



Full wwPDB X-ray Structure Validation Report ⓘ

Sep 23, 2024 – 12:11 AM EDT

PDB ID : 7U9F
Title : Integrin alpha IIB beta3 complex with BMS compound 4 in Mn2+
Authors : Lin, F.-Y.; Zhu, J.; Zhu, J.; Springer, T.A.
Deposited on : 2022-03-10
Resolution : 2.70 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 : 4.02b-467
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 1.20.1
EDS : 3.0
buster-report : 1.1.7 (2018)
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.002 (Gargrove)
Density-Fitness : 1.0.11
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.38.3

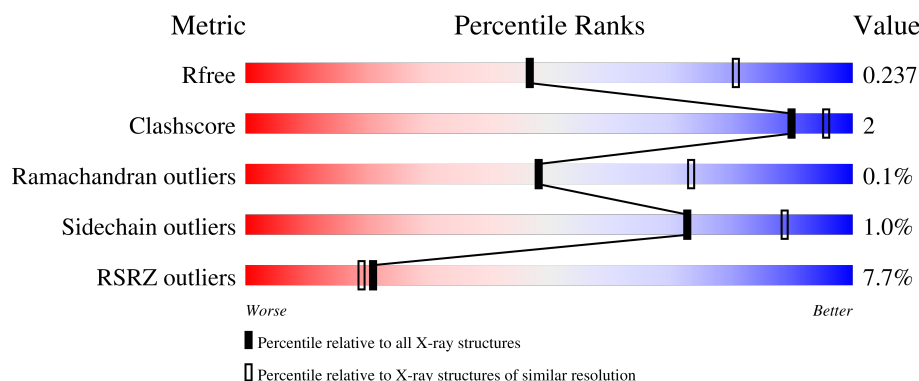
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.70 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.



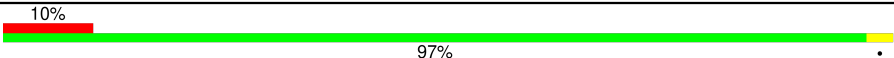
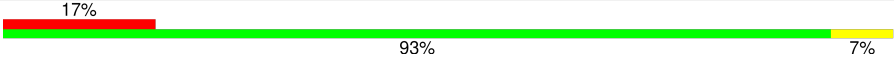
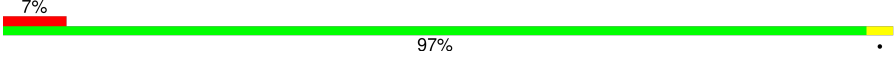

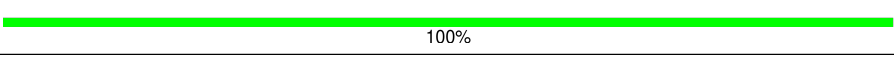
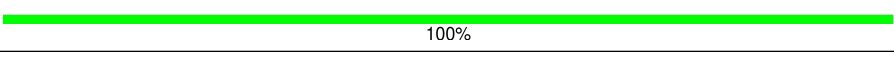

Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	3333 (2.70-2.70)
Clashscore	180529	3684 (2.70-2.70)
Ramachandran outliers	177936	3633 (2.70-2.70)
Sidechain outliers	177891	3633 (2.70-2.70)
RSRZ outliers	164620	3333 (2.70-2.70)

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	454	<div> <div>0%</div> <div>95%</div> <div>5%</div> </div>
1	C	454	<div> <div>2%</div> <div>93%</div> <div>7%</div> </div>
2	B	471	<div> <div>5%</div> <div>93%</div> <div>6%</div> </div>
2	D	471	<div> <div>6%</div> <div>94%</div> <div>6%</div> </div>
3	E	216	<div> <div>33%</div> <div>94%</div> <div>5%</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	216	
4	F	214	
4	L	214	
5	G	5	
6	I	2	
6	K	2	
7	J	4	

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 22211 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 Integrin alpha-IIb.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	454	Total	C	N	O	S	0	4	0
			3499	2226	601	664	8			
1	C	453	Total	C	N	O	S	0	4	0
			3502	2224	604	666	8			

- Molecule 2 is a protein called Integrin beta-3.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	466	Total	C	N	O	S	4	4	0
			3618	2252	617	715	34			
2	D	471	Total	C	N	O	S	3	0	0
			3623	2255	619	715	34			

- Molecule 3 is a protein called Fab heavy chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	E	214	Total	C	N	O	S	0	0	0
			1631	1035	264	326	6			
3	H	216	Total	C	N	O	S	0	0	0
			1642	1041	266	329	6			

- Molecule 4 is a protein called Fab light chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	F	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			
4	L	214	Total	C	N	O	S	0	0	0
			1637	1019	268	341	9			

- Molecule 5 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
5	G	5	Total	C	N	O	0	0	0
			61	34	2	25			

- Molecule 6 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
6	I	2	Total	C	N	O	0	0	0
			28	16	2	10			
6	K	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 7 is an oligosaccharide called alpha-D-mannopyranose-(1-3)-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
7	J	4	Total	C	N	O	0	0	0
			50	28	2	20			

- Molecule 8 is SULFATE ION (three-letter code: SO4) (formula: O₄S).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	A	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	C	1	Total	O	S	0	0
			5	4	1		
8	L	1	Total	O	S	0	0
			5	4	1		

- Molecule 9 is CALCIUM ION (three-letter code: CA) (formula: Ca).

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

- Molecule 10 is MANGANESE (II) ION (three-letter code: MN) (formula: Mn).

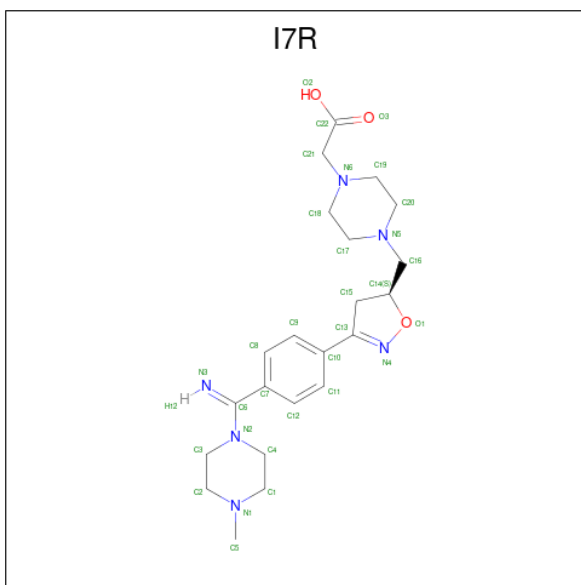
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	B	3	Total	Mn	0	0
			3	3		
10	D	3	Total	Mn	0	0
			3	3		

- Molecule 11 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: $C_8H_{15}NO_6$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
11	B	1	Total	C	N	O	0	0
			14	8	1	5		
11	D	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 12 is (4-{[(5S)-3-{4-[(E)-imino(4-methylpiperazin-1-yl)methyl]phenyl}-4,5-dihydro-1,2-oxazol-5-yl]methyl}piperazin-1-yl)acetic acid (three-letter code: I7R) (formula: $C_{22}H_{32}N_6O_3$) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
12	B	1	Total	C	N	O	0	0
			31	22	6	3		
12	D	1	Total	C	N	O	0	0
			31	22	6	3		

- Molecule 13 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
13	C	1	Total	Cl	0	0
			1	1		
13	D	1	Total	Cl	0	0
			1	1		

- Molecule 14 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	A	408	Total	O	0	0
			408	408		
14	B	226	Total	O	0	0
			226	226		
14	C	185	Total	O	0	0
			185	185		
14	D	152	Total	O	0	0
			152	152		
14	E	19	Total	O	0	0
			19	19		

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	F	18	Total	O	0	0
			18	18		
14	H	34	Total	O	0	0
			34	34		
14	L	62	Total	O	0	0
			62	62		

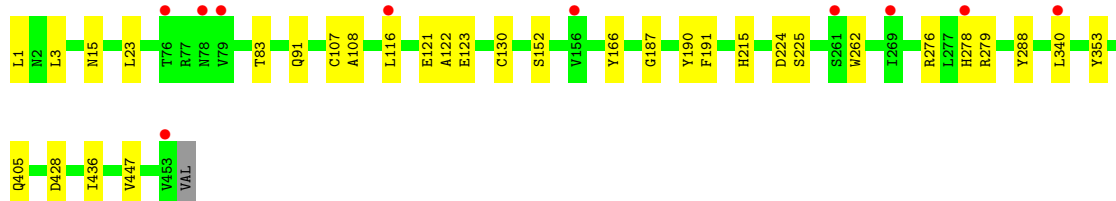
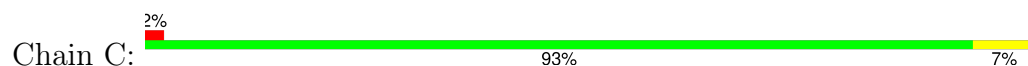
3 Residue-property plots [i](#)

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.

