



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 5, 2026 – 12:45 AM UTC

PDB ID : 3EJJ / pdb_00003ejj
Title : Structure of M-CSF bound to the first three domains of FMS
Authors : Chen, X.; Liu, H.; Focia, P.J.; Shim, A.; He, X.
Deposited on : 2008-09-18
Resolution : 2.40 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

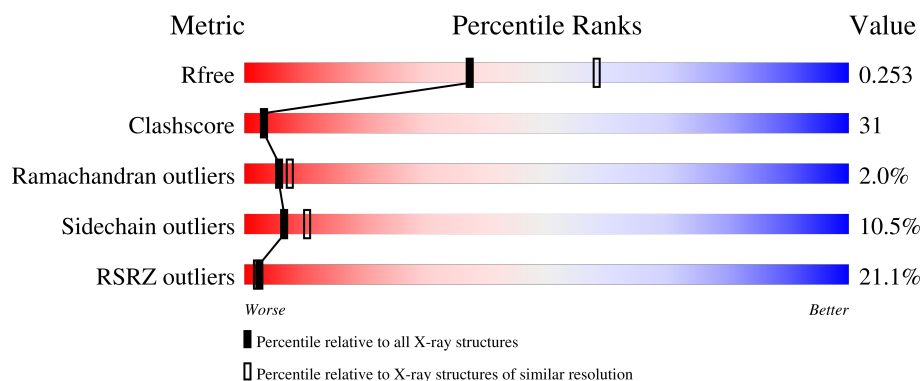
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	4912 (2.40-2.40)
Clashscore	190562	5391 (2.40-2.40)
Ramachandran outliers	187476	5320 (2.40-2.40)
Sidechain outliers	187428	5321 (2.40-2.40)
RSRZ outliers	180081	4916 (2.40-2.40)

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	155	
1	B	155	
2	X	289	
3	C	2	
3	D	2	

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	C	2	X	-	-	-
3	NAG	D	1	X	-	-	-
3	NAG	D	2	X	-	-	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5213 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 Colony stimulating factor-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	148	Total	C	N	O	S	0	0	0
			1204	752	203	239	10			
1	B	145	Total	C	N	O	S	0	0	0
			1184	740	200	234	10			

There are 20 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	1	ALA	-	expression tag	UNP Q3U395
A	2	ASP	-	expression tag	UNP Q3U395
A	3	PRO	-	expression tag	UNP Q3U395
A	149	HIS	-	expression tag	UNP Q3U395
A	150	HIS	-	expression tag	UNP Q3U395
A	151	HIS	-	expression tag	UNP Q3U395
A	152	HIS	-	expression tag	UNP Q3U395
A	153	HIS	-	expression tag	UNP Q3U395
A	154	HIS	-	expression tag	UNP Q3U395
A	155	HIS	-	expression tag	UNP Q3U395
B	1	ALA	-	expression tag	UNP Q3U395
B	2	ASP	-	expression tag	UNP Q3U395
B	3	PRO	-	expression tag	UNP Q3U395
B	149	HIS	-	expression tag	UNP Q3U395
B	150	HIS	-	expression tag	UNP Q3U395
B	151	HIS	-	expression tag	UNP Q3U395
B	152	HIS	-	expression tag	UNP Q3U395
B	153	HIS	-	expression tag	UNP Q3U395
B	154	HIS	-	expression tag	UNP Q3U395
B	155	HIS	-	expression tag	UNP Q3U395

- Molecule 2 is a protein called Macrophage colony-stimulating factor 1 receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	X	272	Total	C	N	O	S	0	0	0
			2115	1336	364	406	9			

There are 12 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
X	17	ALA	-	expression tag	UNP P09581
X	18	ASP	-	expression tag	UNP P09581
X	19	PRO	-	expression tag	UNP P09581
X	297	GLU	-	expression tag	UNP P09581
X	298	SER	-	expression tag	UNP P09581
X	299	HIS	-	expression tag	UNP P09581
X	300	HIS	-	expression tag	UNP P09581
X	301	HIS	-	expression tag	UNP P09581
X	302	HIS	-	expression tag	UNP P09581
X	303	HIS	-	expression tag	UNP P09581
X	304	HIS	-	expression tag	UNP P09581
X	305	HIS	-	expression tag	UNP P09581

- Molecule 3 is an oligosaccharide called 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	2	Total	C	N	O		0	0	0
			28	16	2	10				
3	D	2	Total	C	N	O		0	0	0
			28	16	2	10				

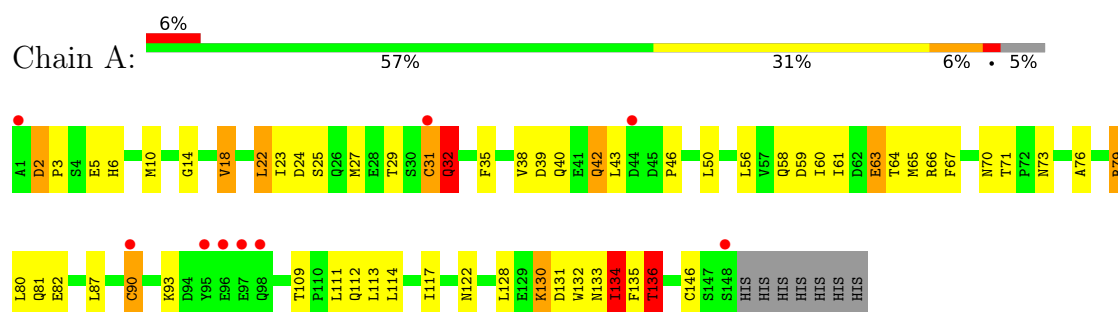
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	187	Total	O	0	0
			187	187		
4	B	114	Total	O	0	0
			114	114		
4	X	353	Total	O	0	0
			353	353		

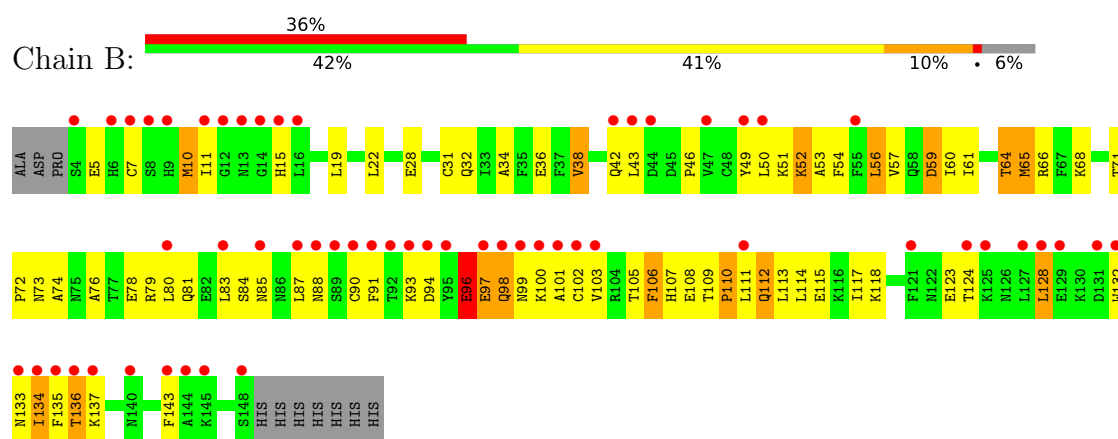
3 Residue-property plots [i](#)

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.

