



Full wwPDB X-ray Structure Validation Report ⓘ

Apr 28, 2025 – 07:13 PM EDT

PDB ID : 3T3P / pdb_00003t3p
Title : A Novel High Affinity Integrin α IIb β 3 Receptor Antagonist That Unexpectedly Displaces Mg^{2+} from the β 3 MIDAS
Authors : Zhu, J.; Zhu, J.; Springer, T.A.
Deposited on : 2011-07-25
Resolution : 2.20 Å (reported)

This is a Full wwPDB X-ray Structure Validation Report for a publicly released PDB entry.

We welcome your comments at validation@mail.wwpdb.org

A user guide is available at

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The 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 Phenix2.0rc1
Mogul : 2022.3.0, CSD as543be (2022)
Xtriage (Phenix) : 2.0rc1
EDS : 3.0
Percentile statistics : 20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4 : 9.0.006 (Gargrove)
Density-Fitness : 1.0.12
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.43.1

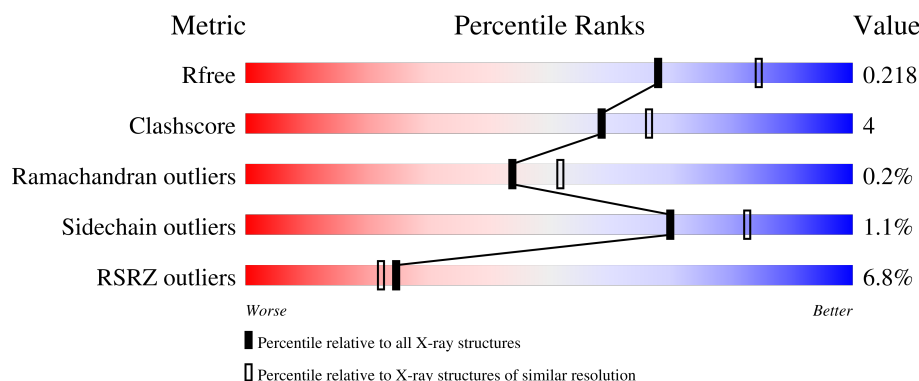
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 Å.

Percentile scores (ranging between 0-100) for global validation metrics of the entry are shown in the following graphic. The table shows the number of entries on which the scores are based.



Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	5791 (2.20-2.20)
Clashscore	180529	6634 (2.20-2.20)
Ramachandran outliers	177936	6560 (2.20-2.20)
Sidechain outliers	177891	6561 (2.20-2.20)
RSRZ outliers	164620	5791 (2.20-2.20)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments 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	457	<div> <div>93%</div> <div>5%</div> </div>
1	C	457	<div> <div>91%</div> <div>7%</div> </div>
2	B	472	<div> <div>4%</div> <div>87%</div> <div>11%</div> </div>
2	D	472	<div> <div>4%</div> <div>90%</div> <div>9%</div> </div>
3	E	221	<div> <div>33%</div> <div>79%</div> <div>18%</div> </div>

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Mol	Chain	Length	Quality of chain
3	H	221	<p>7% 84% 13%</p>
4	F	214	<p>21% 80% 20%</p>
4	L	214	<p>% 93% 7%</p>
5	G	5	<p>100%</p>
6	I	2	<p>100%</p>
6	K	2	<p>50% 50%</p>
7	J	4	<p>75% 25%</p>

2 Entry composition

There are 14 unique types of molecules in this entry. The entry contains 22411 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	8	0
			3532	2245	611	668	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	7	0
			3643	2269	622	718	34			
2	D	471	Total	C	N	O	S	3	2	0
			3642	2270	621	716	35			

- Molecule 3 is a protein called Monoclonal antibody 10E5 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 Monoclonal antibody 10E5 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 (CCD ID: 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	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 GLYCEROL (CCD ID: GOL) (formula: C₃H₈O₃).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
9	A	1	Total	C	O	0	0
			6	3	3		

- Molecule 10 is CALCIUM ION (CCD ID: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
10	A	4	Total	Ca	0	0
			4	4		
10	B	2	Total	Ca	0	0
			2	2		
10	C	4	Total	Ca	0	0
			4	4		
10	D	2	Total	Ca	0	0
			2	2		

