



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 06:58 AM UTC

PDB ID : 4L37 / pdb_00004l37
Title : SP2-SP3 - a complex of two storage proteins from Bombyx mori hemolymph
Authors : Pietrzyk, A.J.; Bujacz, A.; Mueller-Dieckmann, J.; Jaskolski, M.; Bujacz, G.
Deposited on : 2013-06-05
Resolution : 2.90 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	:	4-5-2 with Phenix2.0
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

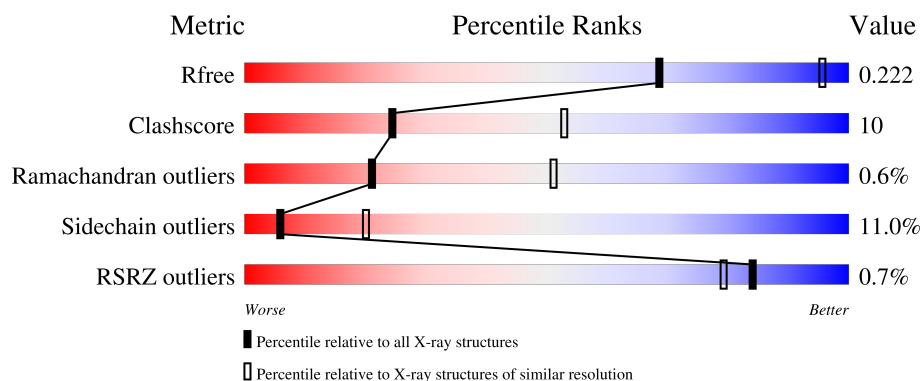
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.90 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}	180053	2481 (2.90-2.90)
Clashscore	190562	2690 (2.90-2.90)
Ramachandran outliers	187476	2623 (2.90-2.90)
Sidechain outliers	187428	2625 (2.90-2.90)
RSRZ outliers	180081	2481 (2.90-2.90)

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	680	70% 25% 5%
2	B	687	69% 24% 5%
3	C	5	100%
3	D	5	80% 20%

2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 11673 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.

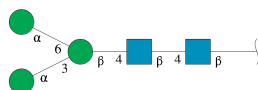
- Molecule 1 is a protein called Silkworm storage protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	674	Total	C	N	O	S	0	1	0
			5723	3780	886	1031	26			

- Molecule 2 is a protein called Arylphorin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	667	Total	C	N	O	S	0	1	0
			5664	3723	892	1024	25			

- Molecule 3 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	C	5	Total	C	N	O	0	0	0
			61	34	2	25			
3	D	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 4 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



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

- Molecule 5 is SODIUM ION (CCD ID: NA) (formula: Na).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	2	Total	Na	0	0
			2	2		
5	B	1	Total	Na	0	0
			1	1		

- Molecule 6 is THIOCYANATE ION (CCD ID: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	S	0	0
			3	1	1	1		
6	A	1	Total	C	N	S	0	0
			3	1	1	1		
6	A	1	Total	C	N	S	0	0
			3	1	1	1		
6	B	1	Total	C	N	S	0	0
			3	1	1	1		
6	B	1	Total	C	N	S	0	0
			3	1	1	1		

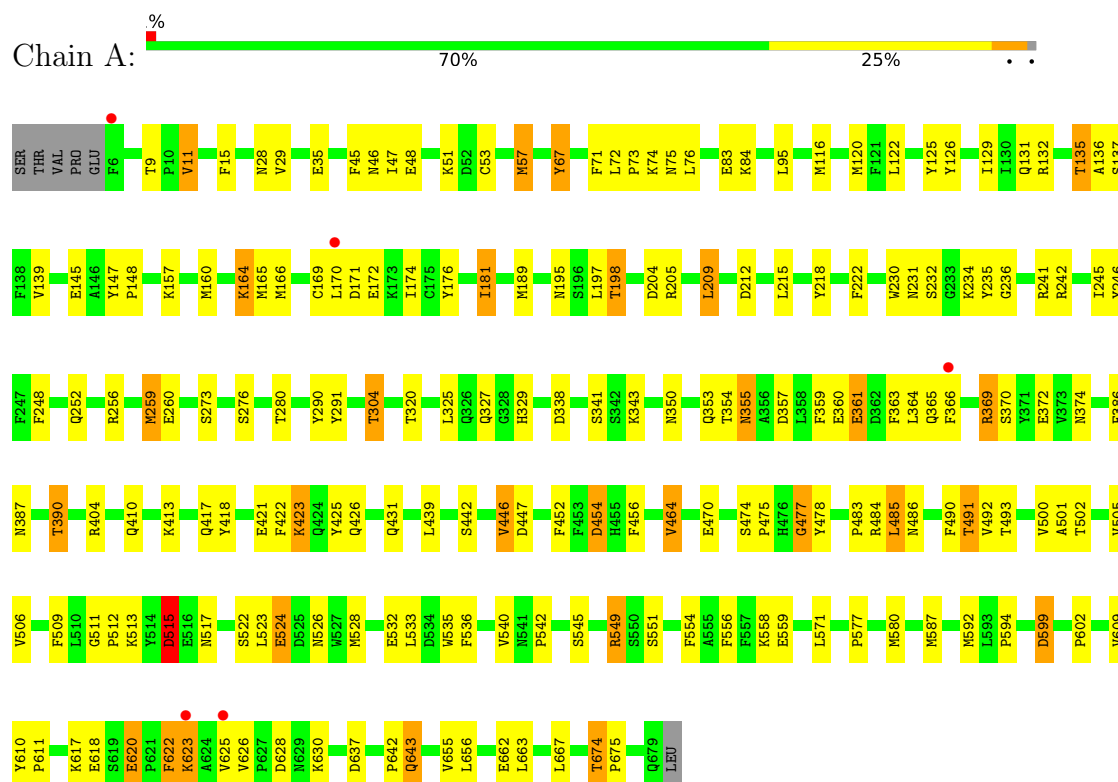
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	84	Total	O	0	0
			84	84		
7	B	52	Total	O	0	0
			52	52		