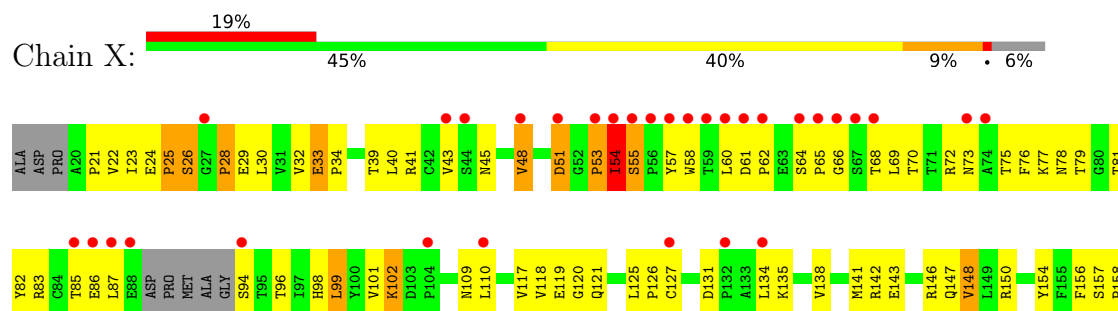
• Molecule 1: Colony stimulating factor-1

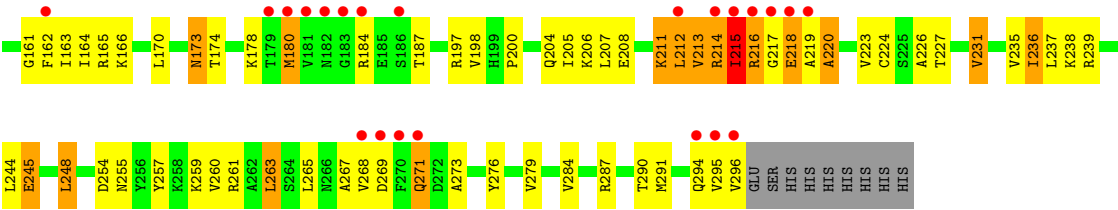


• Molecule 1: Colony stimulating factor-1

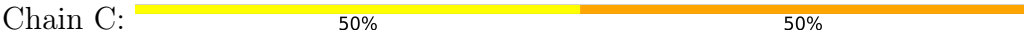


• Molecule 2: Macrophage colony-stimulating factor 1 receptor





● Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



● Molecule 3: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose



4 Data and refinement statistics

Property	Value	Source
Space group	H 3 2	Depositor
Cell constants a, b, c, α , β , γ	158.85Å 158.85Å 237.95Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	20.00 – 2.40 20.00 – 2.40	Depositor EDS
% Data completeness (in resolution range)	5.0 (20.00-2.40) 98.9 (20.00-2.40)	Depositor EDS
R_{merge}	0.04	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.53 (at 2.41Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.238 , 0.265 0.250 , 0.253	Depositor DCC
R_{free} test set	2249 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	55.9	Xtriage
Anisotropy	0.228	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.32 , 67.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5213	wwPDB-VP
Average B, all atoms (Å ²)	68.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.33% 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: 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	0.88	0/1226	1.06	6/1653 (0.4%)
1	B	0.50	0/1205	1.03	7/1623 (0.4%)
2	X	0.72	0/2159	1.28	26/2942 (0.9%)
All	All	0.72	0/4590	1.16	39/6218 (0.6%)

There are no bond length outliers.

All (39) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	X	218	GLU	N-CA-C	16.54	132.66	108.34
2	X	54	ILE	N-CA-C	11.80	123.16	108.06
2	X	213	VAL	N-CA-C	-11.36	91.77	108.12
2	X	219	ALA	N-CA-C	10.49	126.03	110.30
2	X	214	ARG	N-CA-C	-10.12	89.23	110.80
2	X	217	GLY	N-CA-C	-10.06	102.83	115.31
2	X	216	ARG	N-CA-C	-8.74	94.95	108.42
2	X	268	VAL	N-CA-C	7.88	119.29	108.89
1	B	97	GLU	N-CA-C	-7.86	99.94	110.55
1	A	136	THR	N-CA-C	-7.82	103.30	112.92
1	B	96	GLU	N-CA-C	7.81	123.34	112.72
2	X	26	SER	N-CA-C	7.79	120.57	108.96
1	B	49	TYR	N-CA-C	-7.36	102.86	111.03
2	X	25	PRO	CA-C-N	-6.92	110.52	121.87
2	X	25	PRO	C-N-CA	-6.92	110.52	121.87
1	A	90	CYS	CA-CB-SG	-6.89	98.55	114.40
1	A	31	CYS	CB-CA-C	-6.74	102.52	113.37
2	X	125	LEU	CA-C-N	6.74	128.26	119.84
2	X	125	LEU	C-N-CA	6.74	128.26	119.84
2	X	239	ARG	N-CA-C	-6.65	97.56	108.41
1	B	64	THR	N-CA-C	6.57	118.24	111.14

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	88	ASN	N-CA-C	-6.56	104.54	112.54
2	X	142	ARG	N-CA-C	-6.17	101.06	109.95
2	X	25	PRO	N-CA-C	-6.12	96.19	112.10
2	X	157	SER	CA-C-N	6.11	126.29	119.32
2	X	157	SER	C-N-CA	6.11	126.29	119.32
2	X	220	ALA	N-CA-C	6.01	118.29	108.55
1	A	134	ILE	N-CA-C	-5.96	100.36	109.78
2	X	215	ILE	N-CA-C	-5.94	101.05	108.89
2	X	218	GLU	CB-CA-C	-5.93	107.88	116.54
1	A	81	GLN	N-CA-C	-5.89	104.86	111.28
2	X	96	THR	N-CA-C	5.58	118.50	109.40
1	B	59	ASP	N-CA-C	-5.48	104.95	111.03
2	X	223	VAL	N-CA-C	5.48	115.99	107.99
2	X	51	ASP	N-CA-C	-5.46	99.62	108.41
1	B	110	PRO	N-CA-C	-5.28	106.52	113.65
1	A	130	LYS	N-CA-C	-5.22	105.50	111.14
2	X	33	GLU	N-CA-C	-5.16	103.17	110.29
2	X	55	SER	N-CA-C	-5.05	98.64	109.81

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	1204	0	1148	56	0
1	B	1184	0	1129	80	0
2	X	2115	0	2105	145	0
3	C	28	0	25	3	0
3	D	28	0	25	2	0
4	A	187	0	0	6	0
4	B	114	0	0	9	0
4	X	353	0	0	27	0
All	All	5213	0	4432	278	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 31.