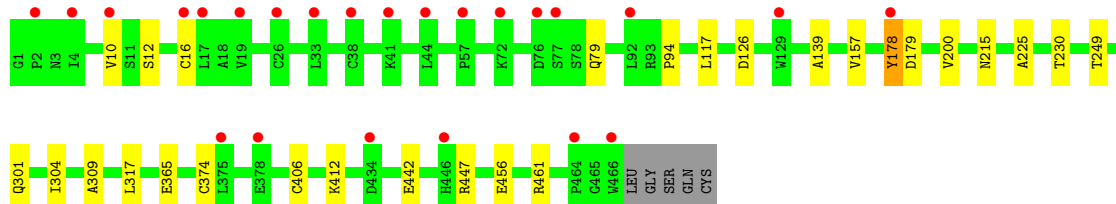
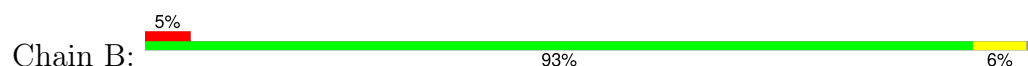
- Molecule 1: Integrin alpha-IIb



- Molecule 1: Integrin alpha-IIb

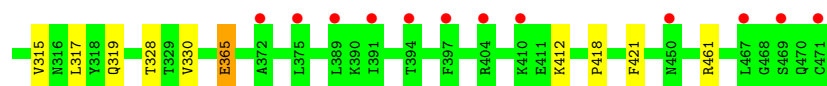


- Molecule 2: Integrin beta-3

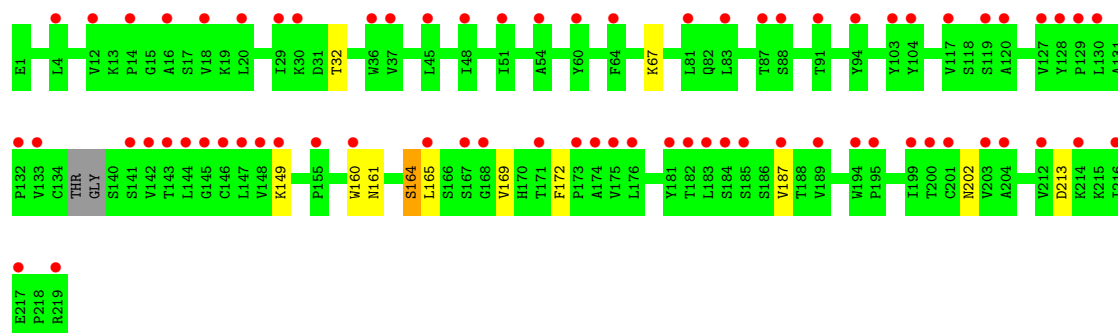


- Molecule 2: Integrin beta-3

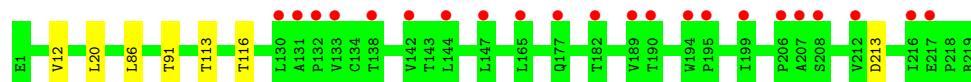




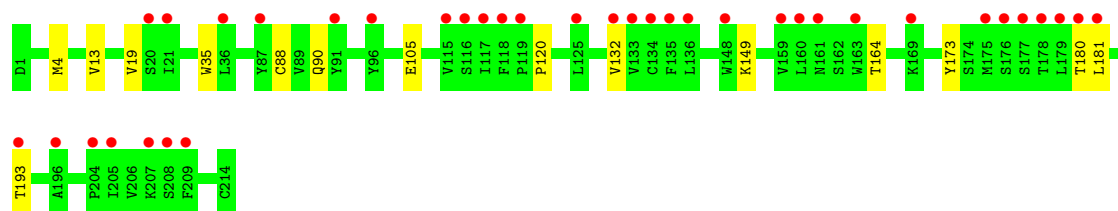
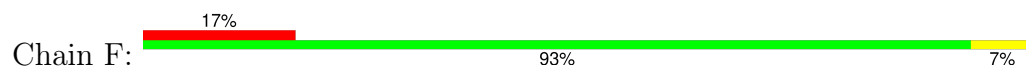
• Molecule 3: Fab heavy chain



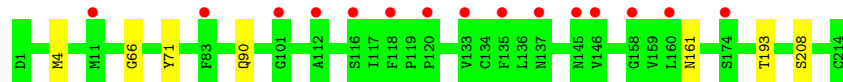
• Molecule 3: Fab heavy chain



• Molecule 4: Fab light chain



• Molecule 4: Fab light chain



• Molecule 5: 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





- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain I:  100%



- Molecule 6: 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain K:  100%



- Molecule 7: alpha-D-mannopyranose-(1-3)-beta-D-mannopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose

Chain J:  75% 25%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	259.40Å 144.29Å 104.92Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	46.09 – 2.70 46.09 – 2.70	Depositor EDS
% Data completeness (in resolution range)	98.7 (46.09-2.70) 89.4 (46.09-2.70)	Depositor EDS
R_{merge}	0.10	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.16 (at 2.69Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, R_{free}	0.217 , 0.237 0.215 , 0.237	Depositor DCC
R_{free} test set	106687 reflections (1.85%)	wwPDB-VP
Wilson B-factor (Å ²)	48.9	Xtriage
Anisotropy	0.366	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 43.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	22211	wwPDB-VP
Average B, all atoms (Å ²)	80.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.38% 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 [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: I7R, MN, SO4, CL, NAG, BMA, CA, 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	0.25	0/3608	0.46	0/4918
1	C	0.26	0/3605	0.45	0/4912
2	B	0.24	0/3688	0.44	0/5000
2	D	0.24	0/3690	0.42	0/5003
3	E	0.24	0/1673	0.45	0/2290
3	H	0.24	0/1684	0.45	0/2305
4	F	0.24	0/1673	0.43	0/2269
4	L	0.24	0/1673	0.45	0/2269
All	All	0.24	0/21294	0.44	0/28966

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 [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	3499	0	3345	10	0
1	C	3502	0	3334	16	0
2	B	3618	0	3533	14	0
2	D	3623	0	3540	13	0
3	E	1631	0	1590	8	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	H	1642	0	1600	4	0
4	F	1637	0	1553	8	0
4	L	1637	0	1553	4	0
5	G	61	0	52	0	0
6	I	28	0	25	0	0
6	K	28	0	25	0	0
7	J	50	0	43	0	0
8	A	20	0	0	0	0
8	C	20	0	0	0	0
8	L	5	0	0	0	0
9	A	4	0	0	0	0
9	C	4	0	0	0	0
10	B	3	0	0	0	0
10	D	3	0	0	0	0
11	B	14	0	13	0	0
11	D	14	0	13	0	0
12	B	31	0	0	0	0
12	D	31	0	0	1	0
13	C	1	0	0	0	0
13	D	1	0	0	0	0
14	A	408	0	0	0	1
14	B	226	0	0	1	0
14	C	185	0	0	1	1
14	D	152	0	0	0	0
14	E	19	0	0	0	0
14	F	18	0	0	0	0
14	H	34	0	0	0	0
14	L	62	0	0	1	0
All	All	22211	0	20219	71	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 2.