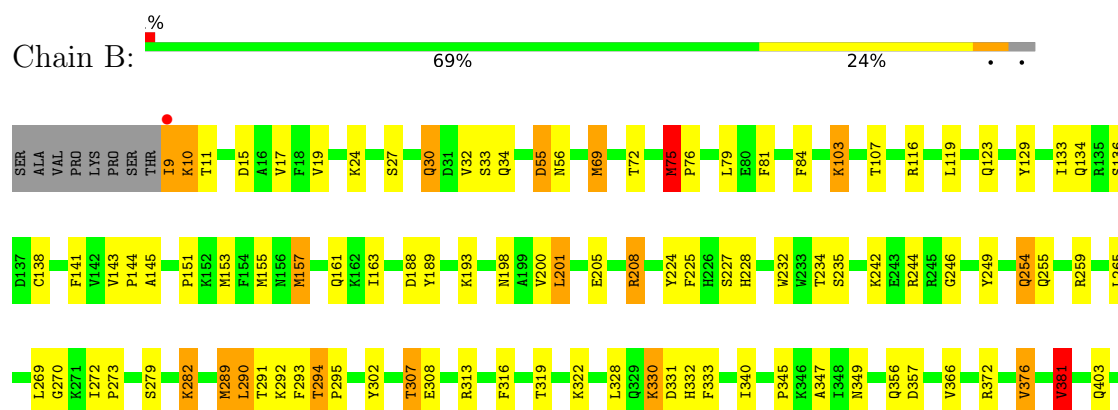
3 Residue-property plots

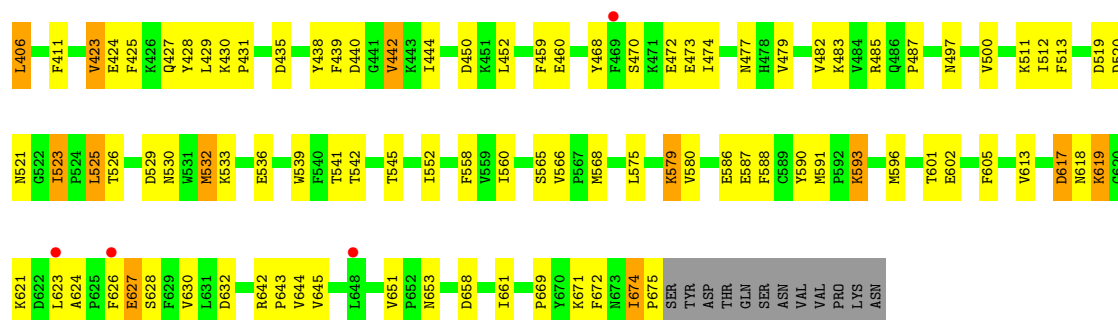
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Silkworm storage protein



• Molecule 2: Arylphorin





- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain C: 100%



- Molecule 3: alpha-D-mannopyranose-(1-3)-[alpha-D-mannopyranose-(1-6)]beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain D: 80% 20%



4 Data and refinement statistics

Property	Value	Source
Space group	P 63 2 2	Depositor
Cell constants a, b, c, α , β , γ	192.75Å 192.75Å 180.82Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	48.00 – 2.90 48.00 – 2.90	Depositor EDS
% Data completeness (in resolution range)	99.7 (48.00-2.90) 99.6 (48.00-2.90)	Depositor EDS
R_{merge}	0.11	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.79 (at 2.91Å)	Xtriage
Refinement program	REFMAC 5.7.0032	Depositor
R, R_{free}	0.166 , 0.223 0.166 , 0.222	Depositor DCC
R_{free} test set	1096 reflections (2.47%)	wwPDB-VP
Wilson B-factor (Å ²)	46.8	Xtriage
Anisotropy	0.543	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 51.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	11673	wwPDB-VP
Average B, all atoms (Å ²)	51.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.87% 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: SO4, MAN, NA, NAG, BMA, SCN

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	0.87	0/5924	1.11	15/8026 (0.2%)
2	B	0.83	0/5848	1.05	16/7912 (0.2%)
All	All	0.85	0/11772	1.08	31/15938 (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

There are no bond length outliers.

All (31) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	622	PHE	N-CA-C	8.13	118.70	108.45
2	B	270	GLY	N-CA-C	6.92	124.40	111.80
2	B	279	SER	CA-C-N	-6.85	113.25	120.03
2	B	279	SER	C-N-CA	-6.85	113.25	120.03
1	A	477	GLY	N-CA-C	6.72	122.59	113.99
2	B	75	MET	CA-C-N	6.63	126.59	120.03
2	B	75	MET	C-N-CA	6.63	126.59	120.03
1	A	361	GLU	N-CA-C	6.32	119.45	109.96
1	A	327	GLN	N-CA-C	-6.12	102.89	110.41
2	B	119	LEU	N-CA-C	6.01	118.84	109.52
1	A	515	ASP	CB-CA-C	-6.00	98.49	110.42
2	B	381	VAL	N-CA-CB	5.99	119.56	110.58
2	B	330	LYS	CA-C-N	-5.98	112.31	122.11
2	B	330	LYS	C-N-CA	-5.98	112.31	122.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	359	PHE	N-CA-C	5.86	117.55	109.29
1	A	355	ASN	CB-CA-C	-5.83	98.81	110.42
2	B	290	LEU	N-CA-C	5.82	116.78	108.74
1	A	145	GLU	N-CA-C	-5.74	106.41	113.41
1	A	276	SER	CA-C-N	-5.68	113.85	119.99
1	A	276	SER	C-N-CA	-5.68	113.85	119.99
1	A	474	SER	CA-C-N	5.61	125.37	119.76
1	A	474	SER	C-N-CA	5.61	125.37	119.76
2	B	626	PHE	N-CA-C	5.55	117.33	111.28
1	A	571	LEU	N-CA-C	-5.38	105.44	112.23
2	B	588	PHE	N-CA-C	5.36	117.82	111.33
1	A	242	ARG	N-CA-C	5.17	117.33	111.02
2	B	424	GLU	N-CA-C	-5.12	105.82	111.71
2	B	193	LYS	N-CA-C	-5.10	101.39	109.96
2	B	512	ILE	N-CA-C	5.04	115.11	107.75
2	B	331	ASP	N-CA-C	-5.04	107.52	113.97
1	A	533	LEU	N-CA-C	-5.02	107.29	113.41

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	360	GLU	Peptide
1	A	477	GLY	Peptide

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	5723	0	5443	123	0
2	B	5664	0	5426	108	0
3	C	61	0	52	0	0
3	D	61	0	52	1	0
4	A	5	0	0	0	0
4	B	5	0	0	0	0
5	A	2	0	0	0	0
5	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
6	A	9	0	0	0	0
6	B	6	0	0	1	0
7	A	84	0	0	7	0
7	B	52	0	0	3	0
All	All	11673	0	10973	223	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 10.

All (223) 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:497:ASN:HD22	2:B:552:ILE:HD12	1.22	1.02
1:A:256:ARG:HH12	1:A:260:GLU:HG2	1.31	0.95
1:A:515:ASP:HB3	1:A:517:ASN:H	1.31	0.95
1:A:132:ARG:HB2	1:A:135:THR:HG22	1.49	0.93
2:B:470:SER:HB3	2:B:473:GLU:HG3	1.55	0.85
1:A:132:ARG:HB2	1:A:135:THR:CG2	2.10	0.81
1:A:554:PHE:CE2	1:A:592:MET:HE1	2.21	0.74
2:B:291:THR:O	2:B:293:PHE:N	2.21	0.74
1:A:116:MET:HE2	1:A:120:MET:HE3	1.67	0.74
1:A:166:MET:HE3	2:B:468:TYR:HD1	1.52	0.74
2:B:56:ASN:HA	2:B:103:LYS:HD3	1.70	0.74
2:B:313[A]:ARG:HD3	2:B:381:VAL:HG12	1.69	0.73
1:A:350:ASN:OD1	1:A:355:ASN:ND2	2.24	0.70
1:A:259:MET:HE1	1:A:512:PRO:N	2.07	0.69
1:A:176:TYR:HD2	1:A:181:ILE:HD11	1.56	0.69
1:A:230:TRP:HZ3	1:A:363:PHE:CZ	2.11	0.68
2:B:27:SER:HA	2:B:30:GLN:HG3	1.75	0.66
1:A:628:ASP:HB3	1:A:630:LYS:H	1.59	0.66
1:A:246:TYR:CE2	1:A:353:GLN:HB2	2.31	0.66
2:B:254:GLN:OE1	2:B:255:GLN:NE2	2.29	0.66
2:B:587:GLU:HG2	2:B:590:TYR:HD2	1.61	0.65
1:A:51:LYS:HD2	1:A:57:MET:HE2	1.79	0.64
1:A:136:ALA:O	1:A:137:SER:HB3	1.97	0.64
1:A:248:PHE:O	1:A:252:GLN:HB2	1.99	0.63
1:A:338:ASP:O	1:A:341:SER:HB3	1.98	0.63
1:A:485:LEU:HD22	1:A:486:ASN:H	1.63	0.63
2:B:163:ILE:HD13	2:B:482:VAL:HG11	1.80	0.63
2:B:259:ARG:HG2	2:B:591:MET:HE1	1.80	0.63
1:A:256:ARG:NH1	1:A:260:GLU:HG2	2.10	0.62