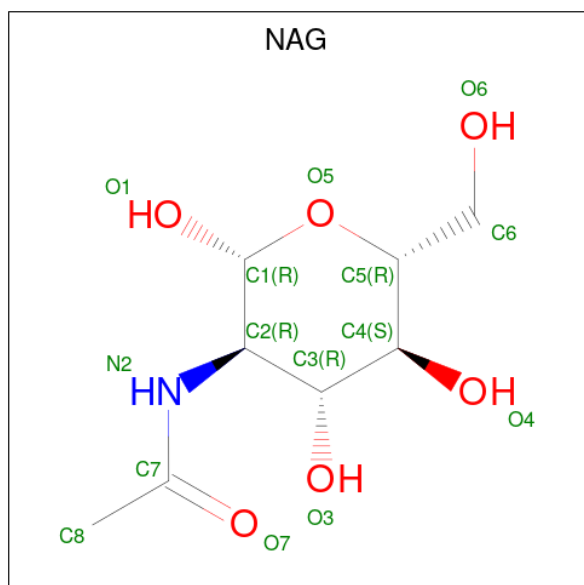
- Molecule 11 is CHLORIDE ION (CCD ID: CL) (formula: Cl).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
11	B	1	Total	Cl	0	0
			1	1		
11	C	2	Total	Cl	0	0
			2	2		
11	D	1	Total	Cl	0	0
			1	1		

- Molecule 12 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
12	B	1	Total Mg 1 1	0	0
12	D	1	Total Mg 1 1	0	0

- Molecule 13 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: $C_8H_{15}NO_6$).



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

- Molecule 14 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
14	A	463	Total O 463 463	0	0
14	B	249	Total O 249 249	0	0
14	C	274	Total O 274 274	0	0
14	D	200	Total O 200 200	0	0
14	E	17	Total O 17 17	0	0

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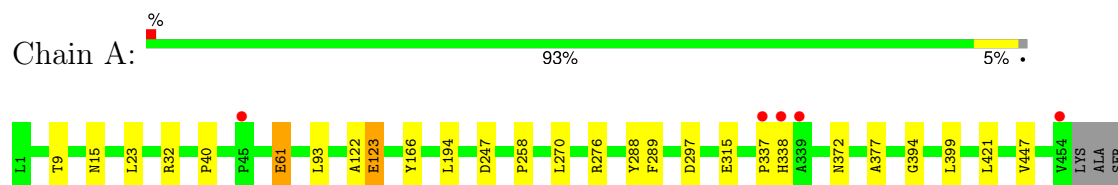
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
14	F	13	Total 13	O 13	0	0
14	H	29	Total 29	O 29	0	0
14	L	46	Total 46	O 46	0	0

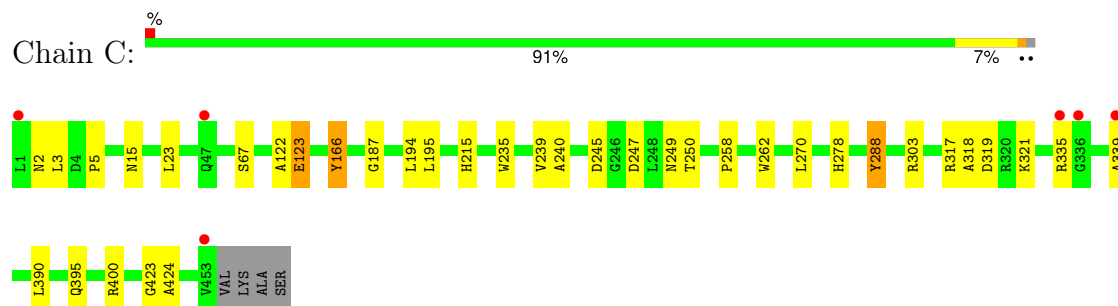
3 Residue-property plots

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.