All (278) 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:X:138:VAL:HG12	2:X:162:PHE:CZ	1.63	1.32
2:X:138:VAL:CG1	2:X:162:PHE:CZ	2.32	1.13
2:X:54:ILE:HG12	2:X:58:TRP:HD1	1.11	1.09
2:X:138:VAL:HG12	2:X:162:PHE:HZ	0.90	1.06
2:X:138:VAL:CG1	2:X:162:PHE:CE1	2.46	0.99
2:X:54:ILE:HG12	2:X:58:TRP:CD1	2.02	0.95
2:X:110:LEU:HD23	2:X:110:LEU:H	1.33	0.94
1:B:19:LEU:HD13	1:B:80:LEU:HD21	1.55	0.89
2:X:23:ILE:O	2:X:26:SER:HB2	1.77	0.85
1:B:124:THR:HG23	1:B:135:PHE:HE1	1.40	0.84
1:B:124:THR:HG23	1:B:135:PHE:CE1	2.16	0.81
2:X:215:ILE:HB	2:X:295:VAL:HA	1.62	0.81
2:X:138:VAL:CG1	2:X:162:PHE:HZ	1.77	0.79
1:A:71:THR:HG22	1:A:73:ASN:H	1.48	0.78
1:B:51:LYS:HD2	1:B:143:PHE:HZ	1.48	0.78
2:X:173:ASN:HD22	2:X:174:THR:H	1.32	0.77
1:A:109:THR:HG21	4:A:190:HOH:O	1.83	0.77
2:X:60:LEU:HG	2:X:62:PRO:HD3	1.66	0.76
2:X:204:GLN:HG3	4:X:390:HOH:O	1.87	0.75
2:X:150:ARG:HD3	4:X:513:HOH:O	1.86	0.74
2:X:58:TRP:NE1	2:X:78:ASN:HD22	1.87	0.73
1:A:5:GLU:CD	1:A:5:GLU:H	1.97	0.73
2:X:141:MET:HG3	2:X:178:LYS:HD2	1.69	0.73
1:B:134:ILE:O	1:B:135:PHE:HB2	1.90	0.72
2:X:138:VAL:HG11	2:X:162:PHE:CE1	2.23	0.71
2:X:218:GLU:HA	2:X:267:ALA:HA	1.70	0.71
2:X:57:TYR:CE2	2:X:77:LYS:HD2	2.26	0.70
2:X:81:THR:OG1	2:X:98:HIS:HD2	1.74	0.70
2:X:57:TYR:CZ	2:X:77:LYS:HD2	2.26	0.70
2:X:28:PRO:HG2	2:X:29:GLU:H	1.56	0.70
1:B:65:MET:HE1	1:B:117:ILE:HG21	1.74	0.70
1:B:112:GLN:O	1:B:115:GLU:N	2.25	0.69
2:X:118:VAL:O	2:X:121:GLN:HB2	1.93	0.69
1:A:79:ARG:HD2	2:X:255:ASN:ND2	2.08	0.68
4:X:559:HOH:O	3:C:2:NAG:H3	1.92	0.68
2:X:215:ILE:HG12	2:X:295:VAL:HG13	1.74	0.68
1:A:59:ASP:O	1:A:63:GLU:HG2	1.93	0.67
2:X:138:VAL:HG11	2:X:162:PHE:CZ	2.29	0.67