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:509:PHE:CE1	1:A:532:GLU:HG2	2.36	0.61
2:B:460:GLU:HG2	2:B:485:ARG:HB3	1.81	0.61
1:A:536:PHE:CE1	1:A:549:ARG:HG3	2.35	0.61
2:B:153:MET:HE1	2:B:403:GLN:NE2	2.16	0.60
1:A:132:ARG:CB	1:A:135:THR:HG22	2.27	0.60
2:B:511:LYS:HE3	2:B:539:TRP:HD1	1.65	0.60
1:A:361:GLU:HG2	1:A:363:PHE:O	2.02	0.60
2:B:601:THR:HG23	2:B:605:PHE:HB2	1.84	0.60
1:A:129:ILE:HA	1:A:135:THR:HG21	1.83	0.59
1:A:11:VAL:HG13	1:A:15:PHE:HB3	1.84	0.59
1:A:259:MET:HE1	1:A:512:PRO:CD	2.33	0.59
1:A:554:PHE:CD2	1:A:592:MET:HE1	2.37	0.58
1:A:325:LEU:HD21	1:A:422:PHE:HB2	1.85	0.58
2:B:332:HIS:HA	2:B:340:ILE:O	2.04	0.58
2:B:235:SER:OG	2:B:242:LYS:HG3	2.04	0.57
1:A:361:GLU:CG	1:A:363:PHE:O	2.52	0.57
1:A:620:GLU:HA	1:A:620:GLU:OE1	2.05	0.57
2:B:642:ARG:HB2	2:B:643:PRO:HD2	1.87	0.57
1:A:209:LEU:HG	1:A:260:GLU:HG3	1.87	0.57
1:A:166:MET:HE3	2:B:468:TYR:CD1	2.38	0.57
1:A:166:MET:CE	2:B:468:TYR:HD1	2.16	0.56
1:A:129:ILE:HA	1:A:135:THR:CG2	2.35	0.56
2:B:291:THR:C	2:B:293:PHE:H	2.13	0.56
1:A:353:GLN:NE2	1:A:355:ASN:OD1	2.39	0.56
2:B:519:ASP:CG	2:B:523:ILE:HG12	2.32	0.56
1:A:290:TYR:CD1	2:B:200:VAL:HG21	2.41	0.55
2:B:497:ASN:ND2	2:B:552:ILE:HD12	2.07	0.55
1:A:129:ILE:O	1:A:135:THR:HG23	2.06	0.55
1:A:136:ALA:O	1:A:137:SER:CB	2.54	0.55
1:A:423:LYS:HG3	1:A:426:GLN:HE21	1.71	0.55
2:B:587:GLU:HG2	2:B:590:TYR:CD2	2.41	0.55
2:B:9:ILE:O	2:B:11:THR:HG23	2.07	0.55
1:A:230:TRP:CZ3	1:A:363:PHE:CE1	2.95	0.54
1:A:230:TRP:CZ3	1:A:363:PHE:CZ	2.95	0.54
1:A:259:MET:HE1	1:A:511:GLY:C	2.31	0.54
1:A:535:TRP:HD1	1:A:556:PHE:HE2	1.54	0.54
2:B:671:LYS:HA	2:B:674:ILE:HD12	1.89	0.54
1:A:83:GLU:CD	1:A:366:PHE:HB2	2.32	0.54
2:B:529:ASP:O	2:B:532:MET:HE1	2.07	0.54
1:A:73:PRO:HD2	1:A:76:LEU:HD12	1.89	0.54
1:A:369:ARG:NH1	1:A:374:ASN:OD1	2.41	0.54