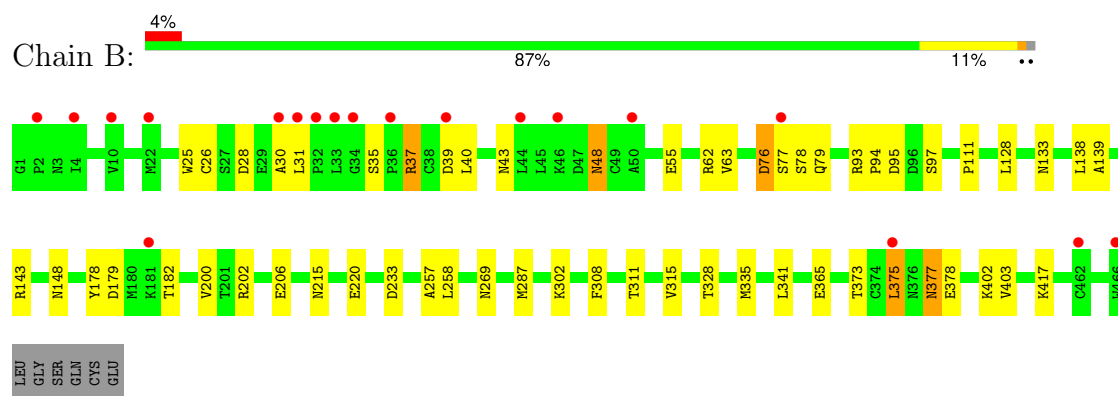
• Molecule 1: Integrin alpha-IIb



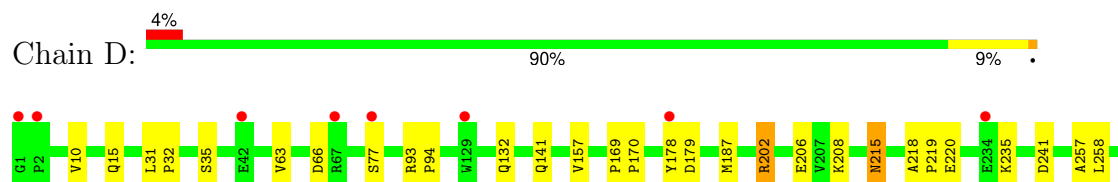
• Molecule 1: Integrin alpha-IIb

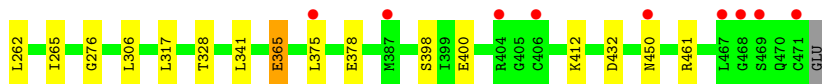


• Molecule 2: Integrin beta-3

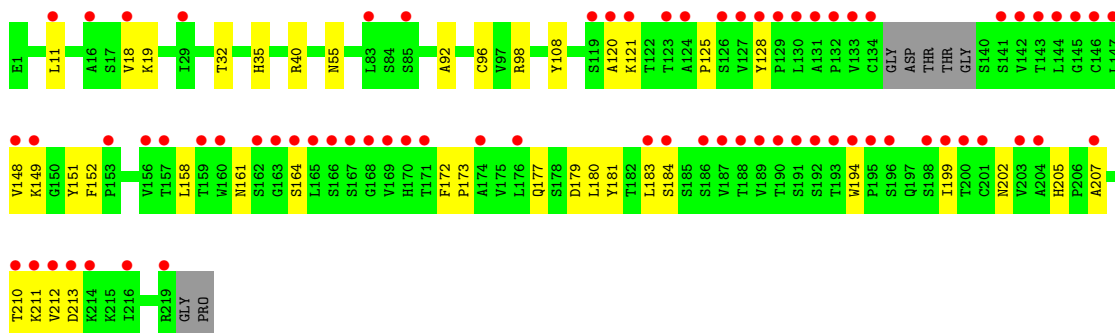
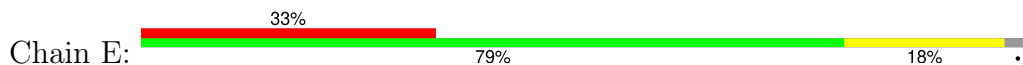


• Molecule 2: Integrin beta-3

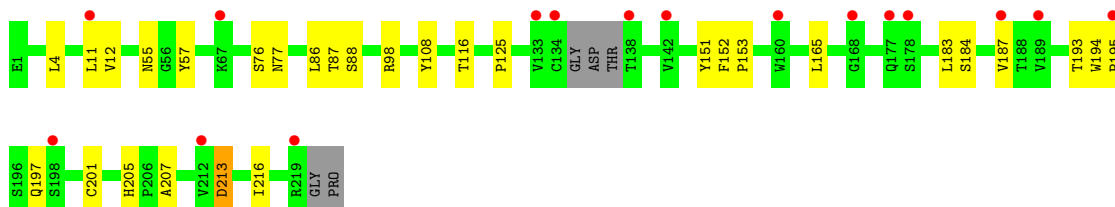
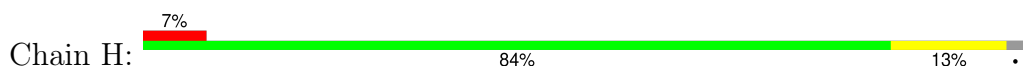