All (71) 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)
3:E:161:ASN:HB2	3:E:164:SER:HB3	1.67	0.75
3:E:165:LEU:HD21	3:E:187:VAL:HG21	1.82	0.60
2:D:12:SER:HB3	2:D:461:ARG:HD3	1.82	0.60
2:B:139:ALA:HB2	2:B:200:VAL:HG11	1.87	0.56
1:C:121:GLU:HG3	1:C:123:GLU:H	1.71	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:306:LEU:HB3	2:D:328:THR:HG22	1.89	0.55
2:D:121:SER:HB2	12:D:2006:I7R:O2	2.07	0.53
2:B:230:THR:HG23	2:B:304:ILE:HG13	1.91	0.52
1:C:83:THR:HB	1:C:116:LEU:HB2	1.91	0.52
3:E:160:TRP:HE1	3:E:169:VAL:HG11	1.75	0.51
1:A:262:TRP:HB3	2:B:317:LEU:HD13	1.91	0.51
2:B:10:VAL:HG21	2:B:16:CYS:HB2	1.92	0.50
1:A:9:THR:HB	1:A:447:VAL:HB	1.92	0.50
2:D:117:LEU:HD11	2:D:225:ALA:HB1	1.94	0.50
2:D:365:GLU:OE2	2:D:412:LYS:NZ	2.44	0.49
2:B:126[A]:ASP:OD1	2:B:126[A]:ASP:N	2.44	0.49
3:H:20:LEU:HD22	3:H:113:THR:HG21	1.94	0.49
1:A:394:GLY:HA2	1:A:399:LEU:HD23	1.95	0.49
1:C:262:TRP:HB3	2:D:317:LEU:HD13	1.94	0.48
1:A:377:ALA:HB2	1:A:421:LEU:HD11	1.96	0.48
1:A:187:GLY:HA2	1:A:191:PHE:HA	1.96	0.48
2:B:117:LEU:HD11	2:B:225:ALA:HB1	1.95	0.48
4:L:193:THR:HG23	4:L:208:SER:HB3	1.96	0.47
2:B:365:GLU:OE2	2:B:412:LYS:NZ	2.39	0.47
1:A:314:MET:HB3	1:A:322:LEU:HB3	1.97	0.47
2:D:319:GLN:HA	2:D:330:VAL:HG21	1.97	0.46
4:L:4:MET:HE2	4:L:90:GLN:HB3	1.97	0.46
1:C:353:TYR:OH	2:D:297:GLU:OE1	2.27	0.45
4:F:13:VAL:HG11	4:F:19:VAL:HG11	1.99	0.45
3:H:12:VAL:HG21	3:H:86:LEU:HD13	1.97	0.45
4:F:120:PRO:HD3	4:F:132:VAL:HG22	1.99	0.45
3:H:91:THR:HG23	3:H:116:THR:HA	1.99	0.45
3:E:149:LYS:NZ	4:F:180:THR:HG21	2.31	0.45
1:C:224:ASP:OD1	1:C:225:SER:N	2.43	0.45
1:C:107:CYS:HA	1:C:130:CYS:HA	1.98	0.45
1:C:276:ARG:HD2	1:C:279:ARG:HB2	1.99	0.45
4:L:161:ASN:ND2	14:L:404:HOH:O	2.49	0.45
1:A:107:CYS:HA	1:A:130:CYS:HA	1.97	0.44
3:E:172:PHE:CD2	4:F:164:THR:HG23	2.52	0.44
1:A:3:LEU:O	1:A:5:PRO:HD3	2.18	0.44
1:C:278[A]:HIS:NE2	1:C:340:LEU:O	2.50	0.44
3:E:202:ASN:HA	3:E:213:ASP:HB3	1.99	0.44
1:C:187:GLY:HA2	1:C:191:PHE:HA	2.00	0.44
2:B:442:GLU:OE1	2:B:447:ARG:NH1	2.51	0.43
1:C:215:HIS:CE1	3:E:32:THR:HG22	2.53	0.43
2:D:22:MET:HG2	2:D:40:LEU:HD22	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:178:TYR:CG	2:D:179:ASP:N	2.86	0.43
3:H:213:ASP:OD1	3:H:213:ASP:N	2.52	0.43
2:B:456:GLU:OE2	2:B:461:ARG:NH1	2.52	0.43
1:A:122:ALA:O	1:A:123:GLU:HB2	2.19	0.42
3:E:67:LYS:HE3	3:E:67:LYS:HB2	1.90	0.42
2:B:301:GLN:NE2	14:B:2107:HOH:O	2.43	0.42
1:C:123:GLU:HG3	1:C:152:SER:HB2	2.02	0.42
4:F:35:TRP:CZ3	4:F:88:CYS:HB3	2.55	0.42
1:C:122:ALA:O	1:C:123:GLU:HB2	2.18	0.42
2:D:311:THR:O	2:D:315:VAL:HG23	2.21	0.41
2:D:418:PRO:HB2	2:D:421:PHE:CD1	2.55	0.41
2:B:178:TYR:CG	2:B:179:ASP:N	2.88	0.41
2:B:249:THR:HA	2:B:309:ALA:O	2.19	0.41
1:C:3:LEU:O	1:C:405:GLN:NE2	2.47	0.41
1:C:428:ASP:CG	14:C:602:HOH:O	2.59	0.41
4:F:105:GLU:OE1	4:F:173:TYR:OH	2.27	0.41
4:F:149:LYS:HB2	4:F:193:THR:HB	2.03	0.41
2:B:94:PRO:HG3	2:B:406:CYS:HB2	2.03	0.41
1:A:109:PRO:O	1:A:168:GLU:HA	2.21	0.41
2:B:12:SER:HB3	2:B:461:ARG:HD3	2.03	0.41
1:C:436:ILE:HG22	1:C:447:VAL:HG22	2.03	0.41
2:D:235:LYS:HE3	2:D:276:GLY:O	2.21	0.41
4:F:4:MET:HE2	4:F:90:GLN:HB3	2.02	0.41
4:L:66:GLY:HA3	4:L:71:TYR:HA	2.03	0.41
1:C:91:GLN:HB2	1:C:108:ALA:HB1	2.04	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)
14:A:902:HOH:O	14:C:761:HOH:O[1_554]	2.19	0.01

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	456/454 (100%)	440 (96%)	15 (3%)	1 (0%)	44	68
1	C	455/454 (100%)	438 (96%)	17 (4%)	0	100	100
2	B	468/471 (99%)	451 (96%)	16 (3%)	1 (0%)	44	68
2	D	469/471 (100%)	445 (95%)	24 (5%)	0	100	100
3	E	210/216 (97%)	194 (92%)	16 (8%)	0	100	100
3	H	212/216 (98%)	203 (96%)	9 (4%)	0	100	100
4	F	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
4	L	212/214 (99%)	205 (97%)	7 (3%)	0	100	100
All	All	2694/2710 (99%)	2580 (96%)	112 (4%)	2 (0%)	48	73

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
2	B	157	VAL

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	366/362 (101%)	361 (99%)	5 (1%)	62	84
1	C	365/362 (101%)	359 (98%)	6 (2%)	58	82
2	B	416/416 (100%)	412 (99%)	4 (1%)	73	89
2	D	416/416 (100%)	411 (99%)	5 (1%)	67	86
3	E	186/187 (100%)	185 (100%)	1 (0%)	86	95
3	H	187/187 (100%)	187 (100%)	0	100	100
4	F	188/188 (100%)	187 (100%)	1 (0%)	86	95
4	L	188/188 (100%)	188 (100%)	0	100	100

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Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
All	All	2312/2306 (100%)	2290 (99%)	22 (1%)	73	89