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:75:MET:HE1	2:B:81:PHE:HB2	1.88	0.54
2:B:618:ASN:O	2:B:619:LYS:CB	2.55	0.54
2:B:84:PHE:HD1	2:B:376:VAL:HG22	1.72	0.54
1:A:387:ASN:OD1	1:A:390:THR:HG23	2.07	0.54
1:A:456:PHE:HB3	1:A:484:ARG:HG3	1.89	0.53
2:B:9:ILE:CG2	2:B:10:LYS:N	2.71	0.53
2:B:497:ASN:ND2	2:B:552:ILE:HG23	2.23	0.53
2:B:406:LEU:HD22	2:B:411:PHE:CE2	2.44	0.53
2:B:75:MET:HE2	2:B:123:GLN:CD	2.33	0.53
2:B:618:ASN:O	2:B:619:LYS:HB2	2.07	0.52
1:A:74:LYS:O	1:A:75:ASN:HB2	2.08	0.52
2:B:558:PHE:HE2	2:B:596:MET:HE1	1.74	0.52
2:B:198:ASN:HA	2:B:201:LEU:O	2.10	0.52
1:A:67:TYR:C	1:A:67:TYR:CD2	2.87	0.52
1:A:491:THR:HG22	7:A:866:HOH:O	2.09	0.52
2:B:232:TRP:O	2:B:366:VAL:HA	2.10	0.51
2:B:558:PHE:CE2	2:B:596:MET:HE1	2.46	0.51
2:B:11:THR:OG1	2:B:579:LYS:HE3	2.09	0.51
2:B:9:ILE:CG2	2:B:10:LYS:H	2.24	0.51
2:B:624:ALA:O	2:B:628:SER:HB2	2.09	0.51
1:A:610:TYR:HB2	1:A:611:PRO:HD2	1.93	0.51
2:B:619:LYS:C	2:B:621:LYS:H	2.19	0.51
1:A:361:GLU:CD	1:A:365:GLN:HG2	2.36	0.50
1:A:241:ARG:NH2	1:A:630:LYS:O	2.45	0.50
2:B:249:TYR:CE1	2:B:356:GLN:HB2	2.46	0.50
2:B:487:PRO:HG3	2:B:672:PHE:HB2	1.93	0.50
1:A:610:TYR:OH	1:A:628:ASP:OD2	2.24	0.50
2:B:75:MET:HE1	2:B:81:PHE:CD1	2.46	0.50
1:A:164:LYS:NZ	1:A:470:GLU:OE1	2.44	0.50
1:A:160:MET:HE2	1:A:478:TYR:HB3	1.93	0.49
1:A:577:PRO:HB2	1:A:580:MET:HG3	1.94	0.49
1:A:628:ASP:HB2	7:A:834:HOH:O	2.11	0.49
1:A:524:GLU:HG3	1:A:642:PRO:HG3	1.94	0.49
2:B:56:ASN:O	2:B:103:LYS:HB2	2.12	0.49
1:A:662:GLU:OE1	1:A:667:LEU:HD13	2.12	0.49
2:B:658:ASP:HB3	7:B:848:HOH:O	2.12	0.49
1:A:446:VAL:HG13	1:A:492:VAL:HG22	1.94	0.49
1:A:46:ASN:ND2	1:A:48:GLU:OE1	2.46	0.49
2:B:423:VAL:HG23	2:B:427:GLN:HE21	1.78	0.48
1:A:195:ASN:HB3	1:A:197:LEU:H	1.79	0.48
1:A:304:THR:HB	7:A:836:HOH:O	2.13	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:330:LYS:HD3	2:B:333:PHE:HB3	1.95	0.47
2:B:291:THR:C	2:B:293:PHE:N	2.72	0.47
2:B:316:PHE:CE1	2:B:372:ARG:HD3	2.49	0.47
2:B:328:LEU:O	2:B:428:TYR:OH	2.32	0.47
1:A:164:LYS:HG2	1:A:478:TYR:OH	2.14	0.47
1:A:454:ASP:O	1:A:483:PRO:HA	2.15	0.47
2:B:144:PRO:HB3	2:B:568:MET:HG3	1.95	0.47
1:A:423:LYS:CG	1:A:426:GLN:HE21	2.28	0.47
1:A:610:TYR:HB2	1:A:611:PRO:CD	2.43	0.47
1:A:259:MET:HE1	1:A:512:PRO:HD3	1.96	0.46
2:B:9:ILE:HG23	2:B:10:LYS:N	2.30	0.46
1:A:125:TYR:CZ	1:A:129:ILE:HD11	2.50	0.46
1:A:522:SER:HB2	1:A:524:GLU:OE1	2.15	0.46
2:B:205:GLU:O	2:B:208:ARG:HB2	2.15	0.46
1:A:122:LEU:HA	1:A:122:LEU:HD23	1.71	0.46
2:B:513:PHE:CE2	2:B:536:GLU:HB2	2.51	0.46
1:A:165:MET:HE2	2:B:468:TYR:H	1.79	0.46
1:A:554:PHE:CD2	1:A:592:MET:CE	2.98	0.46
2:B:294:THR:HG22	2:B:295:PRO:HD2	1.96	0.46
2:B:75:MET:HE2	2:B:123:GLN:NE2	2.31	0.45
2:B:627:GLU:HA	2:B:630:VAL:HG22	1.98	0.45
2:B:188:ASP:OD1	2:B:188:ASP:N	2.50	0.45
1:A:222:PHE:HD2	1:A:622:PHE:CZ	2.35	0.45
1:A:404:ARG:NH1	7:A:806:HOH:O	2.48	0.45
1:A:413:LYS:O	1:A:417:GLN:HG2	2.15	0.45
1:A:505:VAL:HB	1:A:610:TYR:CE2	2.52	0.45
2:B:617:ASP:O	2:B:618:ASN:C	2.59	0.45
1:A:198:THR:HB	7:A:860:HOH:O	2.16	0.45
2:B:444:ILE:HD11	2:B:613:VAL:HG23	1.99	0.45
1:A:222:PHE:CD2	1:A:622:PHE:CZ	3.04	0.45
2:B:157:MET:HE3	2:B:157:MET:HB2	1.79	0.45
1:A:45:PHE:HE2	1:A:47:ILE:HD12	1.81	0.45
1:A:71:PHE:CD2	1:A:116:MET:HE3	2.51	0.45
2:B:459:PHE:O	2:B:485:ARG:HA	2.17	0.45
1:A:580:MET:HE2	1:A:580:MET:HB3	1.83	0.44
1:A:674:THR:HA	1:A:675:PRO:HD3	1.76	0.44
2:B:138:CYS:O	2:B:141:PHE:HB2	2.16	0.44
2:B:532:MET:SD	2:B:532:MET:N	2.87	0.44
1:A:626:VAL:O	1:A:628:ASP:N	2.46	0.44
1:A:643:GLN:CD	1:A:643:GLN:H	2.26	0.44
1:A:423:LYS:HE3	1:A:637:ASP:O	2.18	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:129:TYR:O	2:B:133:ILE:HG13	2.17	0.44
2:B:282:LYS:HB2	2:B:302:TYR:CZ	2.53	0.44
2:B:319:THR:HG22	7:B:839:HOH:O	2.17	0.44
2:B:189:TYR:CD1	2:B:483:LYS:HG3	2.53	0.43
2:B:272:ILE:HA	2:B:273:PRO:HD3	1.84	0.43
1:A:234:LYS:HD3	1:A:235:TYR:CZ	2.53	0.43
1:A:622:PHE:HE2	7:A:813:HOH:O	2.01	0.43
1:A:260:GLU:OE2	1:A:594:PRO:HA	2.19	0.43
1:A:599:ASP:OD1	1:A:599:ASP:N	2.51	0.43
2:B:357:ASP:O	2:B:357:ASP:CG	2.61	0.43
2:B:347:ALA:HA	7:B:830:HOH:O	2.18	0.43
1:A:355:ASN:HB3	1:A:357:ASP:H	1.84	0.43
1:A:452:PHE:HE1	1:A:454:ASP:OD1	2.02	0.43
2:B:675:PRO:HG3	3:D:2:NAG:H61	2.00	0.43
1:A:501:ALA:HA	1:A:540:VAL:O	2.19	0.43
2:B:669:PRO:HD2	6:B:709:SCN:S	2.59	0.43
1:A:171:ASP:HB3	1:A:174:ILE:HD12	2.00	0.43
2:B:9:ILE:HG22	2:B:10:LYS:H	1.83	0.43
1:A:290:TYR:CD1	2:B:200:VAL:CG2	3.02	0.42
1:A:386:PHE:HB3	1:A:390:THR:OG1	2.19	0.42
1:A:72:LEU:HA	1:A:73:PRO:HD3	1.82	0.42
1:A:291:TYR:OH	2:B:200:VAL:HG22	2.19	0.42
2:B:55:ASP:OD1	2:B:55:ASP:N	2.52	0.42
2:B:75:MET:HE1	2:B:81:PHE:HD1	1.85	0.42
2:B:593:LYS:HB3	2:B:593:LYS:HE3	1.79	0.42
2:B:145:ALA:HB2	2:B:565:SER:CB	2.49	0.42
1:A:506:VAL:HG22	1:A:609:VAL:HG22	2.00	0.42
2:B:32:VAL:HA	2:B:116:ARG:HH12	1.85	0.42
2:B:69:MET:HE3	2:B:69:MET:HB2	1.71	0.42
2:B:246:GLY:HA3	2:B:349:ASN:HA	2.00	0.42
1:A:325:LEU:O	1:A:425:TYR:OH	2.31	0.42
1:A:524:GLU:HG3	1:A:642:PRO:CG	2.49	0.42
1:A:642:PRO:HD2	1:A:643:GLN:OE1	2.20	0.42
2:B:289:MET:HE3	2:B:289:MET:HB2	1.64	0.42
1:A:212:ASP:CG	1:A:484:ARG:HH11	2.28	0.42
1:A:353:GLN:HG2	1:A:353:GLN:O	2.20	0.42
1:A:418:TYR:O	1:A:421:GLU:HB3	2.19	0.42
2:B:619:LYS:C	2:B:621:LYS:N	2.77	0.42
1:A:558:LYS:HD2	1:A:559:GLU:O	2.19	0.42
2:B:224:TYR:O	2:B:225:PHE:C	2.63	0.42
2:B:133:ILE:HD12	2:B:227:SER:HB3	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:151:PRO:O	2:B:155:MET:HE3	2.20	0.41
1:A:166:MET:HE2	2:B:34:GLN:NE2	2.35	0.41
1:A:372:GLU:HB3	7:A:801:HOH:O	2.21	0.41
2:B:525:LEU:HG	2:B:530:ASN:ND2	2.34	0.41
1:A:506:VAL:O	1:A:535:TRP:HA	2.21	0.41
2:B:438:TYR:CE1	2:B:440:ASP:HA	2.56	0.41
1:A:204:ASP:O	1:A:205:ARG:C	2.64	0.41
2:B:345:PRO:HB3	2:B:429:LEU:HD13	2.03	0.41
2:B:430:LYS:HA	2:B:431:PRO:HD3	1.93	0.41
2:B:470:SER:CB	2:B:473:GLU:HG3	2.37	0.41
1:A:215:LEU:O	1:A:218:TYR:HB3	2.21	0.41
1:A:447:ASP:HB2	1:A:490:PHE:HB2	2.02	0.41
1:A:602:PRO:HA	1:A:656:LEU:HD23	2.03	0.41
2:B:468:TYR:CD2	2:B:468:TYR:N	2.87	0.41
2:B:672:PHE:CD1	2:B:672:PHE:N	2.89	0.41
1:A:147:TYR:O	1:A:148:PRO:C	2.64	0.41
1:A:181:ILE:HD13	1:A:181:ILE:HA	1.72	0.41
2:B:19:VAL:HG13	2:B:575:LEU:HB3	2.02	0.41
1:A:164:LYS:HG3	1:A:464:VAL:HG13	2.03	0.40
1:A:212:ASP:OD2	1:A:484:ARG:NH1	2.54	0.40
1:A:501:ALA:HB2	1:A:542:PRO:HD3	2.02	0.40
1:A:512:PRO:HG2	1:A:526:ASN:OD1	2.21	0.40
2:B:75:MET:HA	2:B:76:PRO:HD3	1.84	0.40
2:B:613:VAL:O	2:B:653:ASN:HB2	2.21	0.40
2:B:307:THR:O	2:B:308:GLU:C	2.65	0.40
2:B:439:PHE:HB3	2:B:442:VAL:HG22	2.02	0.40
1:A:587:MET:HE2	1:A:587:MET:HB2	1.84	0.40
2:B:134:GLN:NE2	2:B:228:HIS:O	2.52	0.40
1:A:28:ASN:OD1	1:A:475:PRO:HD2	2.22	0.40
2:B:265:LEU:HD23	2:B:265:LEU:HA	1.64	0.40