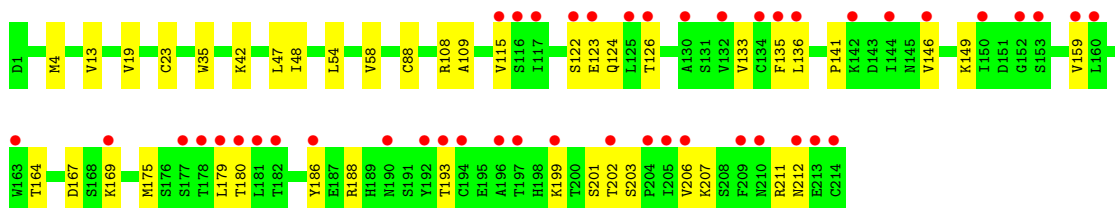
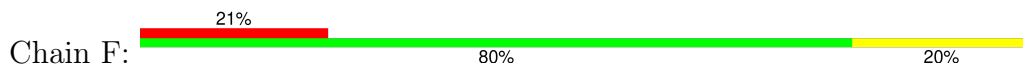
- Molecule 3: Monoclonal antibody 10E5 heavy chain



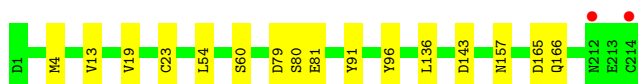
- Molecule 3: Monoclonal antibody 10E5 heavy chain



- Molecule 4: Monoclonal antibody 10E5 light chain



- Molecule 4: Monoclonal antibody 10E5 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

Chain G:  100%

HA31
HA32
BUA3
MAN4
MAN5

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

Chain I:  100%

HA31
HA32

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

Chain K:  50% 50%

HA31
HA32

- 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%

HA31
HA32
BUA3
MAN4

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, α , β , γ	259.53Å 145.26Å 104.80Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.39 – 2.20 48.39 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.3 (48.39-2.20) 99.3 (48.39-2.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.93 (at 2.20Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.7.1_743)	Depositor
R, R_{free}	0.189 , 0.220 0.182 , 0.218	Depositor DCC
R_{free} test set	991 reflections (0.50%)	wwPDB-VP
Wilson B-factor (Å ²)	33.8	Xtriage
Anisotropy	0.000	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.33 , 46.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	22411	wwPDB-VP
Average B, all atoms (Å ²)	41.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.14% 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: CA, SO4, BMA, GOL, NAG, MAN, CL, MG

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	0.47	0/3647	0.71	0/4969
1	C	0.39	0/3605	0.69	0/4912
2	B	0.41	0/3716	0.72	1/5037 (0.0%)
2	D	0.37	0/3714	0.69	1/5036 (0.0%)
3	E	0.28	0/1673	0.65	0/2290
3	H	0.30	0/1684	0.64	0/2305
4	F	0.28	0/1673	0.63	0/2269
4	L	0.31	0/1673	0.63	0/2269
All	All	0.38	0/21385	0.68	2/29087 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	79	GLN	N-CA-C	-5.88	106.35	112.93
2	D	265	ILE	CB-CA-C	-5.14	104.74	110.96

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	3532	0	3383	15	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	C	3502	0	3334	20	0
2	B	3643	0	3566	32	0
2	D	3642	0	3558	32	0
3	E	1631	0	1590	30	0
3	H	1642	0	1600	19	0
4	F	1637	0	1553	28	0
4	L	1637	0	1553	9	0
5	G	61	0	52	0	0
6	I	28	0	25	0	0
6	K	28	0	25	2	0
7	J	50	0	43	0	0
8	A	15	0	0	1	0
8	C	15	0	0	0	0
8	L	5	0	0	0	0
9	A	6	0	8	0	0
10	A	4	0	0	0	0
10	B	2	0	0	0	0
10	C	4	0	0	0	0
10	D	2	0	0	0	0
11	B	1	0	0	0	0
11	C	2	0	0	0	0
11	D	1	0	0	0	0
12	B	1	0	0	0	0
12	D	1	0	0	0	0
13	B	14	0	13	0	0
13	D	14	0	13	0	0
14	A	463	0	0	4	0
14	B	249	0	0	6	0
14	C	274	0	0	0	0
14	D	200	0	0	2	0
14	E	17	0	0	0	0
14	F	13	0	0	0	0
14	H	29	0	0	0	0
14	L	46	0	0	1	0
All	All	22411	0	20316	180	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 4.