All (22) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LEU
1	A	166	TYR
1	A	190	TYR
1	A	270	LEU
1	A	288	TYR
2	B	79	GLN
2	B	178	TYR
2	B	215	ASN
2	B	374	CYS
1	C	1	LEU
1	C	15	ASN
1	C	23	LEU
1	C	166	TYR
1	C	190	TYR
1	C	288	TYR
2	D	143	ARG
2	D	202	ARG
2	D	215	ASN
2	D	241	ASP
2	D	365	GLU
3	E	164	SER
4	F	181	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
2	D	280	HIS
2	D	301	GLN
2	D	438	GLN

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 ⓘ

13 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
5	NAG	G	1	5,2	14,14,15	0.34	0	17,19,21	0.49	0
5	NAG	G	2	5	14,14,15	0.15	0	17,19,21	0.47	0
5	BMA	G	3	5	11,11,12	0.94	0	15,15,17	0.86	0
5	MAN	G	4	5	11,11,12	0.70	0	15,15,17	1.05	2 (13%)
5	MAN	G	5	5	11,11,12	1.20	1 (9%)	15,15,17	2.07	1 (6%)
6	NAG	I	1	2,6	14,14,15	0.38	0	17,19,21	0.42	0
6	NAG	I	2	6	14,14,15	0.19	0	17,19,21	0.40	0
7	NAG	J	1	2,7	14,14,15	0.30	0	17,19,21	0.53	0
7	NAG	J	2	7	14,14,15	0.32	0	17,19,21	0.40	0
7	BMA	J	3	7	11,11,12	0.81	0	15,15,17	0.87	0
7	MAN	J	4	7	11,11,12	0.74	0	15,15,17	1.06	2 (13%)
6	NAG	K	1	2,6	14,14,15	0.31	0	17,19,21	0.43	0
6	NAG	K	2	6	14,14,15	0.18	0	17,19,21	0.47	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
5	NAG	G	1	5,2	-	0/6/23/26	0/1/1/1
5	NAG	G	2	5	-	0/6/23/26	0/1/1/1
5	BMA	G	3	5	-	2/2/19/22	0/1/1/1
5	MAN	G	4	5	-	0/2/19/22	0/1/1/1
5	MAN	G	5	5	-	1/2/19/22	0/1/1/1
6	NAG	I	1	2,6	-	1/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
6	NAG	I	2	6	-	3/6/23/26	0/1/1/1
7	NAG	J	1	2,7	-	0/6/23/26	0/1/1/1
7	NAG	J	2	7	-	0/6/23/26	0/1/1/1
7	BMA	J	3	7	-	2/2/19/22	0/1/1/1
7	MAN	J	4	7	-	2/2/19/22	0/1/1/1
6	NAG	K	1	2,6	-	2/6/23/26	0/1/1/1
6	NAG	K	2	6	-	4/6/23/26	0/1/1/1

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	G	5	MAN	O5-C5	3.44	1.50	1.43

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	G	5	MAN	C1-O5-C5	7.04	121.62	112.19
5	G	4	MAN	C1-O5-C5	2.97	116.16	112.19
7	J	4	MAN	C1-O5-C5	2.90	116.07	112.19
7	J	4	MAN	O2-C2-C3	-2.14	105.72	110.15
5	G	4	MAN	O2-C2-C3	-2.12	105.76	110.15

There are no chirality outliers.

All (17) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	G	3	BMA	O5-C5-C6-O6
5	G	3	BMA	C4-C5-C6-O6
7	J	3	BMA	O5-C5-C6-O6
6	K	1	NAG	O5-C5-C6-O6
7	J	3	BMA	C4-C5-C6-O6
6	K	2	NAG	O5-C5-C6-O6
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2
6	K	2	NAG	C8-C7-N2-C2
6	K	2	NAG	O7-C7-N2-C2
6	K	1	NAG	C4-C5-C6-O6
6	K	2	NAG	C4-C5-C6-O6
7	J	4	MAN	O5-C5-C6-O6
6	I	2	NAG	O5-C5-C6-O6