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:109:THR:HG22	1:A:112:GLN:OE1	1.95	0.67
2:X:131:ASP:HB3	2:X:134:LEU:HD13	1.75	0.67
1:A:22:LEU:HD11	1:A:67:PHE:HZ	1.61	0.66
2:X:197:ARG:NH1	2:X:197:ARG:HB2	2.11	0.65
2:X:53:PRO:HD3	2:X:81:THR:O	1.97	0.65
1:B:96:GLU:H	1:B:96:GLU:CD	2.05	0.65
2:X:54:ILE:HG21	2:X:58:TRP:CD1	2.32	0.65
2:X:165:ARG:HB3	4:X:530:HOH:O	1.97	0.65
2:X:138:VAL:HG12	2:X:162:PHE:CE1	2.20	0.64
1:B:110:PRO:O	1:B:114:LEU:HD23	1.97	0.64
2:X:215:ILE:HG13	2:X:296:VAL:N	2.11	0.64
1:A:134:ILE:O	1:A:135:PHE:HB2	1.98	0.64
2:X:206:LYS:HD2	4:X:554:HOH:O	1.96	0.64
1:B:84:SER:HB2	4:B:253:HOH:O	1.96	0.63
1:A:2:ASP:H	1:A:3:PRO:HD2	1.62	0.63
2:X:138:VAL:CG1	2:X:162:PHE:HE1	2.07	0.63
1:A:22:LEU:HD11	1:A:67:PHE:CZ	2.33	0.63
1:B:100:LYS:O	1:B:103:VAL:HG22	1.99	0.62
2:X:215:ILE:HG13	2:X:296:VAL:H	1.64	0.62
2:X:110:LEU:HB2	4:X:389:HOH:O	1.98	0.62
2:X:269:ASP:HB3	4:X:605:HOH:O	1.98	0.62
2:X:119:GLU:HB2	2:X:197:ARG:HA	1.82	0.62
2:X:48:VAL:HG23	2:X:66:GLY:HA2	1.82	0.62
2:X:236:ILE:HD11	2:X:279:VAL:HB	1.82	0.62
1:A:2:ASP:N	1:A:3:PRO:HD2	2.16	0.61
2:X:148:VAL:HG12	4:X:357:HOH:O	2.00	0.61
1:B:109:THR:HB	1:B:111:LEU:HD13	1.83	0.61
2:X:215:ILE:HA	2:X:295:VAL:HG22	1.82	0.61
1:B:11:ILE:HG12	1:B:83:LEU:HD11	1.81	0.60
1:A:109:THR:HG22	1:A:112:GLN:CD	2.28	0.59
2:X:53:PRO:HD2	2:X:82:TYR:CD2	2.37	0.59
1:A:29:THR:CG2	1:A:31:CYS:SG	2.90	0.59
2:X:197:ARG:HD3	4:X:324:HOH:O	2.03	0.59
2:X:75:THR:HG23	2:X:77:LYS:H	1.68	0.59
1:B:112:GLN:O	1:B:113:LEU:C	2.44	0.58
1:B:68:LYS:O	1:B:74:ALA:HB2	2.03	0.58
1:B:132:TRP:CD1	1:B:132:TRP:H	2.20	0.58
2:X:271:GLN:HB2	4:X:497:HOH:O	2.04	0.58
1:A:56:LEU:O	1:A:60:ILE:HG12	2.03	0.57
1:A:5:GLU:HG3	1:A:132:TRP:CZ2	2.39	0.57
1:B:111:LEU:HG	4:B:166:HOH:O	2.05	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:178:LYS:HB3	4:X:387:HOH:O	2.04	0.57
2:X:60:LEU:HD11	4:X:356:HOH:O	2.05	0.57
1:A:109:THR:HG23	1:A:112:GLN:H	1.69	0.56
1:B:115:GLU:HG2	4:B:182:HOH:O	2.03	0.56
2:X:216:ARG:C	2:X:218:GLU:N	2.59	0.56
1:A:5:GLU:HB3	4:A:215:HOH:O	2.05	0.56
1:A:42:GLN:HG3	1:A:146:CYS:HA	1.87	0.56
1:A:133:ASN:O	1:A:136:THR:HB	2.05	0.56
2:X:211:LYS:HG2	4:X:617:HOH:O	2.05	0.56
1:A:79:ARG:HD3	1:A:82:GLU:OE2	2.06	0.56
1:A:130:LYS:HD3	4:A:254:HOH:O	2.05	0.56
2:X:117:VAL:HG22	2:X:118:VAL:H	1.71	0.56
2:X:216:ARG:C	2:X:218:GLU:H	2.13	0.56
1:B:111:LEU:H	1:B:111:LEU:CD1	2.18	0.55
2:X:110:LEU:H	2:X:110:LEU:CD2	2.10	0.55
2:X:215:ILE:HD13	2:X:215:ILE:C	2.31	0.55
2:X:178:LYS:HD3	4:X:387:HOH:O	2.07	0.55
2:X:212:LEU:CD1	2:X:214:ARG:HB2	2.36	0.55
1:B:133:ASN:O	1:B:136:THR:HB	2.06	0.55
1:A:113:LEU:HD23	1:A:113:LEU:C	2.32	0.55
2:X:39:THR:HG23	2:X:68:THR:HG23	1.89	0.55
2:X:21:PRO:HD3	2:X:94:SER:HB2	1.88	0.55
1:A:111:LEU:HB3	4:A:231:HOH:O	2.06	0.54
1:B:51:LYS:HE3	1:B:94:ASP:OD1	2.08	0.54
2:X:220:ALA:HA	4:X:448:HOH:O	2.08	0.54
2:X:118:VAL:O	2:X:119:GLU:C	2.51	0.54
2:X:236:ILE:CD1	2:X:279:VAL:HB	2.37	0.54
1:A:18:VAL:HG13	1:A:76:ALA:HB1	1.89	0.54
1:A:6:HIS:HD2	4:X:336:HOH:O	1.91	0.53
1:B:109:THR:OG1	1:B:111:LEU:HB2	2.09	0.53
2:X:207:LEU:HD13	2:X:291:MET:HB3	1.90	0.53
1:B:68:LYS:HB3	1:B:71:THR:HG21	1.89	0.53
1:B:22:LEU:HD22	1:B:73:ASN:OD1	2.08	0.53
1:B:76:ALA:O	1:B:80:LEU:HB2	2.09	0.53
1:B:56:LEU:O	1:B:60:ILE:HG12	2.09	0.53
2:X:117:VAL:CG2	2:X:121:GLN:HB3	2.39	0.53
2:X:231:VAL:HG13	2:X:257:TYR:CE2	2.44	0.53
1:B:137:LYS:HG3	4:B:167:HOH:O	2.08	0.53
1:B:111:LEU:HD12	1:B:111:LEU:N	2.24	0.52
2:X:73:ASN:CG	3:D:1:NAG:HN2	2.16	0.52
2:X:276:TYR:HB2	2:X:291:MET:HG3	1.91	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:51:LYS:HD2	1:B:143:PHE:CZ	2.37	0.52
2:X:218:GLU:CA	2:X:267:ALA:HA	2.38	0.52
1:B:123:GLU:HG2	4:B:170:HOH:O	2.08	0.52
2:X:117:VAL:HG22	2:X:121:GLN:HB3	1.91	0.52
1:A:58:GLN:OE1	2:X:146:ARG:NH1	2.42	0.52
2:X:21:PRO:CD	2:X:94:SER:HB2	2.40	0.52
1:A:109:THR:HG22	1:A:112:GLN:CG	2.40	0.52
2:X:51:ASP:OD2	2:X:83:ARG:HD2	2.10	0.52
2:X:218:GLU:HG2	4:X:454:HOH:O	2.09	0.52
2:X:263:LEU:HD22	2:X:265:LEU:HG	1.92	0.52
1:A:23:ILE:C	1:A:25:SER:H	2.19	0.51
1:B:85:ASN:C	1:B:87:LEU:H	2.18	0.51
2:X:79:THR:HA	2:X:99:LEU:O	2.09	0.51
1:A:29:THR:HG23	1:A:31:CYS:SG	2.50	0.51
1:B:91:PHE:CZ	1:B:135:PHE:CE1	2.99	0.51
1:B:111:LEU:H	1:B:111:LEU:HD12	1.74	0.51
1:A:35:PHE:CD2	1:A:113:LEU:HD12	2.46	0.51
1:B:65:MET:HE3	1:B:117:ILE:HG12	1.93	0.51
2:X:200:PRO:HB2	2:X:284:VAL:HG21	1.91	0.51
1:B:50:LEU:HD11	1:B:123:GLU:HB2	1.92	0.51
1:A:66:ARG:HD3	4:A:264:HOH:O	2.10	0.51
1:B:34:ALA:HA	1:B:106:PHE:O	2.11	0.51
2:X:77:LYS:HA	2:X:109:ASN:OD1	2.11	0.50
1:B:81:GLN:HG3	4:B:214:HOH:O	2.11	0.50
2:X:75:THR:HG23	2:X:77:LYS:N	2.25	0.50
1:B:57:VAL:O	1:B:61:ILE:HG12	2.10	0.50
2:X:102:LYS:O	2:X:102:LYS:HG2	2.11	0.50
2:X:178:LYS:HG2	2:X:187:THR:OG1	2.12	0.50
2:X:197:ARG:HB2	2:X:197:ARG:HH11	1.77	0.50
1:B:60:ILE:HG21	1:B:117:ILE:HD11	1.92	0.50
2:X:148:VAL:HG23	4:X:430:HOH:O	2.11	0.50
1:A:5:GLU:CD	1:A:5:GLU:N	2.68	0.49
2:X:30:LEU:CD1	2:X:32:VAL:HG13	2.43	0.49
2:X:170:LEU:HD12	2:X:170:LEU:C	2.37	0.49
1:B:59:ASP:O	1:B:60:ILE:C	2.55	0.49
2:X:248:LEU:HD21	2:X:259:LYS:HB3	1.94	0.49
2:X:213:VAL:HG22	2:X:294:GLN:HB2	1.95	0.49
3:D:2:NAG:H3	3:D:2:NAG:H83	1.94	0.48
1:B:19:LEU:HD21	1:B:118:LYS:HA	1.95	0.48
1:A:27:MET:HE1	1:B:114:LEU:HD21	1.94	0.48