All (180) 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)
8:A:460:SO4:O4	14:A:691:HOH:O	2.14	0.65
1:A:122:ALA:O	1:A:123:GLU:HB2	1.99	0.62
2:B:202:ARG:NH2	2:B:206:GLU:OE2	2.33	0.61
2:D:157:VAL:HG12	2:D:187[B]:MET:HE1	1.82	0.60
3:E:202:ASN:HA	3:E:213:ASP:HB3	1.83	0.60
2:D:178:TYR:CG	2:D:179:ASP:N	2.70	0.59
2:D:375:LEU:O	2:D:378:GLU:HG2	2.03	0.59
3:H:12:VAL:HG21	3:H:86:LEU:HD13	1.84	0.59
4:F:201:SER:OG	4:F:203:SER:O	2.19	0.59
3:H:87:THR:HG22	3:H:88:SER:N	2.19	0.57
1:C:122:ALA:O	1:C:123:GLU:HB2	2.04	0.57
2:D:400:GLU:HB2	6:K:1:NAG:H83	1.86	0.56
1:A:337:PRO:O	1:A:338:HIS:CG	2.59	0.56
3:E:173:PRO:HD3	4:F:164:THR:HG22	1.88	0.56
4:F:193:THR:HG23	4:F:206:VAL:HG13	1.89	0.55
2:D:257:ALA:O	2:D:258:LEU:HB2	2.08	0.54
1:A:194:LEU:HD12	1:A:194:LEU:C	2.32	0.54
2:D:235:LYS:HE3	2:D:276:GLY:O	2.08	0.54
4:F:4:MET:HE3	4:F:23:CYS:SG	2.49	0.53
3:H:4:LEU:HD12	3:H:4:LEU:N	2.24	0.53
3:E:177:GLN:N	3:E:180:LEU:O	2.37	0.53
2:B:62:ARG:HD3	14:B:1066:HOH:O	2.09	0.53
2:D:202:ARG:NH2	2:D:206:GLU:OE2	2.39	0.53
2:B:26:CYS:O	2:B:37:ARG:NH1	2.42	0.53
3:H:194:TRP:CG	3:H:195:PRO:HA	2.44	0.52
3:E:125:PRO:HB2	3:E:148:VAL:HG13	1.92	0.52
3:E:98:ARG:HG3	3:E:108:TYR:HB2	1.91	0.52
4:F:159:VAL:HG22	4:F:179:LEU:HD13	1.91	0.52
4:F:141:PRO:HD3	4:F:199:LYS:HD3	1.93	0.51
3:H:193:THR:O	3:H:197:GLN:N	2.35	0.51
1:A:247:ASP:C	1:A:247:ASP:OD2	2.54	0.51
1:C:2:ASN:OD1	1:C:2:ASN:N	2.42	0.51
4:L:136:LEU:HD12	4:L:136:LEU:N	2.26	0.51
1:C:194:LEU:C	1:C:194:LEU:HD12	2.36	0.51
1:C:245:ASP:OD1	1:C:250:THR:OG1	2.29	0.51
3:E:158:LEU:HD23	3:E:158:LEU:C	2.36	0.51
3:E:40:ARG:CG	3:E:92:ALA:HB2	2.41	0.51
4:F:47:LEU:HA	4:F:58:VAL:HG21	1.93	0.50
3:E:205:HIS:CE1	3:E:207:ALA:HB3	2.46	0.50
1:C:303:ARG:NH1	1:C:335:ARG:HD3	2.27	0.50
4:F:136:LEU:HD12	4:F:136:LEU:N	2.26	0.50
2:D:341:LEU:C	2:D:341:LEU:HD23	2.37	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:149:LYS:HB2	4:F:193:THR:HB	1.93	0.50
2:D:202:ARG:HD3	14:D:754:HOH:O	2.12	0.50
2:B:335:MET:HE2	14:B:518:HOH:O	2.10	0.50
3:E:149:LYS:NZ	4:F:180:THR:HG21	2.26	0.50
4:F:108:ARG:NE	4:F:109:ALA:O	2.43	0.50
2:B:93:ARG:HB2	2:B:94:PRO:HD2	1.94	0.49
3:E:183:LEU:C	3:E:183:LEU:HD23	2.37	0.49
4:L:4:MET:HE3	4:L:23:CYS:SG	2.52	0.49
3:E:120:ALA:HB2	3:E:179:ASP:HB3	1.93	0.49
4:F:167:ASP:OD1	4:F:169:LYS:HB3	2.13	0.48