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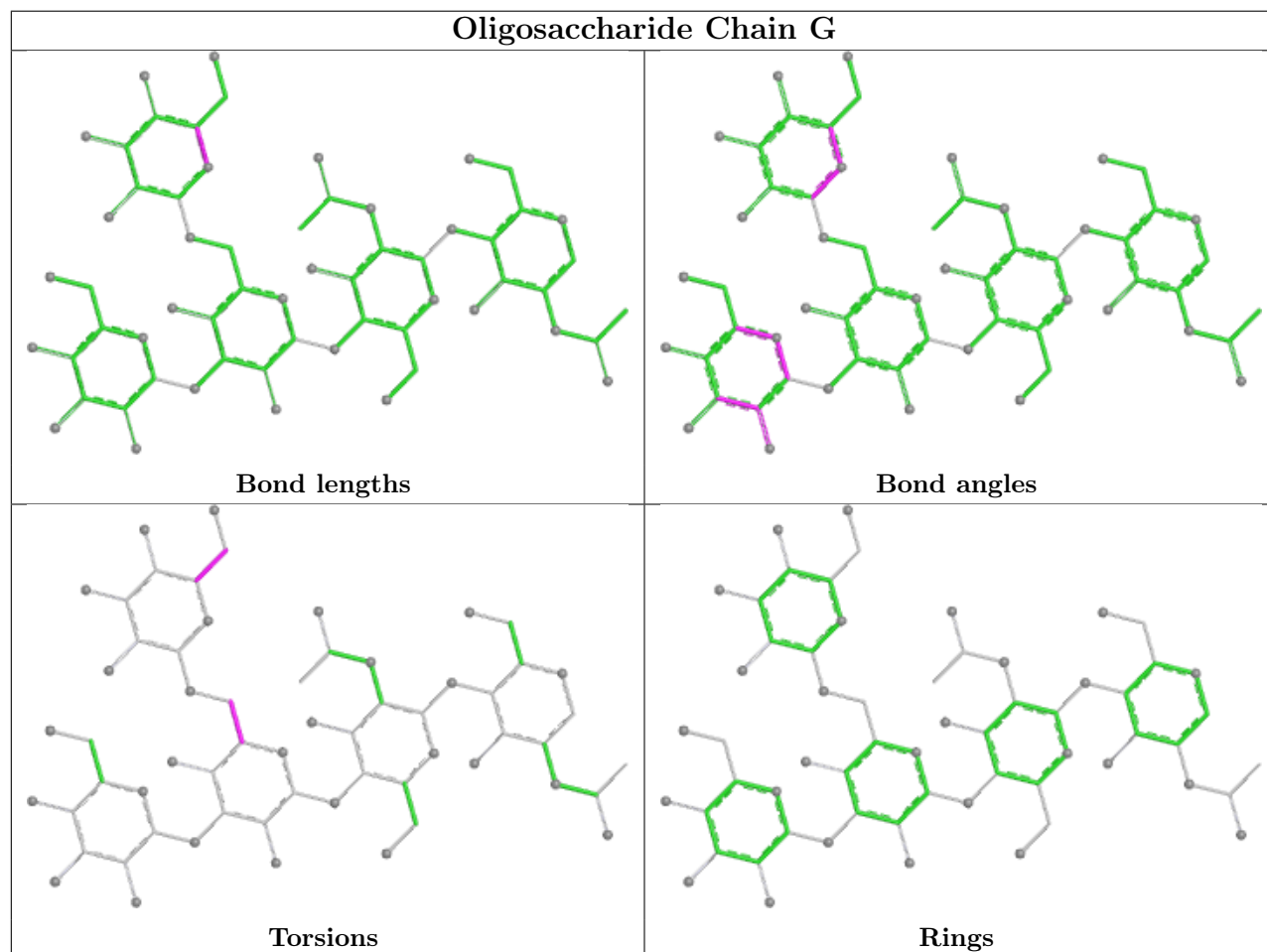
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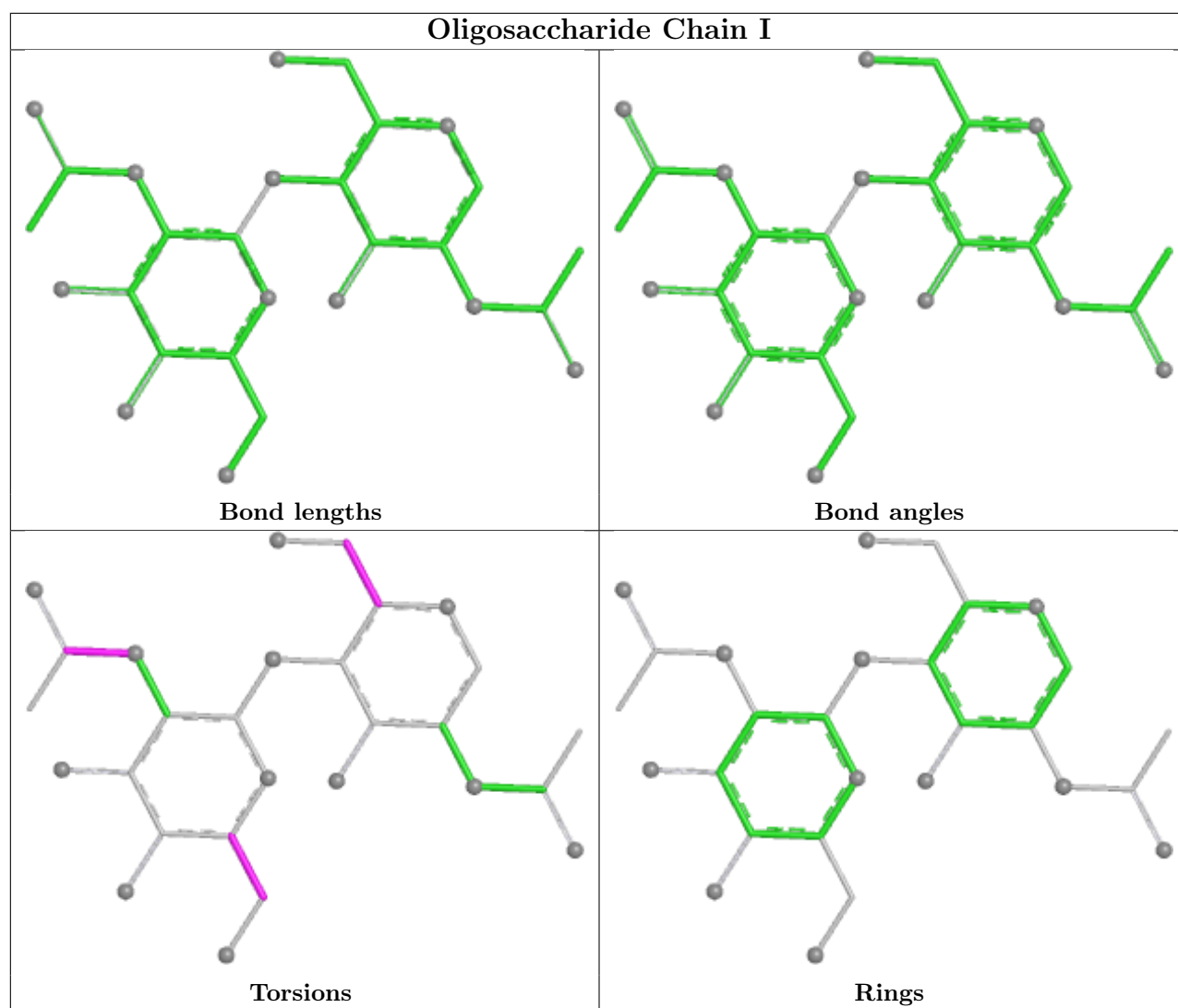
Mol	Chain	Res	Type	Atoms
5	G	5	MAN	C4-C5-C6-O6
7	J	4	MAN	C4-C5-C6-O6
6	I	1	NAG	C4-C5-C6-O6

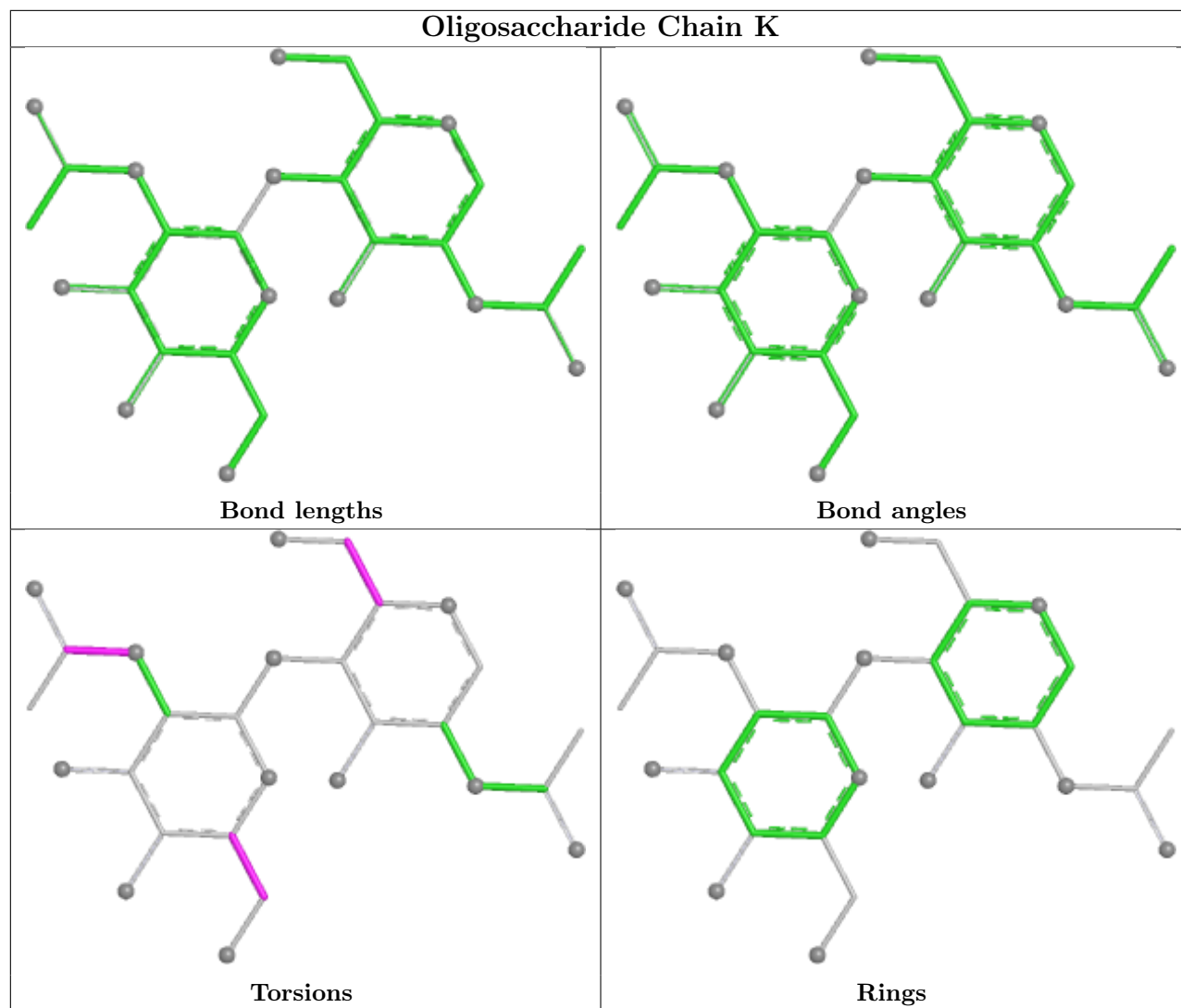
There are no ring outliers.