1:A:2:ASP:H	1:A:3:PRO:CD	2.27	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:39:THR:OG1	2:X:70:THR:HG23	2.12	0.48
1:B:51:LYS:HZ2	1:B:143:PHE:HE2	1.60	0.48
2:X:245:GLU:HA	4:X:509:HOH:O	2.12	0.48
2:X:296:VAL:HG22	4:X:487:HOH:O	2.13	0.48
2:X:127:CYS:O	2:X:161:GLY:HA2	2.14	0.48
1:B:38:VAL:HG21	1:B:43:LEU:HD13	1.96	0.47
2:X:110:LEU:O	2:X:110:LEU:HG	2.14	0.47
1:B:133:ASN:O	1:B:136:THR:HG22	2.14	0.47
2:X:48:VAL:HG12	2:X:85:THR:O	2.14	0.47
2:X:45:ASN:HB3	3:C:1:NAG:N2	2.29	0.47
1:B:133:ASN:O	1:B:136:THR:CG2	2.62	0.47
2:X:33:GLU:HG3	2:X:34:PRO:HD2	1.96	0.47
1:A:61:ILE:HA	1:A:65:MET:HE3	1.97	0.47
1:B:60:ILE:CG2	1:B:113:LEU:HD21	2.44	0.47
1:A:136:THR:HG23	1:A:136:THR:O	2.14	0.47
1:B:107:HIS:HD2	4:B:255:HOH:O	1.97	0.47
2:X:143:GLU:HG3	4:X:368:HOH:O	2.14	0.47
1:A:2:ASP:N	1:A:3:PRO:CD	2.78	0.47
2:X:244:LEU:N	2:X:244:LEU:HD12	2.30	0.47
1:B:100:LYS:HD2	1:B:100:LYS:N	2.29	0.46
2:X:154:TYR:HB2	2:X:163:ILE:O	2.15	0.46
2:X:53:PRO:HD2	2:X:82:TYR:CE2	2.51	0.46
2:X:213:VAL:HG13	2:X:294:GLN:O	2.16	0.46
2:X:53:PRO:O	2:X:54:ILE:HD12	2.16	0.46
2:X:226:ALA:HB3	2:X:235:VAL:HG21	1.98	0.46
1:B:128:LEU:HD12	1:B:128:LEU:HA	1.82	0.46
2:X:41:ARG:HH11	2:X:41:ARG:HG3	1.81	0.46
1:B:51:LYS:HD3	1:B:51:LYS:C	2.41	0.45
1:A:23:ILE:O	1:A:25:SER:N	2.49	0.45
2:X:273:ALA:HB1	4:X:311:HOH:O	2.16	0.45
1:B:94:ASP:O	1:B:96:GLU:HG3	2.17	0.45
2:X:206:LYS:HE2	2:X:208:GLU:CD	2.42	0.45
2:X:23:ILE:O	2:X:26:SER:CB	2.57	0.45
2:X:22:VAL:HB	2:X:43:VAL:HB	1.99	0.45
2:X:64:SER:N	2:X:65:PRO:HD2	2.31	0.45
1:B:99:ASN:HB3	1:B:100:LYS:HD2	1.98	0.45
2:X:204:GLN:O	2:X:226:ALA:HA	2.17	0.45
2:X:215:ILE:HG13	2:X:296:VAL:C	2.42	0.45
2:X:40:LEU:HB2	2:X:69:LEU:HB2	1.98	0.45
2:X:24:GLU:HB2	2:X:41:ARG:HB2	1.98	0.45
2:X:273:ALA:CB	4:X:311:HOH:O	2.65	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:X:76:PHE:HA	2:X:101:VAL:HB	1.99	0.44
2:X:180:MET:HA	2:X:184:ARG:O	2.16	0.44
1:A:23:ILE:C	1:A:25:SER:N	2.74	0.44
1:B:111:LEU:CD1	1:B:111:LEU:N	2.81	0.44
2:X:120:GLY:O	2:X:166:LYS:HA	2.18	0.44
1:A:32:GLN:HA	1:A:32:GLN:HE21	1.83	0.44
1:B:133:ASN:C	1:B:134:ILE:O	2.57	0.44
2:X:22:VAL:O	2:X:43:VAL:N	2.49	0.44
2:X:24:GLU:HA	2:X:25:PRO:C	2.43	0.44
1:A:65:MET:HE2	1:A:117:ILE:HG13	2.00	0.43
1:A:131:ASP:O	1:A:134:ILE:HB	2.17	0.43
2:X:75:THR:HG22	2:X:78:ASN:OD1	2.18	0.43
2:X:238:LYS:O	2:X:276:TYR:HA	2.17	0.43
1:B:46:PRO:O	1:B:50:LEU:HD23	2.18	0.43
2:X:216:ARG:HB2	2:X:218:GLU:H	1.83	0.43
1:B:5:GLU:C	1:B:7:CYS:N	2.75	0.43
1:B:133:ASN:O	1:B:136:THR:CB	2.66	0.43
1:A:134:ILE:O	1:A:135:PHE:CB	2.65	0.43
2:X:58:TRP:CD1	2:X:78:ASN:HD22	2.36	0.43
1:B:64:THR:O	1:B:66:ARG:N	2.50	0.43
1:B:78:GLU:O	1:B:81:GLN:HB3	2.19	0.43
1:A:22:LEU:C	1:A:22:LEU:HD12	2.43	0.43
2:X:236:ILE:HD13	2:X:236:ILE:H	1.83	0.43
1:A:10:MET:HG3	2:X:231:VAL:HG21	2.01	0.42
1:A:64:THR:O	1:A:64:THR:CG2	2.66	0.42
1:A:61:ILE:HG12	1:A:65:MET:CE	2.49	0.42
1:B:36:GLU:OE1	1:B:105:THR:HA	2.19	0.42
1:B:71:THR:O	1:B:72:PRO:C	2.63	0.42
1:B:111:LEU:HA	4:B:166:HOH:O	2.19	0.42
1:A:42:GLN:NE2	1:A:42:GLN:HA	2.34	0.42
2:X:215:ILE:O	2:X:216:ARG:CG	2.68	0.42
1:B:53:ALA:O	1:B:54:PHE:C	2.62	0.42
1:B:97:GLU:O	1:B:98:GLN:NE2	2.52	0.42
2:X:60:LEU:HG	2:X:61:ASP:N	2.33	0.42
2:X:51:ASP:HB2	2:X:83:ARG:HB3	2.01	0.42
1:A:29:THR:HG21	1:A:31:CYS:SG	2.59	0.42
1:B:60:ILE:HG21	1:B:113:LEU:HD21	2.01	0.42
2:X:260:VAL:HG12	2:X:261:ARG:N	2.35	0.42
1:B:101:ALA:O	1:B:102:CYS:HB2	2.20	0.42
1:B:5:GLU:C	1:B:5:GLU:CD	2.88	0.42
1:B:28:GLU:HB2	4:B:164:HOH:O	2.20	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:52:LYS:NZ	1:B:101:ALA:O	2.46	0.42
1:B:10:MET:HG2	1:B:87:LEU:HD13	2.02	0.41
1:A:39:ASP:O	1:A:39:ASP:OD2	2.37	0.41
2:X:23:ILE:C	2:X:26:SER:HB2	2.41	0.41
2:X:72:ARG:HG3	4:X:590:HOH:O	2.18	0.41
2:X:147:GLN:HE21	2:X:147:GLN:HB2	1.61	0.41
1:B:71:THR:O	1:B:74:ALA:N	2.53	0.41
1:B:111:LEU:O	1:B:115:GLU:HG3	2.20	0.41
2:X:164:ILE:HD12	2:X:164:ILE:N	2.36	0.41
1:A:14:GLY:O	1:A:18:VAL:HB	2.20	0.41
2:X:200:PRO:HA	4:X:524:HOH:O	2.19	0.41
2:X:216:ARG:CB	2:X:218:GLU:H	2.33	0.41
1:B:108:GLU:HB3	1:B:112:GLN:OE1	2.20	0.41
2:X:197:ARG:HG3	2:X:198:VAL:HG13	2.01	0.41
2:X:117:VAL:HG22	2:X:121:GLN:CB	2.50	0.41
2:X:215:ILE:O	2:X:216:ARG:HG3	2.20	0.41
1:A:65:MET:HE1	1:A:117:ILE:HG21	2.03	0.41
2:X:156:PHE:HB2	2:X:162:PHE:CE2	2.55	0.41
1:A:66:ARG:HG2	2:X:150:ARG:NH2	2.36	0.41
1:B:31:CYS:SG	1:B:32:GLN:N	2.94	0.41
1:B:71:THR:O	1:B:74:ALA:HB3	2.21	0.41
1:B:79:ARG:C	1:B:81:GLN:N	2.77	0.41
2:X:85:THR:HA	2:X:94:SER:N	2.36	0.41
2:X:254:ASP:HB3	4:X:431:HOH:O	2.21	0.41
1:A:46:PRO:HD2	4:A:162:HOH:O	2.21	0.40
1:B:85:ASN:C	1:B:87:LEU:N	2.77	0.40
2:X:45:ASN:HB3	3:C:1:NAG:HN2	1.85	0.40
2:X:86:GLU:O	2:X:87:LEU:C	2.62	0.40
1:B:136:THR:O	1:B:136:THR:HG23	2.20	0.40
1:A:6:HIS:CD2	4:X:336:HOH:O	2.71	0.40
1:A:79:ARG:HD3	1:A:79:ARG:HA	1.77	0.40
1:B:113:LEU:HD23	1:B:117:ILE:HD13	2.03	0.40
2:X:205:ILE:HD12	2:X:287:ARG:O	2.21	0.40
2:X:75:THR:HG23	2:X:77:LYS:HB2	2.04	0.40
2:X:163:ILE:C	2:X:164:ILE:HD12	2.46	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	146/155 (94%)	136 (93%)	7 (5%)	3 (2%)	5	7
1	B	143/155 (92%)	122 (85%)	18 (13%)	3 (2%)	5	7
2	X	268/289 (93%)	239 (89%)	24 (9%)	5 (2%)	6	8
All	All	557/599 (93%)	497 (89%)	49 (9%)	11 (2%)	6	7