3:H:125:PRO:HB3	3:H:151:TYR:HB3	1.94	0.48
2:D:77:SER:HB2	2:D:241:ASP:CG	2.38	0.48
2:D:93:ARG:HB2	2:D:94:PRO:HD2	1.95	0.48
2:D:178:TYR:CZ	2:D:179:ASP:HB3	2.48	0.48
3:E:210:THR:C	3:E:211:LYS:HG3	2.38	0.48
3:H:183:LEU:HD23	3:H:183:LEU:C	2.38	0.48
1:A:270:LEU:HD23	1:A:276:ARG:HA	1.96	0.48
3:H:55:ASN:CG	3:H:57:TYR:HD2	2.22	0.48
2:B:95:ASP:HA	2:B:403:VAL:O	2.14	0.47
2:D:306:LEU:HB3	2:D:328:THR:HG22	1.95	0.47
3:H:11:LEU:HD12	3:H:116:THR:HB	1.97	0.47
4:L:157:ASN:ND2	14:L:1197:HOH:O	2.47	0.47
1:A:15[B]:ASN:ND2	14:A:1000:HOH:O	2.34	0.47
2:D:218:ALA:HB3	2:D:219:PRO:HD3	1.95	0.47
3:H:87:THR:CG2	3:H:88:SER:N	2.76	0.47
4:F:141:PRO:CD	4:F:199:LYS:HD3	2.45	0.47
2:B:178:TYR:CG	2:B:179:ASP:N	2.83	0.47
1:A:32[A]:ARG:HD2	14:A:980:HOH:O	2.15	0.47
1:C:215:HIS:CE1	3:E:32:THR:HG22	2.50	0.47
2:D:157:VAL:CG1	2:D:187[B]:MET:HE1	2.44	0.47
4:F:206:VAL:HG12	4:F:207:LYS:N	2.29	0.46
2:B:76:ASP:OD2	2:B:76:ASP:N	2.47	0.46
2:B:133[A]:ASN:OD1	14:B:1138:HOH:O	2.21	0.46
3:E:128:TYR:CZ	4:F:124:GLN:HA	2.51	0.46
2:D:141:GLN:HG3	2:D:341:LEU:HD21	1.97	0.46
2:D:365:GLU:OE2	2:D:412:LYS:NZ	2.48	0.46
2:B:375:LEU:HB2	14:B:932:HOH:O	2.15	0.46
1:C:122:ALA:O	1:C:123:GLU:CB	2.63	0.46
4:L:79:ASP:OD1	4:L:80:SER:N	2.48	0.46
1:A:315:GLU:OE2	14:A:532:HOH:O	2.21	0.46
2:D:398:SER:OG	6:K:1:NAG:O7	2.26	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:F:35:TRP:CZ3	4:F:88:CYS:HB3	2.51	0.46
2:B:138:LEU:HA	2:B:341:LEU:CD1	2.45	0.46
2:D:63:VAL:HG11	2:D:66:ASP:HB2	1.98	0.46
4:F:115:VAL:HG12	4:F:207:LYS:HG3	1.97	0.46
3:H:201:CYS:O	3:H:213:ASP:HA	2.15	0.46
1:A:258:PRO:HA	1:A:289:PHE:O	2.15	0.45
2:B:97:SER:HB3	2:B:402:LYS:HG2	1.98	0.45
1:C:318:ALA:O	1:C:319:ASP:HB2	2.17	0.45
1:C:390:LEU:HD12	1:C:390:LEU:N	2.31	0.45
2:B:378:GLU:HB3	14:B:932:HOH:O	2.15	0.45
3:E:125:PRO:HB2	3:E:148:VAL:CG1	2.46	0.45
2:B:93:ARG:HB2	2:B:94:PRO:CD	2.47	0.45
3:E:152:PHE:CD2	3:E:152:PHE:C	2.94	0.45
4:L:165:ASP:O	4:L:166:GLN:C	2.58	0.45
3:E:194:TRP:CD1	3:E:199:ILE:HD12	2.52	0.45
1:A:9:THR:HB	1:A:447:VAL:HB	1.98	0.45
3:E:205:HIS:HB3	3:E:210:THR:CG2	2.47	0.45
2:B:233:ASP:OD1	2:B:302:LYS:HD2	2.17	0.45
3:E:205:HIS:HB3	3:E:210:THR:HG22	1.99	0.45
3:E:212:VAL:HG12	3:E:213:ASP:N	2.31	0.44
2:B:31:LEU:CD2	2:B:35:SER:HB2	2.47	0.44
2:D:10:VAL:HA	2:D:15:GLN:NE2	2.32	0.44