There are no symmetry-related clashes.

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	673/680 (99%)	644 (96%)	25 (4%)	4 (1%)	21	51
2	B	666/687 (97%)	635 (95%)	27 (4%)	4 (1%)	21	51
All	All	1339/1367 (98%)	1279 (96%)	52 (4%)	8 (1%)	21	51

All (8) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	515	ASP
2	B	292	LYS
2	B	477	ASN
2	B	450	ASP
2	B	619	LYS
1	A	623	LYS
1	A	343	LYS
1	A	236	GLY

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	612/617 (99%)	546 (89%)	66 (11%)	6	21
2	B	608/626 (97%)	540 (89%)	68 (11%)	6	19
All	All	1220/1243 (98%)	1086 (89%)	134 (11%)	6	20

All (134) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	9	THR
1	A	11	VAL
1	A	29	VAL
1	A	35	GLU
1	A	53	CYS

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Mol	Chain	Res	Type
1	A	57	MET
1	A	67	TYR
1	A	84	LYS
1	A	95	LEU
1	A	126	TYR
1	A	131	GLN
1	A	135	THR
1	A	139	VAL
1	A	157	LYS
1	A	164	LYS
1	A	169	CYS
1	A	170	LEU
1	A	172	GLU
1	A	181	ILE
1	A	189	MET
1	A	198	THR
1	A	209	LEU
1	A	231	ASN
1	A	232	SER
1	A	245	ILE
1	A	259	MET
1	A	273	SER
1	A	280	THR
1	A	304	THR
1	A	320	THR
1	A	329	HIS
1	A	354	THR
1	A	364	LEU
1	A	369	ARG
1	A	370	SER
1	A	390	THR
1	A	410	GLN
1	A	423	LYS
1	A	431	GLN
1	A	439	LEU
1	A	442	SER
1	A	446	VAL
1	A	454	ASP
1	A	464	VAL
1	A	485	LEU
1	A	491	THR
1	A	493	THR

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Mol	Chain	Res	Type
1	A	500	VAL
1	A	502	THR
1	A	513	LYS
1	A	523	LEU
1	A	524	GLU
1	A	528	MET
1	A	545	SER
1	A	549	ARG
1	A	551	SER
1	A	599	ASP
1	A	617	LYS
1	A	618	GLU
1	A	620	GLU
1	A	623	LYS
1	A	625	VAL
1	A	643	GLN
1	A	655	VAL
1	A	663	LEU
1	A	674	THR
2	B	9	ILE
2	B	10	LYS
2	B	15	ASP
2	B	17	VAL
2	B	24	LYS
2	B	30	GLN
2	B	33	SER
2	B	55	ASP
2	B	69	MET
2	B	72	THR
2	B	75	MET
2	B	79	LEU
2	B	103	LYS
2	B	107	THR
2	B	136	SER
2	B	143	VAL
2	B	157	MET
2	B	161	GLN
2	B	201	LEU
2	B	208	ARG
2	B	234	THR
2	B	244	ARG
2	B	254	GLN

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Mol	Chain	Res	Type
2	B	269	LEU
2	B	282	LYS
2	B	289	MET
2	B	290	LEU
2	B	294	THR
2	B	307	THR
2	B	322	LYS
2	B	376	VAL
2	B	381	VAL
2	B	406	LEU
2	B	423	VAL
2	B	425	PHE
2	B	435	ASP
2	B	442	VAL
2	B	452	LEU
2	B	472	GLU
2	B	474	ILE
2	B	479	VAL
2	B	500	VAL
2	B	520	ASP
2	B	521	ASN
2	B	523	ILE
2	B	525	LEU
2	B	526	THR
2	B	532	MET
2	B	533	LYS
2	B	541	THR
2	B	542	THR
2	B	545	THR
2	B	560	ILE
2	B	566	VAL
2	B	579	LYS
2	B	580	VAL
2	B	586	GLU
2	B	593	LYS
2	B	602	GLU
2	B	617	ASP
2	B	623	LEU
2	B	627	GLU
2	B	632	ASP
2	B	644	VAL
2	B	645	VAL

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Mol	Chain	Res	Type
2	B	651	VAL
2	B	661	ILE
2	B	674	ILE

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (21) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	46	ASN
1	A	184	ASN
1	A	353	GLN
1	A	355	ASN
1	A	410	GLN
1	A	417	GLN
1	A	426	GLN
1	A	435	HIS
1	A	529	ASN
2	B	97	HIS
2	B	118	HIS
2	B	123	GLN
2	B	156	ASN
2	B	343	HIS
2	B	427	GLN
2	B	477	ASN
2	B	495	ASN
2	B	497	ASN
2	B	530	ASN
2	B	548	GLN
2	B	554	ASN

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 ⓘ

10 monosaccharides 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	C	1	3,1	14,14,15	0.75	0	17,19,21	1.44	3 (17%)
3	NAG	C	2	3	14,14,15	0.91	1 (7%)	17,19,21	2.20	6 (35%)
3	BMA	C	3	3	11,11,12	0.95	0	15,15,17	1.56	4 (26%)
3	MAN	C	4	3	11,11,12	0.90	0	15,15,17	1.95	3 (20%)
3	MAN	C	5	3	11,11,12	0.77	0	15,15,17	1.78	3 (20%)
3	NAG	D	1	3,2	14,14,15	0.72	0	17,19,21	1.19	1 (5%)
3	NAG	D	2	3	14,14,15	0.83	0	17,19,21	1.44	5 (29%)
3	BMA	D	3	3	11,11,12	0.79	0	15,15,17	2.43	4 (26%)
3	MAN	D	4	3	11,11,12	0.66	0	15,15,17	1.07	1 (6%)
3	MAN	D	5	3	11,11,12	0.83	0	15,15,17	1.33	2 (13%)