All (11) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
2	X	55	SER
2	X	102	LYS
1	A	24	ASP
1	A	32	GLN
1	B	112	GLN
2	X	28	PRO
2	X	126	PRO
2	X	135	LYS
1	B	65	MET
1	B	90	CYS
1	A	2	ASP

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	139/146 (95%)	119 (86%)	20 (14%)	3	4

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	B	137/146 (94%)	124 (90%)	13 (10%)	8	13
2	X	239/253 (94%)	218 (91%)	21 (9%)	9	15
All	All	515/545 (94%)	461 (90%)	54 (10%)	6	10

All (54) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	18	VAL
1	A	22	LEU
1	A	32	GLN
1	A	38	VAL
1	A	40	GLN
1	A	42	GLN
1	A	43	LEU
1	A	50	LEU
1	A	63	GLU
1	A	70	ASN
1	A	79	ARG
1	A	80	LEU
1	A	87	LEU
1	A	90	CYS
1	A	93	LYS
1	A	114	LEU
1	A	122	ASN
1	A	128	LEU
1	A	134	ILE
1	A	136	THR
1	B	10	MET
1	B	15	HIS
1	B	38	VAL
1	B	42	GLN
1	B	52	LYS
1	B	56	LEU
1	B	93	LYS
1	B	96	GLU
1	B	98	GLN
1	B	106	PHE
1	B	128	LEU
1	B	134	ILE
1	B	136	THR
2	X	48	VAL

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Mol	Chain	Res	Type
2	X	53	PRO
2	X	54	ILE
2	X	99	LEU
2	X	148	VAL
2	X	158	PRO
2	X	173	ASN
2	X	180	MET
2	X	211	LYS
2	X	212	LEU
2	X	215	ILE
2	X	224	CYS
2	X	227	THR
2	X	231	VAL
2	X	236	ILE
2	X	237	LEU
2	X	245	GLU
2	X	248	LEU
2	X	263	LEU
2	X	271	GLN
2	X	290	THR

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	13	ASN
1	A	21	GLN
1	A	32	GLN
1	A	40	GLN
1	A	88	ASN
1	A	98	GLN
1	A	119	ASN
1	A	141	ASN
1	B	13	ASN
1	B	70	ASN
1	B	75	ASN
1	B	81	GLN
1	B	86	ASN
1	B	88	ASN
1	B	98	GLN
1	B	141	ASN
2	X	98	HIS
2	X	147	GLN

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Mol	Chain	Res	Type
2	X	173	ASN
2	X	199	HIS
2	X	255	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 ⓘ

4 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	2,3	14,14,15	0.61	0	17,19,21	0.67	0
3	NAG	C	2	3	14,14,15	0.61	0	17,19,21	1.01	1 (5%)
3	NAG	D	1	2,3	14,14,15	0.82	1 (7%)	17,19,21	1.00	0
3	NAG	D	2	3	14,14,15	0.73	0	17,19,21	1.40	3 (17%)

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	2,3	-	4/6/23/26	0/1/1/1
3	NAG	C	2	3	1/1/5/7	2/6/23/26	0/1/1/1
3	NAG	D	1	2,3	1/1/5/7	0/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	NAG	D	2	3	1/1/5/7	5/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	D	1	NAG	C1-C2	2.32	1.55	1.52

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	D	2	NAG	C3-C4-C5	3.61	116.78	110.23
3	D	2	NAG	C4-C3-C2	2.89	115.25	111.02
3	D	2	NAG	C2-N2-C7	-2.33	119.78	122.90
3	C	2	NAG	C3-C4-C5	2.07	113.99	110.23

All (3) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
3	C	2	NAG	C1
3	D	1	NAG	C1
3	D	2	NAG	C1

All (11) torsion outliers are listed below:

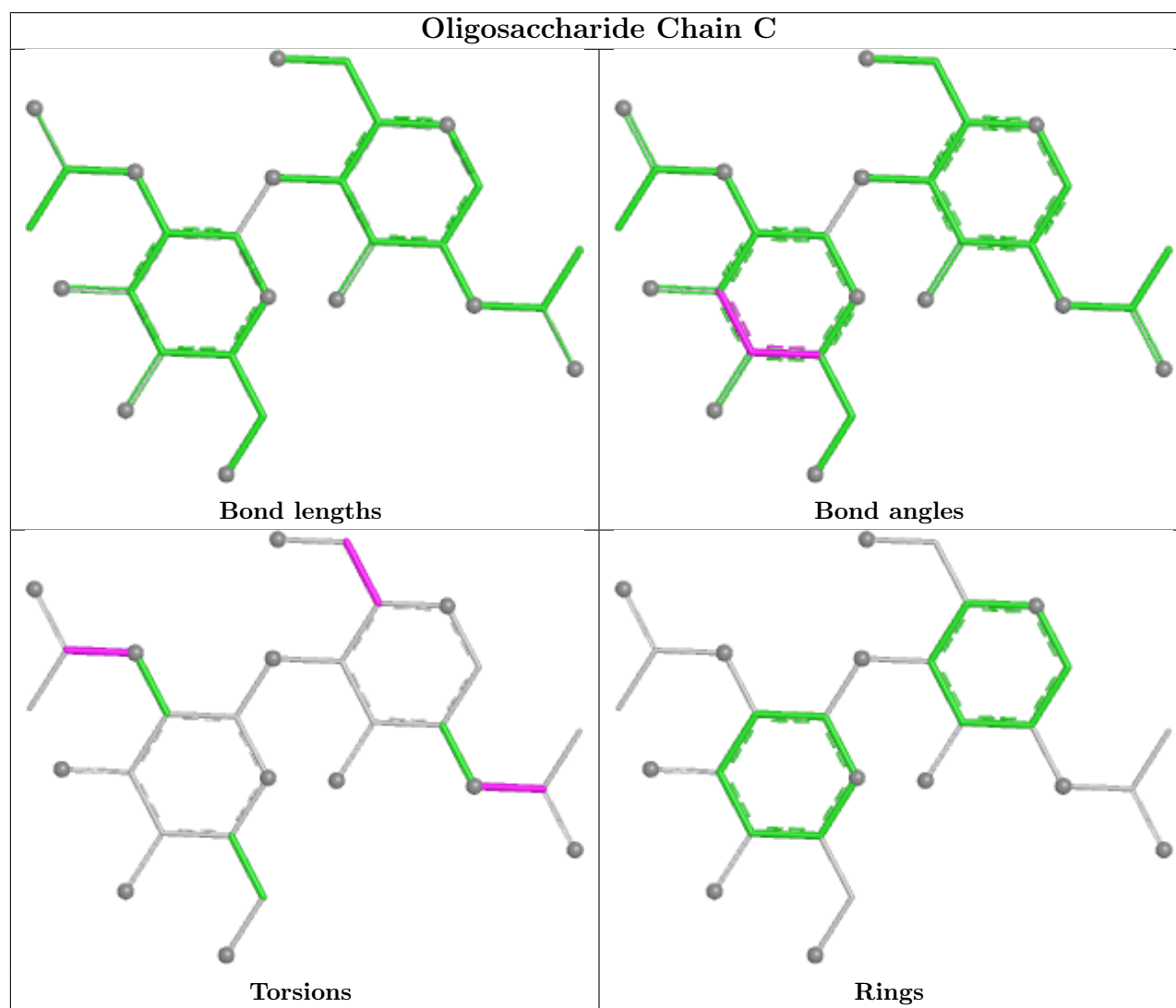
Mol	Chain	Res	Type	Atoms
3	C	1	NAG	C8-C7-N2-C2
3	C	1	NAG	O7-C7-N2-C2
3	C	2	NAG	C8-C7-N2-C2
3	C	2	NAG	O7-C7-N2-C2
3	D	2	NAG	C8-C7-N2-C2
3	D	2	NAG	O7-C7-N2-C2
3	D	2	NAG	C4-C5-C6-O6
3	D	2	NAG	O5-C5-C6-O6
3	C	1	NAG	C4-C5-C6-O6
3	D	2	NAG	C3-C2-N2-C7
3	C	1	NAG	O5-C5-C6-O6