1:A:394:GLY:HA2	1:A:399:LEU:HD23	1.99	0.44
4:F:122:SER:O	4:F:126:THR:HG23	2.17	0.44
1:C:278[A]:HIS:CE1	1:C:339:ALA:HB1	2.52	0.44
3:E:213:ASP:N	3:E:213:ASP:OD1	2.51	0.44
2:B:39:ASP:OD2	2:B:43:ASN:ND2	2.51	0.44
3:E:172:PHE:CD1	4:F:164:THR:HG23	2.53	0.44
4:F:186:TYR:CE2	4:F:211:ARG:HG3	2.53	0.44
4:L:54:LEU:HD21	4:L:60:SER:HA	1.99	0.44
1:C:317:ARG:HB2	1:C:321:LYS:HB2	1.99	0.44
2:B:39:ASP:OD2	2:B:40:LEU:N	2.51	0.44
4:F:133:VAL:HG11	4:F:135:PHE:CZ	2.52	0.44
2:B:373:THR:CG2	2:B:377:ASN:HA	2.49	0.43
4:F:123:GLU:O	4:F:126:THR:OG1	2.35	0.43
2:B:220:GLU:HA	2:B:220:GLU:OE1	2.17	0.43
1:C:166:TYR:O	1:C:187:GLY:HA3	2.18	0.43
2:D:132:GLN:OE1	2:D:208:LYS:HG2	2.18	0.43
3:H:165:LEU:HD21	3:H:187:VAL:HG21	2.00	0.43
2:B:308:PHE:CE2	2:B:328:THR:HG21	2.54	0.43
2:D:450:ASN:O	2:D:450:ASN:ND2	2.51	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:H:98:ARG:HG3	3:H:108:TYR:HB2	2.00	0.43
2:B:365:GLU:H	2:B:365:GLU:CD	2.26	0.43
1:C:3:LEU:O	1:C:5:PRO:HD3	2.19	0.43
3:H:194:TRP:CZ2	3:H:216:ILE:HG22	2.54	0.43
3:H:205:HIS:CE1	3:H:207:ALA:HB3	2.54	0.43
1:C:258:PRO:HB2	1:C:288:TYR:CD1	2.54	0.42
3:E:11:LEU:N	3:E:11:LEU:HD12	2.34	0.42
3:E:121:LYS:N	3:E:121:LYS:HD2	2.34	0.42
1:A:297:ASP:O	1:A:372:ASN:HB2	2.19	0.42
3:E:40:ARG:HG3	3:E:92:ALA:HB2	2.01	0.42
1:A:40:PRO:HA	1:A:93:LEU:O	2.20	0.42
1:C:247:ASP:OD2	1:C:249:ASN:HB2	2.19	0.42
3:E:18:VAL:HG22	3:E:19:LYS:N	2.34	0.42
4:F:48:ILE:CD1	4:F:54:LEU:HD23	2.50	0.42
1:A:61:GLU:H	1:A:61:GLU:CD	2.28	0.42
2:D:31:LEU:HD12	2:D:32:PRO:HD2	2.02	0.42
4:F:13:VAL:HG11	4:F:19:VAL:HG11	2.01	0.42
2:B:28:ASP:OD2	2:B:30:ALA:N	2.53	0.42
3:H:183:LEU:HD23	3:H:184:SER:N	2.35	0.42
2:D:461:ARG:NE	14:D:880:HOH:O	2.47	0.41
3:H:12:VAL:HG21	3:H:86:LEU:CD1	2.50	0.41
4:L:13:VAL:HG11	4:L:19:VAL:HG11	2.02	0.41
1:C:262:TRP:HB3	2:D:317:LEU:HD13	2.02	0.41
1:C:423:GLY:O	1:C:424:ALA:HB3	2.20	0.41
2:D:220:GLU:HA	2:D:220:GLU:OE1	2.20	0.41
4:F:202:THR:O	4:F:202:THR:HG22	2.20	0.41
4:L:81:GLU:N	4:L:81:GLU:OE1	2.54	0.41
2:B:139:ALA:HB2	2:B:200:VAL:HG11	2.02	0.41
1:C:395:GLN:OE1	1:C:400:ARG:HD3	2.21	0.41
4:F:146:VAL:HG12	4:F:175:MET:HE1	2.02	0.41
3:H:152:PHE:CD1	3:H:153:PRO:HA	2.55	0.41
1:A:377:ALA:HB2	1:A:421:LEU:HD11	2.03	0.41
4:F:186:TYR:C	4:F:188:ARG:H	2.28	0.41
2:B:77:SER:O	2:B:78:SER:OG	2.29	0.41