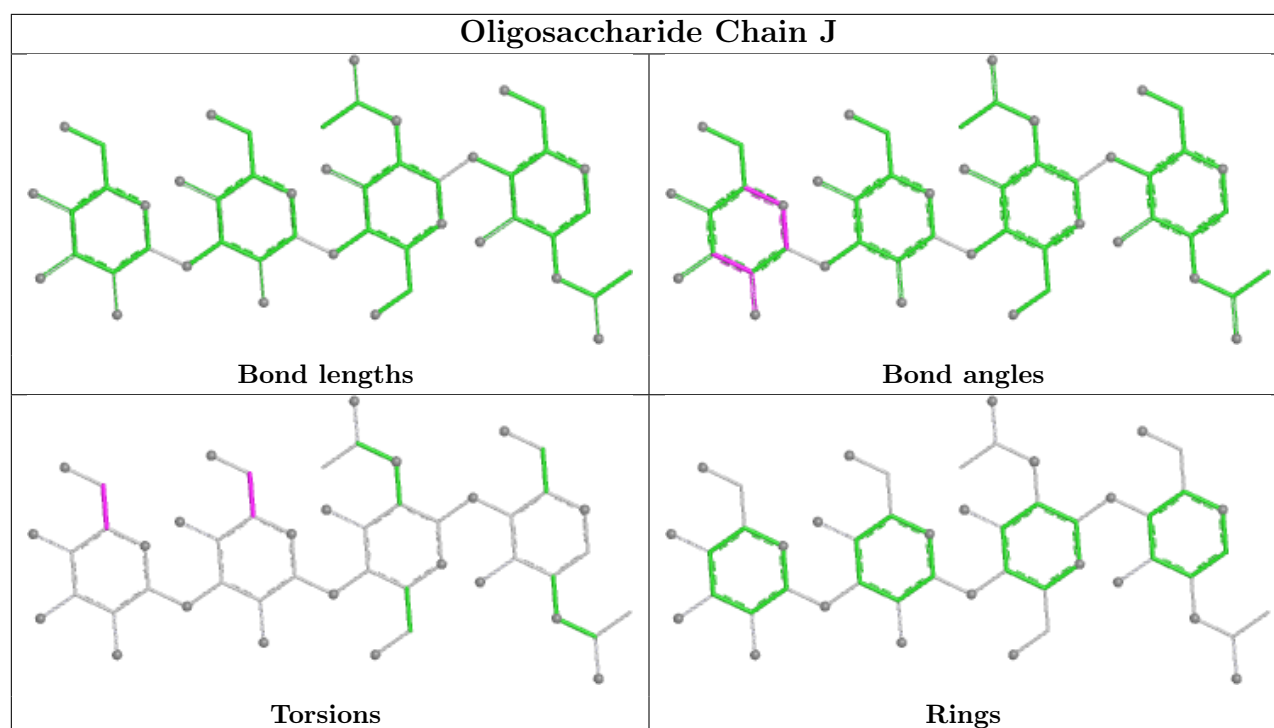
No monomer is involved in short contacts.

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 29 ligands modelled in this entry, 16 are monoatomic - leaving 13 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	$\# Z > 2$
8	SO4	A	508	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	C	502	-	4,4,4	0.24	0	6,6,6	0.09	0
12	I7R	B	2005	10	34,34,34	1.10	2 (5%)	44,47,47	1.05	2 (4%)
8	SO4	C	509	-	4,4,4	0.22	0	6,6,6	0.10	0
8	SO4	A	501	-	4,4,4	0.25	0	6,6,6	0.07	0
8	SO4	A	507	-	4,4,4	0.24	0	6,6,6	0.10	0
11	NAG	D	2004	2	14,14,15	0.35	0	17,19,21	0.60	1 (5%)
12	I7R	D	2006	10	34,34,34	1.09	2 (5%)	44,47,47	0.96	1 (2%)
8	SO4	L	301	-	4,4,4	0.24	0	6,6,6	0.09	0
8	SO4	A	502	-	4,4,4	0.24	0	6,6,6	0.08	0
11	NAG	B	2004	2	14,14,15	0.33	0	17,19,21	0.69	1 (5%)

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
8	SO4	C	503	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	C	501	-	4,4,4	0.23	0	6,6,6	0.08	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
12	I7R	D	2006	10	-	4/18/49/49	0/4/4/4
12	I7R	B	2005	10	-	4/18/49/49	0/4/4/4
11	NAG	D	2004	2	-	2/6/23/26	0/1/1/1
11	NAG	B	2004	2	-	2/6/23/26	0/1/1/1

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
12	B	2005	I7R	C6-N3	2.83	1.34	1.27
12	D	2006	I7R	C6-N3	2.82	1.34	1.27
12	D	2006	I7R	O1-C14	-2.50	1.43	1.46
12	B	2005	I7R	O1-C14	-2.44	1.43	1.46

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
11	B	2004	NAG	C1-O5-C5	2.45	115.47	112.19
12	D	2006	I7R	C14-C15-C13	2.23	102.81	100.82
12	B	2005	I7R	C10-C13-N4	2.20	125.55	120.74
12	B	2005	I7R	C14-C15-C13	2.04	102.64	100.82
11	D	2004	NAG	C1-O5-C5	2.01	114.88	112.19

There are no chirality outliers.

All (12) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
12	B	2005	I7R	C15-C14-C16-N5
12	B	2005	I7R	O1-C14-C16-N5
12	D	2006	I7R	O1-C14-C16-N5
11	B	2004	NAG	O5-C5-C6-O6
11	B	2004	NAG	C4-C5-C6-O6

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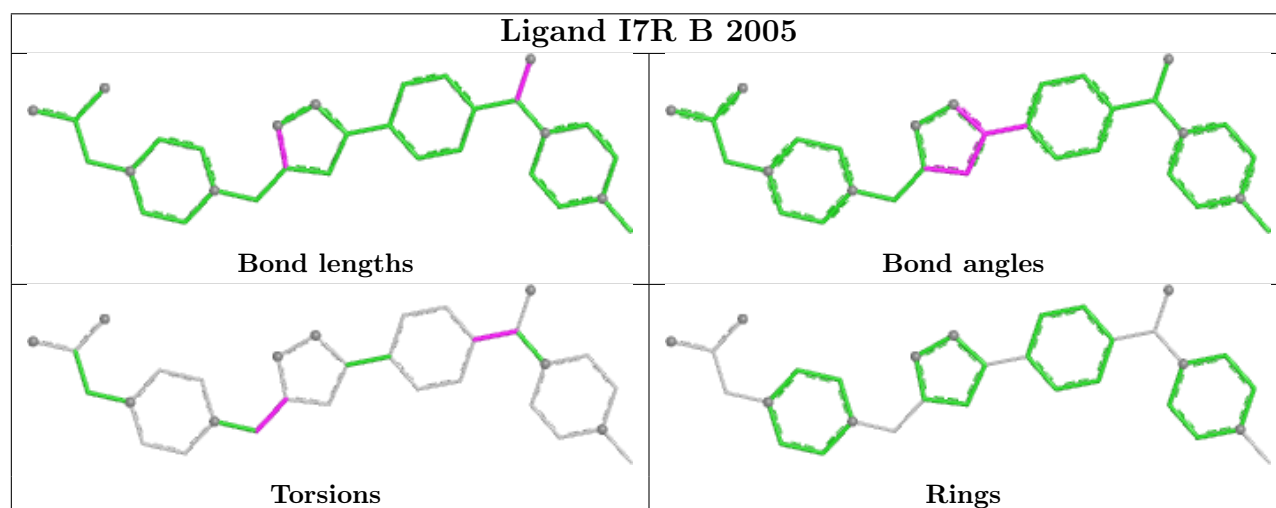
Mol	Chain	Res	Type	Atoms
11	D	2004	NAG	O5-C5-C6-O6
11	D	2004	NAG	C4-C5-C6-O6
12	B	2005	I7R	N3-C6-C7-C12
12	B	2005	I7R	N3-C6-C7-C8
12	D	2006	I7R	N3-C6-C7-C12
12	D	2006	I7R	N3-C6-C7-C8
12	D	2006	I7R	C15-C14-C16-N5