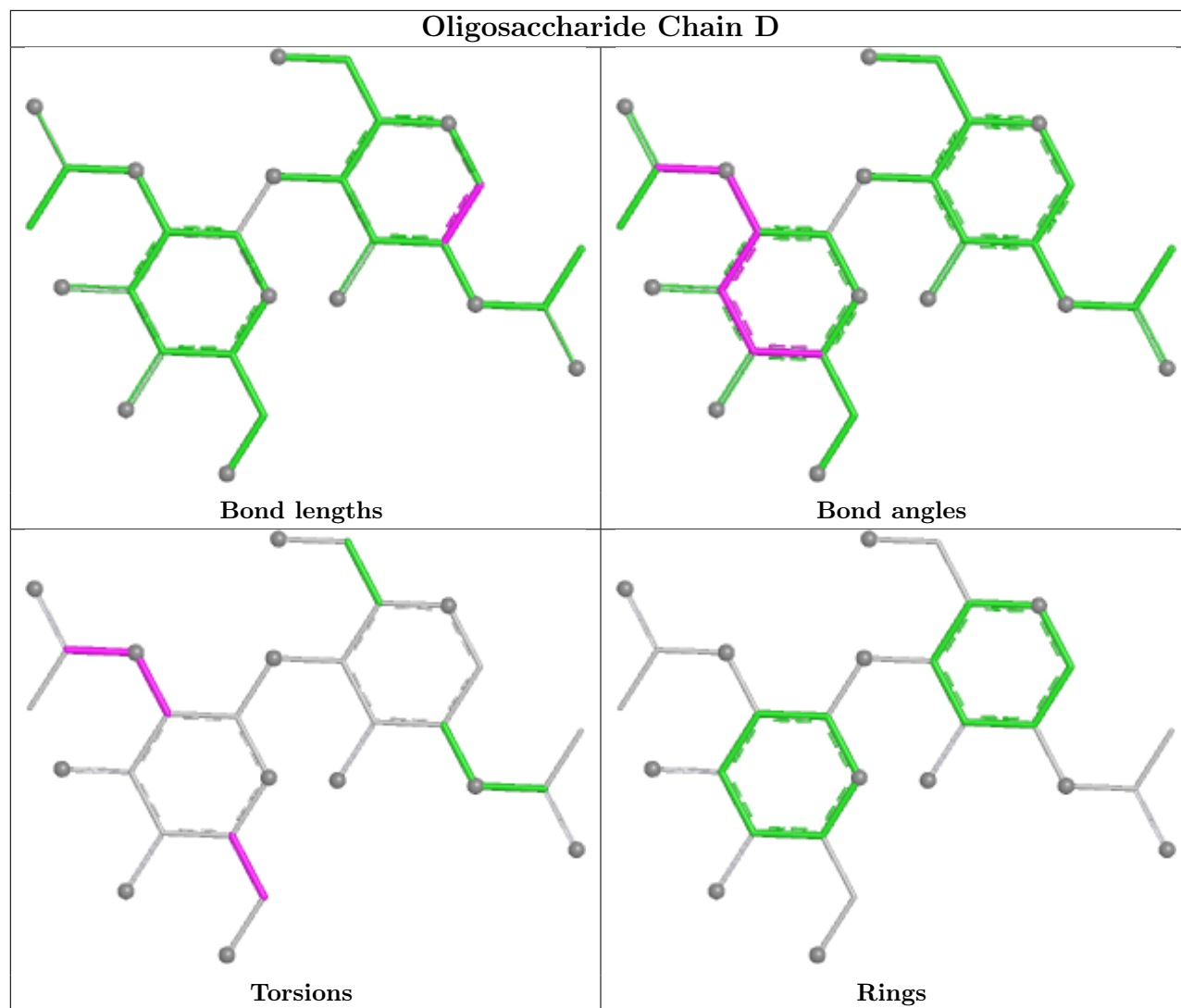
There are no ring outliers.

4 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	1	NAG	2	0
3	C	2	NAG	1	0
3	D	2	NAG	1	0
3	D	1	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](#)

There are no ligands in this entry.

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	148/155 (95%)	0.05	9 (6%) 27 23	24, 37, 81, 138	0
1	B	145/155 (93%)	1.86	56 (38%) 1 0	40, 98, 142, 150	0
2	X	272/289 (94%)	0.84	54 (19%) 3 2	28, 56, 125, 155	0
All	All	565/599 (94%)	0.89	119 (21%) 2 2	24, 56, 134, 155	0

All (119) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	135	PHE	7.5
1	B	4	SER	6.2
1	B	133	ASN	5.6
1	B	132	TRP	5.6
1	B	43	LEU	5.4
1	B	90	CYS	5.3
1	B	136	THR	5.2
2	X	54	ILE	5.1
2	X	86	GLU	4.7
1	B	49	TYR	4.6
1	B	128	LEU	4.6
2	X	216	ARG	4.6
2	X	215	ILE	4.3
2	X	295	VAL	4.3
1	B	95	TYR	4.2
1	B	87	LEU	4.2
2	X	51	ASP	4.2
1	B	134	ILE	4.2
1	A	148	SER	4.1
2	X	296	VAL	4.1
1	B	16	LEU	4.0
1	B	124	THR	4.0
1	A	96	GLU	3.9

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Mol	Chain	Res	Type	RSRZ
1	B	127	LEU	3.8
2	X	180	MET	3.8
2	X	184	ARG	3.8
1	B	55	PHE	3.8
2	X	73	ASN	3.7
1	B	97	GLU	3.7
2	X	217	GLY	3.6
2	X	110	LEU	3.6
1	B	7	CYS	3.6
1	B	137	LYS	3.6
1	A	90	CYS	3.5
1	B	89	SER	3.5
2	X	48	VAL	3.5
2	X	67	SER	3.4
1	B	88	ASN	3.4
2	X	269	ASP	3.3
2	X	44	SER	3.3
1	B	91	PHE	3.3
1	B	131	ASP	3.3
2	X	212	LEU	3.3
2	X	58	TRP	3.2
1	B	148	SER	3.2
2	X	64	SER	3.2
1	B	140	ASN	3.1
2	X	66	GLY	3.1
2	X	74	ALA	3.1
1	B	9	HIS	3.1
1	B	44	ASP	3.1
2	X	179	THR	3.1
2	X	55	SER	3.0
2	X	56	PRO	3.0
2	X	183	GLY	3.0
2	X	59	THR	3.0
2	X	87	LEU	3.0
1	B	8	SER	3.0
1	B	42	GLN	3.0
2	X	88	GLU	2.9
2	X	214	ARG	2.9
2	X	85	THR	2.9
1	B	15	HIS	2.9
2	X	219	ALA	2.9
1	B	98	GLN	2.9