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	C	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	C	2	3	-	0/6/23/26	0/1/1/1
3	BMA	C	3	3	-	2/2/19/22	0/1/1/1
3	MAN	C	4	3	-	1/2/19/22	0/1/1/1
3	MAN	C	5	3	-	0/2/19/22	0/1/1/1
3	NAG	D	1	3,2	-	0/6/23/26	0/1/1/1
3	NAG	D	2	3	-	0/6/23/26	0/1/1/1
3	BMA	D	3	3	-	2/2/19/22	0/1/1/1
3	MAN	D	4	3	-	0/2/19/22	0/1/1/1
3	MAN	D	5	3	-	1/2/19/22	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	C	2	NAG	O5-C1	-2.30	1.39	1.43

All (32) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	3	BMA	C1-O5-C5	6.19	120.48	112.19
3	C	4	MAN	C1-O5-C5	5.74	119.88	112.19
3	C	2	NAG	C1-O5-C5	4.67	118.44	112.19
3	D	3	BMA	C1-C2-C3	-4.23	103.49	109.64
3	C	5	MAN	O2-C2-C3	-4.18	101.50	110.15
3	C	1	NAG	O5-C1-C2	-3.95	105.18	111.29
3	C	5	MAN	C1-C2-C3	3.75	115.11	109.64
3	C	3	BMA	O3-C3-C2	3.67	117.54	110.05
3	D	3	BMA	O5-C1-C2	3.58	119.32	110.79
3	C	2	NAG	C1-C2-N2	-3.31	105.22	110.43
3	C	2	NAG	O7-C7-C8	-3.15	116.45	122.05
3	D	5	MAN	C1-C2-C3	3.13	114.20	109.64
3	C	2	NAG	O5-C5-C6	-2.97	101.88	107.66
3	D	2	NAG	O4-C4-C3	-2.78	103.83	110.38
3	D	5	MAN	C2-C3-C4	2.71	115.62	110.86
3	D	1	NAG	C2-N2-C7	-2.70	119.28	122.90
3	D	2	NAG	O7-C7-C8	-2.68	117.29	122.05
3	C	2	NAG	O7-C7-N2	2.64	126.64	121.98
3	D	3	BMA	C3-C4-C5	2.63	115.00	110.23
3	D	2	NAG	O3-C3-C4	-2.46	104.58	110.38
3	C	1	NAG	C2-N2-C7	-2.41	119.67	122.90
3	C	5	MAN	O5-C1-C2	-2.39	105.10	110.79
3	C	2	NAG	O4-C4-C3	2.35	115.91	110.38
3	C	1	NAG	O5-C5-C4	-2.23	105.40	110.83
3	C	3	BMA	O5-C5-C6	2.15	111.85	107.66
3	C	4	MAN	O5-C1-C2	2.15	115.91	110.79
3	D	2	NAG	C2-N2-C7	-2.15	120.02	122.90
3	D	4	MAN	C1-C2-C3	2.12	112.72	109.64
3	D	2	NAG	O7-C7-N2	2.11	125.70	121.98
3	C	3	BMA	O5-C5-C4	-2.05	105.85	110.83
3	C	4	MAN	C1-C2-C3	2.01	112.57	109.64
3	C	3	BMA	C3-C4-C5	2.01	113.87	110.23

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	3	BMA	O5-C5-C6-O6
3	D	3	BMA	C4-C5-C6-O6
3	C	4	MAN	C4-C5-C6-O6
3	D	5	MAN	C4-C5-C6-O6

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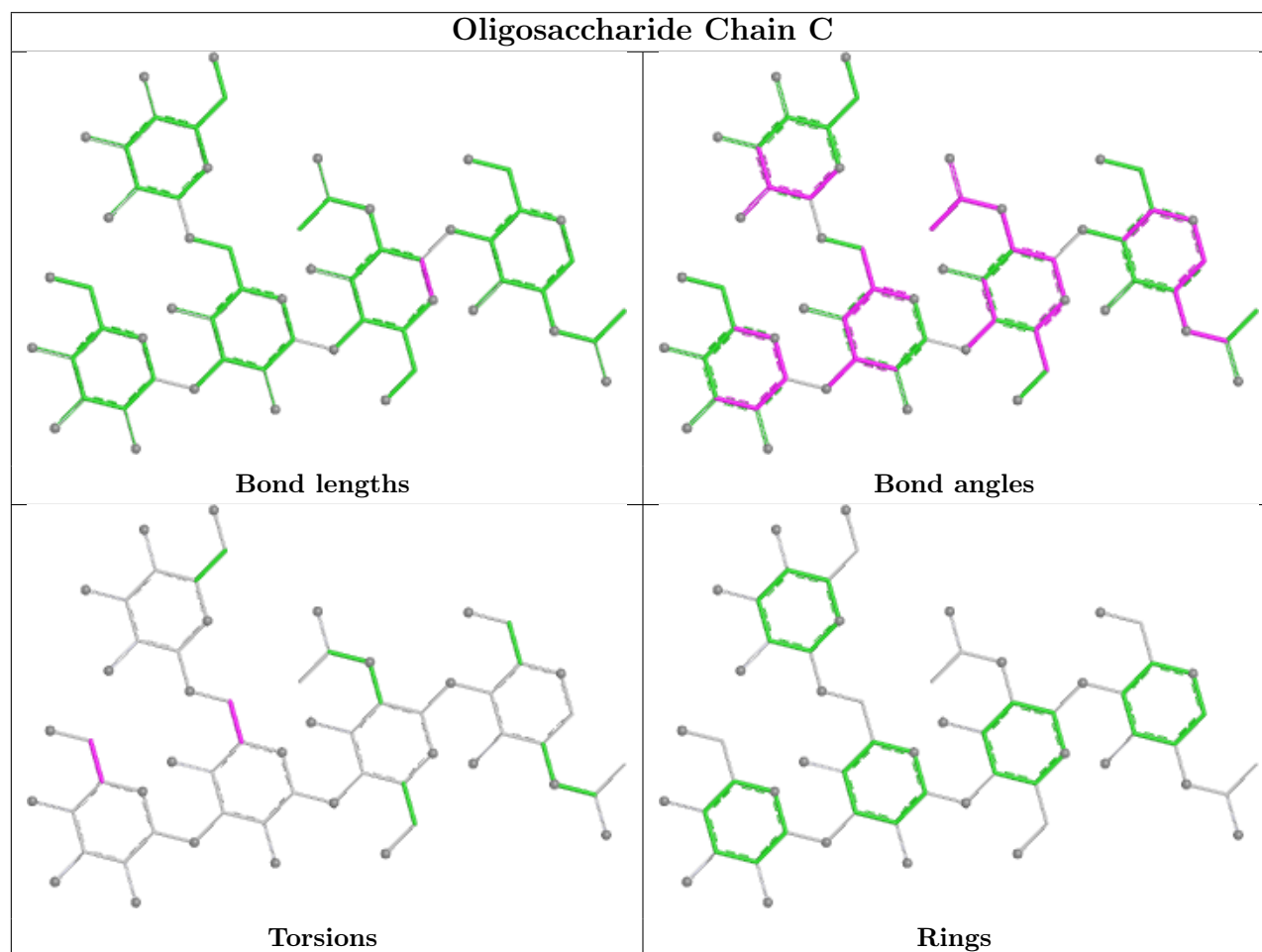
Mol	Chain	Res	Type	Atoms
3	C	3	BMA	C4-C5-C6-O6
3	C	3	BMA	O5-C5-C6-O6