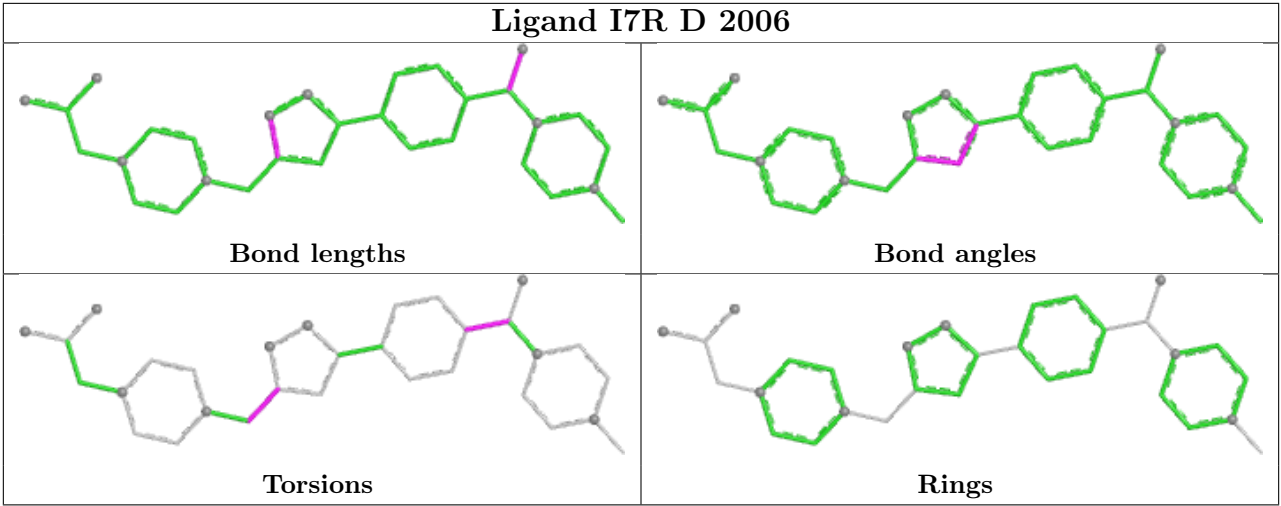
There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
12	D	2006	I7R	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 all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.





5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

The following chains have linkage breaks:

Mol	Chain	Number of breaks
3	H	1

All chain breaks are listed below:

Model	Chain	Residue-1	Atom-1	Residue-2	Atom-2	Distance (Å)
1	H	134:CYS	C	138:THR	N	6.94

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	454/454 (100%)	-0.19	3 (0%) 84 83	24, 43, 61, 76	4 (0%)
1	C	453/454 (99%)	0.41	10 (2%) 62 61	26, 64, 89, 111	4 (0%)
2	B	466/471 (98%)	0.39	24 (5%) 34 31	21, 66, 142, 157	5 (1%)
2	D	471/471 (100%)	0.88	27 (5%) 30 28	46, 82, 117, 132	1 (0%)
3	E	214/216 (99%)	1.70	71 (33%) 1 1	82, 127, 191, 194	0
3	H	216/216 (100%)	0.83	22 (10%) 13 13	54, 90, 138, 144	0
4	F	214/214 (100%)	1.27	37 (17%) 5 5	85, 131, 189, 194	0
4	L	214/214 (100%)	0.81	15 (7%) 24 22	59, 91, 111, 130	0
All	All	2702/2710 (99%)	0.62	209 (7%) 21 19	21, 76, 163, 194	14 (0%)

All (209) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	204	ALA	4.8
4	F	133	VAL	4.6
4	F	135	PHE	4.6
4	F	132	VAL	4.6
4	L	135	PHE	4.5
3	E	147	LEU	4.4
1	A	454	VAL	4.3
3	E	144	LEU	4.3
3	E	127	VAL	4.2
3	E	145	GLY	4.1
3	E	203	VAL	4.1
3	E	199	ILE	4.1
4	F	115	VAL	4.0
4	F	117	ILE	3.9
3	E	128	TYR	3.8
3	E	184	SER	3.7

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Mol	Chain	Res	Type	RSRZ
3	H	142	VAL	3.7
2	D	178	TYR	3.6
4	F	178	THR	3.6
3	H	130	LEU	3.6
3	E	212	VAL	3.5
2	D	375	LEU	3.5
4	F	160	LEU	3.4
4	F	181	LEU	3.4
3	H	189	VAL	3.3
3	E	149	LYS	3.3
4	F	177	SER	3.2
2	D	181	LYS	3.2
3	E	195	PRO	3.2
4	F	193	THR	3.1
1	C	278[A]	HIS	3.1
3	E	168	GLY	3.1
4	F	180	THR	3.1
3	H	194	TRP	3.1
3	E	129	PRO	3.1
4	F	125	LEU	3.1
3	E	146	CYS	3.1
3	E	171	THR	3.1
3	E	201	CYS	3.0
3	E	165	LEU	3.0
4	F	136	LEU	3.0
3	E	187	VAL	3.0
4	F	118	PHE	3.0
3	E	81	LEU	2.9
3	E	130	LEU	2.9
3	E	148	VAL	2.9
3	E	132	PRO	2.9
3	E	133	VAL	2.9
1	A	217	SER	2.9
3	E	142	VAL	2.9
2	D	450	ASN	2.9
2	D	45	LEU	2.8
3	E	183	LEU	2.8
4	F	134	CYS	2.8
4	F	116	SER	2.8
4	F	196	ALA	2.8
3	E	14	PRO	2.8
3	E	189	VAL	2.8

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Mol	Chain	Res	Type	RSRZ
2	B	57	PRO	2.8
3	E	217	GLU	2.7
4	F	119	PRO	2.7
3	E	216	ILE	2.7
3	E	54	ALA	2.7
4	L	112	ALA	2.7
3	E	83	LEU	2.7
4	F	179	LEU	2.7
4	F	175	MET	2.7
2	B	77	SER	2.7
2	D	129	TRP	2.7
2	B	4	ILE	2.7
4	F	205	ILE	2.7
2	D	212	VAL	2.6
3	E	45	LEU	2.6
3	E	194	TRP	2.6
3	H	217	GLU	2.6
2	D	41	LYS	2.6
2	B	41	LYS	2.6
3	E	214	LYS	2.6
2	D	389	LEU	2.6
2	D	188	PHE	2.6
4	L	146	VAL	2.6
2	B	378	GLU	2.5
2	B	178	TYR	2.5
3	E	104	TYR	2.5
3	E	37	VAL	2.5
3	H	212	VAL	2.5
3	H	131	ALA	2.5
2	B	464	PRO	2.5
2	D	394	THR	2.5
3	E	167	SER	2.5
3	E	200	THR	2.5
1	C	340	LEU	2.5
2	B	44	LEU	2.5
4	F	208	SER	2.5
2	B	26	CYS	2.5
3	E	175	VAL	2.5
2	B	76	ASP	2.5
4	F	163	TRP	2.4
3	E	155	PRO	2.4
3	H	132	PRO	2.4

