705	11/12	0.94	0.16	-1.14	66,80,91,97	0
3	NAG	A	708	14/15	0.86	0.13	-	127,146,161,163	0
4	CA	A	713	1/1	0.97	0.06	-	82,82,82,82	0
2	MAN	A	702	11/12	0.94	0.11	-	71,78,86,90	0
3	NAG	A	709	14/15	0.80	0.15	-	94,118,129,129	0
2	MAN	A	704	11/12	0.81	0.31	-	104,114,127,128	0
3	NAG	A	707	14/15	0.93	0.10	-	75,84,99,115	0
2	MAN	A	703	11/12	0.96	0.11	-	75,81,89,91	0

6.5 Other polymers [i](#)

There are no such residues in this entry.