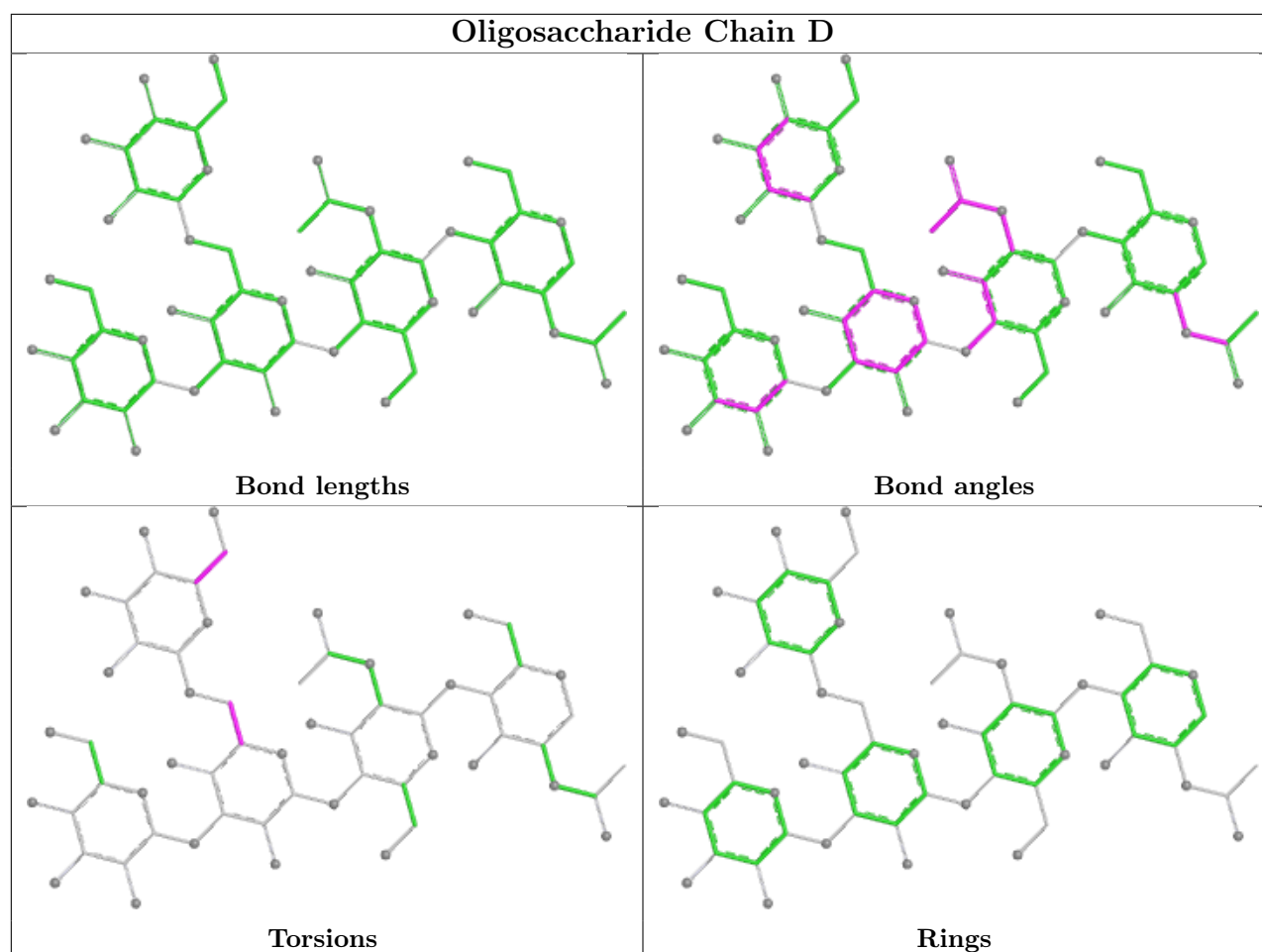
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	D	2	NAG	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for oligosaccharide.





5.6 Ligand geometry [i](#)

Of 10 ligands modelled in this entry, 3 are monoatomic - leaving 7 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	$\# Z > 2$
4	SO4	B	706	-	4,4,4	0.53	0	6,6,6	0.31	0
6	SCN	B	708	-	1,2,2	0.30	0	0,1,1	-	-
6	SCN	A	709	-	1,2,2	1.07	0	0,1,1	-	-
6	SCN	B	709	-	1,2,2	0.99	0	0,1,1	-	-
4	SO4	A	706	-	4,4,4	0.52	0	6,6,6	0.60	0
6	SCN	A	710	-	1,2,2	0.10	0	0,1,1	-	-
6	SCN	A	711	-	1,2,2	0.14	0	0,1,1	-	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	B	709	SCN	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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	674/680 (99%)	-0.51	5 (0%) 84 79	22, 43, 78, 141	1 (0%)
2	B	667/687 (97%)	-0.45	5 (0%) 84 79	15, 49, 94, 170	1 (0%)
All	All	1341/1367 (98%)	-0.48	10 (0%) 84 79	15, 46, 88, 170	2 (0%)

All (10) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	623	LYS	4.6
2	B	626	PHE	3.2
2	B	9	ILE	3.1
2	B	623	LEU	3.0
2	B	648	LEU	2.9
1	A	6	PHE	2.8
1	A	366	PHE	2.5
1	A	170	LEU	2.4
1	A	625	VAL	2.3
2	B	469	PHE	2.0

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

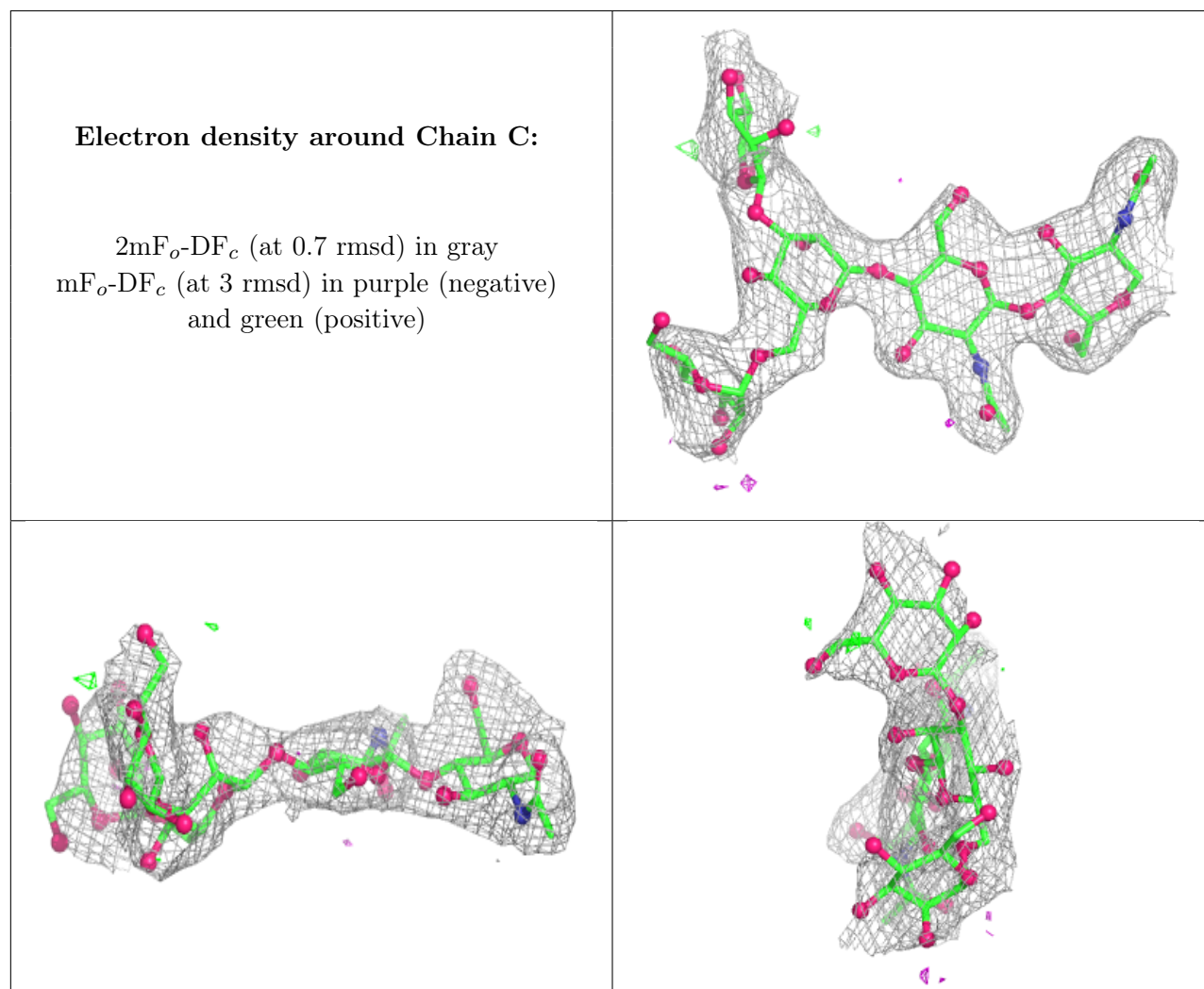
There are no non-standard protein/DNA/RNA residues in this entry.