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Mol	Chain	Res	Type	RSRZ
3	E	18	VAL	2.4
2	D	467	LEU	2.4
3	E	20	LEU	2.4
2	B	129	TRP	2.4
4	L	174	SER	2.4
3	H	216	ILE	2.4
3	H	206	PRO	2.4
3	E	36	TRP	2.4
3	E	51	ILE	2.4
4	L	158	GLY	2.4
2	B	375	LEU	2.4
2	B	466	TRP	2.4
4	F	159	VAL	2.4
2	D	469	SER	2.4
3	H	190	THR	2.3
3	E	12	VAL	2.3
3	H	133	VAL	2.3
3	H	177	GLN	2.3
4	L	133	VAL	2.3
4	L	83	PHE	2.3
4	F	87	TYR	2.3
2	B	38	CYS	2.3
3	H	138	THR	2.3
3	H	144	LEU	2.3
2	D	404	ARG	2.3
4	F	207	LYS	2.3
3	E	117	VAL	2.3
4	L	118	PHE	2.3
2	D	391	ILE	2.3
3	H	208	SER	2.3
3	E	60	TYR	2.3
4	F	91	TYR	2.3
2	D	471	CYS	2.3
3	H	199	ILE	2.3
3	E	174	ALA	2.3
3	H	165	LEU	2.3
4	F	169	LYS	2.3
3	E	29	ILE	2.3
2	D	372	ALA	2.3
3	E	143	THR	2.2
1	C	156	VAL	2.2
2	B	19	VAL	2.2

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Mol	Chain	Res	Type	RSRZ
2	D	112	VAL	2.2
4	F	209	PHE	2.2
4	L	11	MET	2.2
1	C	76	THR	2.2
3	E	103	TYR	2.2
4	F	204	PRO	2.2
2	B	434	ASP	2.2
3	E	16	ALA	2.2
2	B	17	LEU	2.2
2	B	92	LEU	2.2
3	E	160	TRP	2.2
4	L	101	GLY	2.2
2	D	147	SER	2.2
3	E	141	SER	2.2
4	F	161	ASN	2.2
2	B	16	CYS	2.2
2	D	72	LYS	2.2
2	B	33	LEU	2.2
4	F	36	LEU	2.2
3	E	88	SER	2.2
3	H	195	PRO	2.2
2	B	446	HIS	2.2
4	L	137	ASN	2.2
2	D	138	LEU	2.2
2	B	2	PRO	2.1
1	C	261	SER	2.1
2	B	10	VAL	2.1
2	D	207	VAL	2.1
3	E	219	ARG	2.1
3	E	173	PRO	2.1
3	E	30	LYS	2.1
1	C	269	ILE	2.1
4	L	160	LEU	2.1
4	L	120	PRO	2.1
2	B	72	LYS	2.1
3	E	87	THR	2.1
3	E	182	THR	2.1
4	F	20	SER	2.1
4	F	176	SER	2.1
1	C	78	ASN	2.1
1	C	79	VAL	2.1
3	E	48	ILE	2.1

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Mol	Chain	Res	Type	RSRZ
3	E	4	LEU	2.1
2	D	177	CYS	2.1
1	A	61	GLU	2.1
4	F	148	TRP	2.1
2	D	410	LYS	2.1
3	H	182	THR	2.1
2	D	102	ILE	2.1
3	E	185	SER	2.1
1	C	453	VAL	2.1
2	D	397	PHE	2.1
3	E	64	PHE	2.1
3	E	181	TYR	2.1
3	E	120	ALA	2.1
3	E	91	THR	2.0
2	D	131	ILE	2.0
4	F	21	ILE	2.0
3	E	119	SER	2.0
4	L	116	SER	2.0
1	C	116	LEU	2.0
3	E	176	LEU	2.0
4	F	96	TYR	2.0
3	H	207	ALA	2.0
3	H	147	LEU	2.0
4	L	145	ASN	2.0
3	E	94	TYR	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 ⓘ

SUGAR-RSR INFOmissingINFO

6.4 Ligands ⓘ

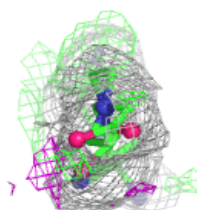
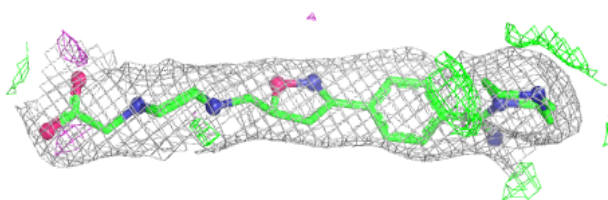
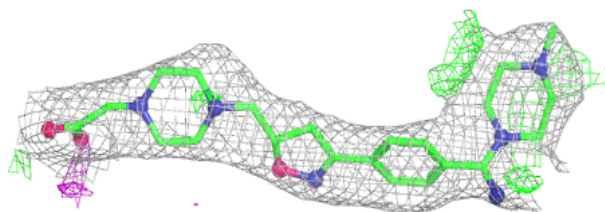
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists the number of atoms with occupancy less than 0.9.

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
11	NAG	D	2004	14/15	0.61	0.15	96,96,96,96	0
11	NAG	B	2004	14/15	0.68	0.14	102,102,102,102	0
8	SO4	C	502	5/5	0.75	0.19	84,84,84,84	0
8	SO4	C	509	5/5	0.76	0.17	92,92,92,92	0
8	SO4	C	503	5/5	0.79	0.20	94,94,94,94	0
8	SO4	A	507	5/5	0.81	0.28	70,70,70,70	0
8	SO4	C	501	5/5	0.82	0.24	76,76,76,76	0
8	SO4	A	508	5/5	0.84	0.20	68,68,68,68	0
12	I7R	D	2006	31/31	0.85	0.15	69,69,69,69	0
13	CL	D	2005	1/1	0.85	0.14	89,89,89,89	0
8	SO4	A	501	5/5	0.89	0.22	56,56,56,56	0
8	SO4	L	301	5/5	0.89	0.16	77,77,77,77	0
8	SO4	A	502	5/5	0.90	0.10	56,56,56,56	0
12	I7R	B	2005	31/31	0.90	0.11	46,46,46,46	0
9	CA	C	505	1/1	0.92	0.09	94,94,94,94	0
13	CL	C	504	1/1	0.94	0.09	68,68,68,68	0
10	MN	D	2002	1/1	0.94	0.10	73,73,73,73	0
10	MN	B	2002	1/1	0.96	0.19	64,64,64,64	0
10	MN	D	2001	1/1	0.96	0.07	64,64,64,64	0
9	CA	A	503	1/1	0.96	0.04	48,48,48,48	0
9	CA	A	504	1/1	0.97	0.04	40,40,40,40	0
9	CA	C	506	1/1	0.97	0.05	75,75,75,75	0
9	CA	C	507	1/1	0.97	0.04	66,66,66,66	0
10	MN	B	2001	1/1	0.98	0.03	35,35,35,35	0
10	MN	D	2003	1/1	0.98	0.11	62,62,62,62	0
9	CA	A	505	1/1	0.98	0.04	38,38,38,38	0
9	CA	C	508	1/1	0.98	0.04	59,59,59,59	0
10	MN	B	2003	1/1	0.99	0.10	42,42,42,42	0
9	CA	A	506	1/1	0.99	0.04	38,38,38,38	0

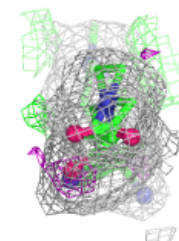
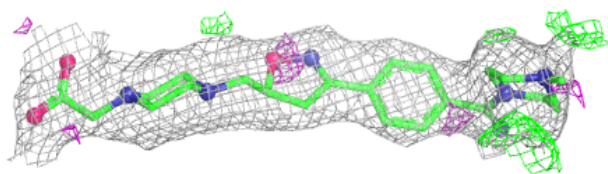
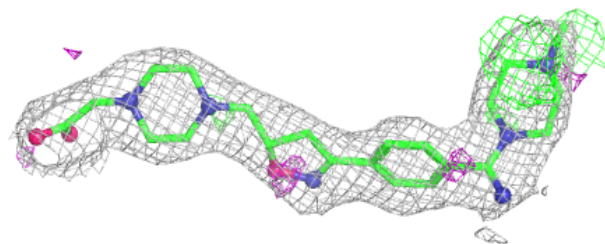
The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around I7R D 2006:

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

**Electron density around I7R B 2005:**

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



6.5 Other polymers [i](#)

There are no such residues in this entry.