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Mol	Chain	Res	Type	RSRZ
1	B	129	GLU	2.9
1	B	47	VAL	2.9
1	B	99	ASN	2.8
2	X	268	VAL	2.8
2	X	94	SER	2.8
2	X	182	ASN	2.8
1	A	1	ALA	2.8
1	B	101	ALA	2.7
1	B	102	CYS	2.7
1	B	121	PHE	2.7
1	B	145	LYS	2.7
2	X	62	PRO	2.6
2	X	53	PRO	2.6
1	A	31	CYS	2.6
2	X	127	CYS	2.6
2	X	218	GLU	2.6
1	A	98	GLN	2.6
1	B	125	LYS	2.6
1	B	92	THR	2.5
2	X	68	THR	2.5
2	X	65	PRO	2.5
2	X	134	LEU	2.5
1	B	14	GLY	2.4
1	B	94	ASP	2.4
2	X	294	GLN	2.4
2	X	162	PHE	2.4
2	X	271	GLN	2.4
2	X	186	SER	2.3
1	B	11	ILE	2.3
1	B	111	LEU	2.3
1	B	12	GLY	2.3
2	X	104	PRO	2.3
2	X	181	VAL	2.3
1	B	144	ALA	2.2
2	X	57	TYR	2.3
2	X	61	ASP	2.2
2	X	43	VAL	2.2
1	B	93	LYS	2.2
1	A	44	ASP	2.2
2	X	270	PHE	2.2
1	B	13	ASN	2.2
2	X	60	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	B	6	HIS	2.2
1	B	85	ASN	2.2
1	B	103	VAL	2.1
1	B	50	LEU	2.1
1	A	97	GLU	2.1
1	B	83	LEU	2.1
1	B	143	PHE	2.1
1	A	95	TYR	2.1
1	B	100	LYS	2.1
2	X	27	GLY	2.1
2	X	132	PRO	2.1
1	B	80	LEU	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](#)

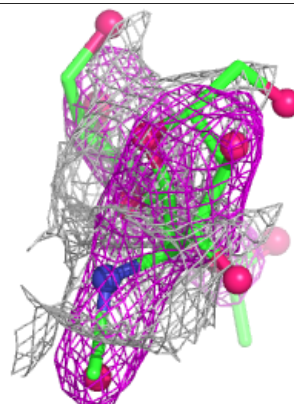
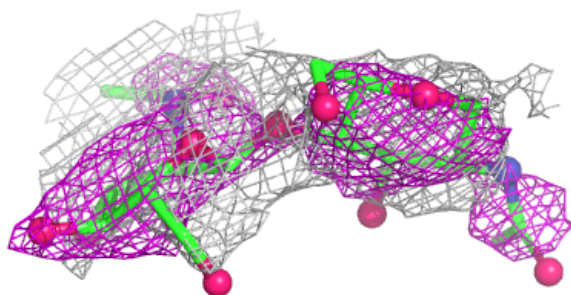
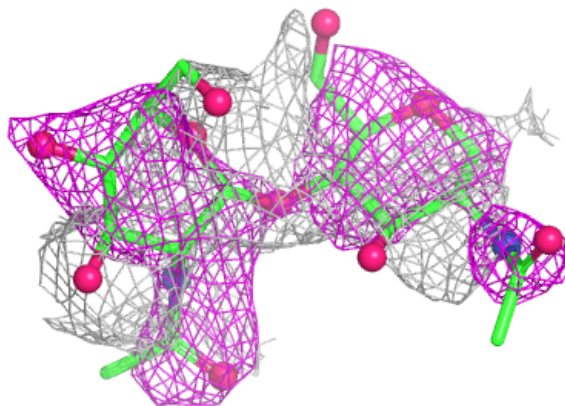
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists 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	NAG	C	1	14/15	-	-	82,88,96,102	0
3	NAG	C	2	14/15	-	-	84,88,93,95	0
3	NAG	D	2	14/15	0.19	0.18	81,83,89,91	0
3	NAG	D	1	14/15	0.20	0.20	79,83,88,88	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.

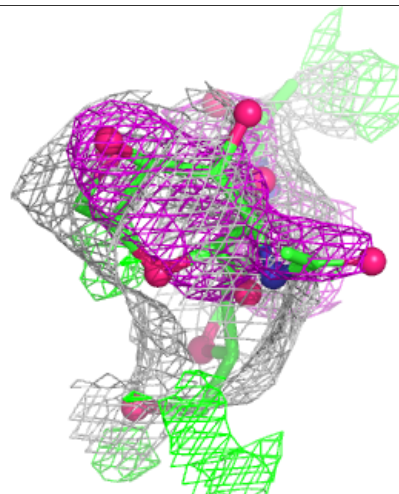
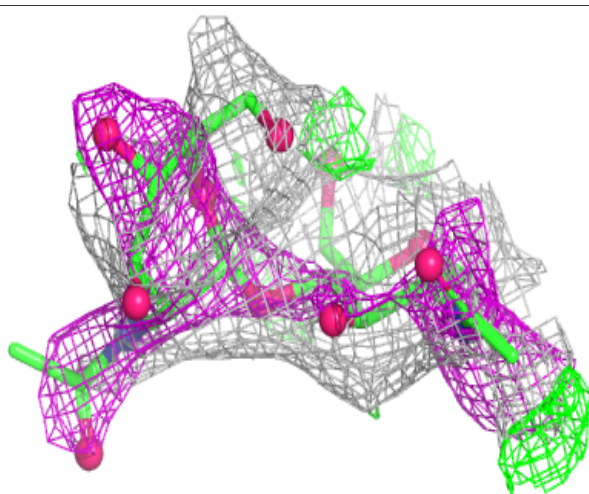
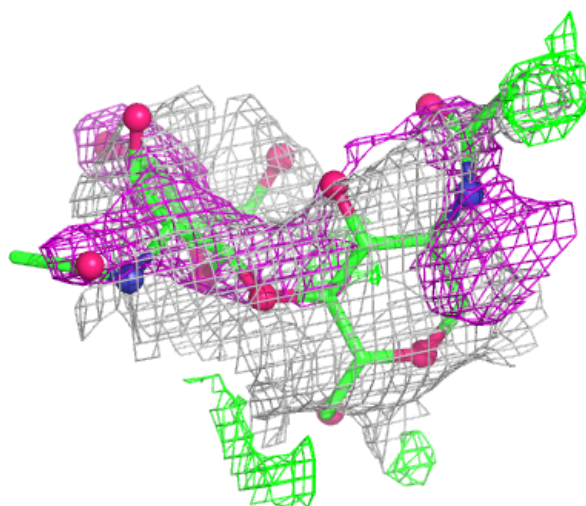
Electron density around Chain C:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



Electron density around Chain D:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)



6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.