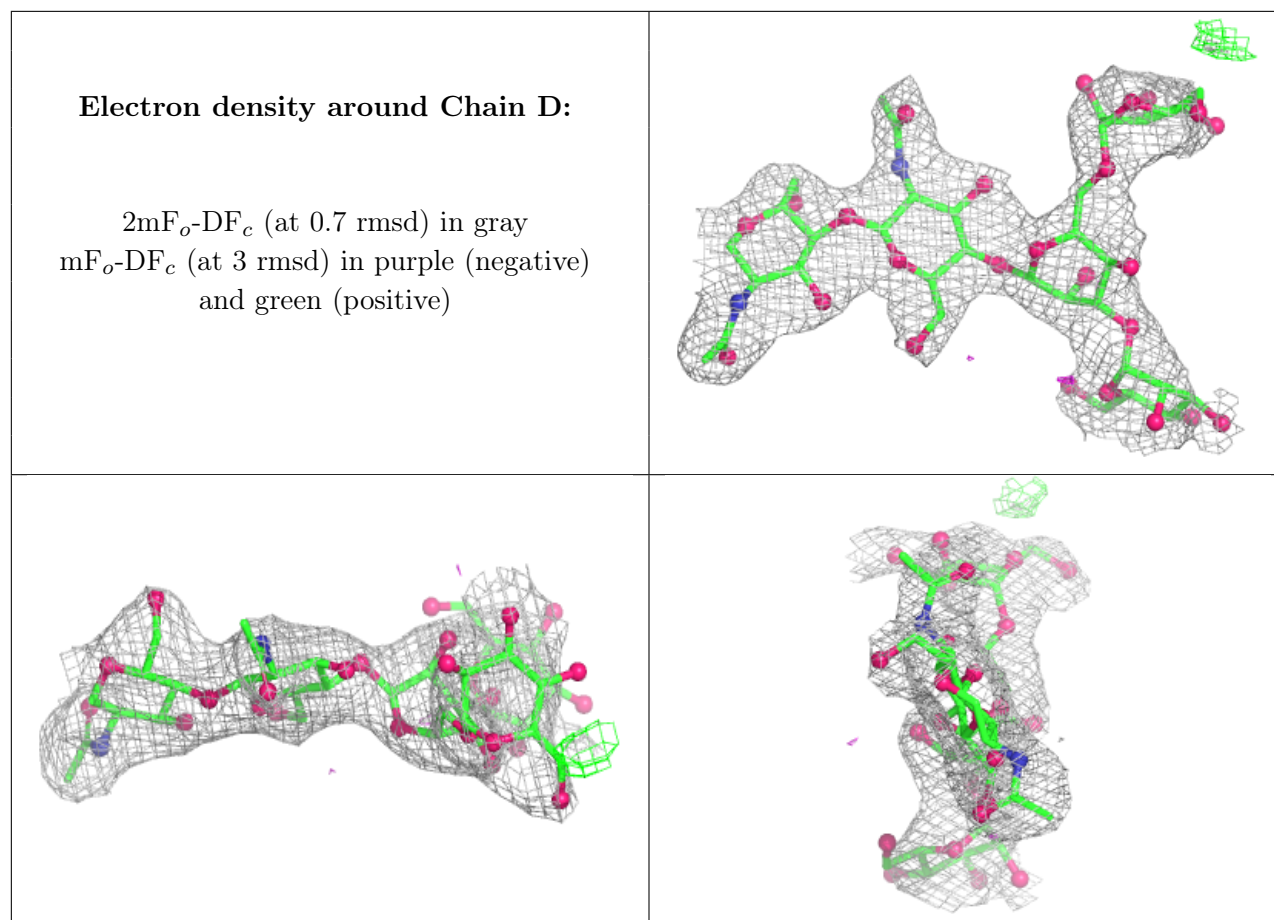
6.3 Carbohydrates [i](#)

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($\text{\AA}^2$)	Q<0.9
3	MAN	C	4	11/12	0.52	0.13	91,114,121,122	0
3	MAN	D	5	11/12	0.55	0.11	97,121,129,132	0
3	MAN	C	5	11/12	0.57	0.12	91,106,111,112	0
3	BMA	C	3	11/12	0.77	0.10	79,83,98,106	0
3	MAN	D	4	11/12	0.79	0.12	113,119,128,138	0
3	BMA	D	3	11/12	0.85	0.09	71,86,103,110	0
3	NAG	C	2	14/15	0.93	0.08	46,59,65,70	0
3	NAG	D	2	14/15	0.96	0.07	51,53,59,76	0
3	NAG	C	1	14/15	0.97	0.05	32,45,56,58	0
3	NAG	D	1	14/15	0.97	0.06	35,40,49,52	0

The following is a graphical depiction of the model fit to experimental electron density for oligosaccharide. Each fit is shown from different orientation to approximate a three-dimensional view.





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($\text{\AA}^2$)	Q<0.9
6	SCN	A	710	3/3	0.81	0.11	72,72,72,77	0
6	SCN	A	711	3/3	0.82	0.27	61,61,73,76	0
6	SCN	B	708	3/3	0.90	0.14	64,64,71,75	0
6	SCN	B	709	3/3	0.90	0.15	68,68,75,80	0
6	SCN	A	709	3/3	0.92	0.10	59,59,74,75	0
4	SO4	B	706	5/5	0.93	0.14	69,78,81,81	5
5	NA	B	707	1/1	0.94	0.07	38,38,38,38	0
4	SO4	A	706	5/5	0.94	0.14	37,45,47,50	5
5	NA	A	707	1/1	0.96	0.07	46,46,46,46	0
5	NA	A	708	1/1	0.99	0.06	36,36,36,36	0

6.5 Other polymers [i](#)

There are no such residues in this entry.