1:C:239:VAL:HG22	1:C:240:ALA:N	2.36	0.41
2:D:93:ARG:HB2	2:D:94:PRO:CD	2.51	0.41
2:D:169:PRO:CB	2:D:170:PRO:CD	2.99	0.41
4:F:42:LYS:N	4:F:42:LYS:HD2	2.35	0.41
3:H:76:SER:O	3:H:77:ASN:C	2.64	0.41
2:B:111:PRO:HB3	2:B:148:ASN:HB3	2.03	0.40
2:B:311:THR:O	2:B:315[B]:VAL:HG23	2.20	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:D:32:PRO:O	2:D:35:SER:HB3	2.21	0.40
3:E:183:LEU:HD23	3:E:184:SER:N	2.37	0.40
4:L:91:TYR:HB2	4:L:96:TYR:CZ	2.55	0.40
2:B:25:TRP:HB3	2:B:55:GLU:HB2	2.02	0.40
2:B:143:ARG:NH1	14:B:797:HOH:O	2.30	0.40
3:E:151:TYR:CZ	3:E:181:TYR:HB2	2.56	0.40
2:B:269:ASN:HA	2:B:287:MET:CG	2.51	0.40
2:D:341:LEU:HD23	2:D:341:LEU:O	2.21	0.40
3:E:35:HIS:O	3:E:96:CYS:HA	2.21	0.40
3:E:161:ASN:O	3:E:164:SER:OG	2.24	0.40
2:B:48:ASN:OD1	2:B:48:ASN:N	2.54	0.40
1:C:235:TRP:CZ2	1:C:270:LEU:HD11	2.56	0.40
2:D:187[A]:MET:HE3	2:D:215:ASN:HB3	2.03	0.40
2:B:257:ALA:O	2:B:258:LEU:HB2	2.22	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	460/457 (101%)	441 (96%)	18 (4%)	1 (0%)	44	52
1	C	455/457 (100%)	441 (97%)	13 (3%)	1 (0%)	44	52
2	B	471/472 (100%)	452 (96%)	17 (4%)	2 (0%)	30	34
2	D	471/472 (100%)	454 (96%)	17 (4%)	0	100	100
3	E	210/221 (95%)	193 (92%)	16 (8%)	1 (0%)	25	28
3	H	212/221 (96%)	197 (93%)	15 (7%)	0	100	100
4	F	212/214 (99%)	195 (92%)	16 (8%)	1 (0%)	25	28
4	L	212/214 (99%)	204 (96%)	8 (4%)	0	100	100
All	All	2703/2728 (99%)	2577 (95%)	120 (4%)	6 (0%)	44	52

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	123	GLU
1	C	123	GLU
2	B	375	LEU
4	F	212	ASN
2	B	377	ASN
3	E	55	ASN

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	370/364 (102%)	366 (99%)	4 (1%)	70	82
1	C	365/364 (100%)	359 (98%)	6 (2%)	58	73
2	B	419/417 (100%)	411 (98%)	8 (2%)	52	67
2	D	418/417 (100%)	413 (99%)	5 (1%)	67	80
3	E	186/190 (98%)	186 (100%)	0	100	100
3	H	187/190 (98%)	186 (100%)	1 (0%)	86	93
4	F	188/188 (100%)	188 (100%)	0	100	100
4	L	188/188 (100%)	187 (100%)	1 (0%)	86	93
All	All	2321/2318 (100%)	2296 (99%)	25 (1%)	70	82

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	23	LEU
1	A	61	GLU
1	A	166	TYR
1	A	288	TYR
2	B	37	ARG
2	B	48	ASN
2	B	63	VAL
2	B	76	ASP

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Mol	Chain	Res	Type
2	B	128	LEU
2	B	182	THR
2	B	215	ASN
2	B	417	LYS
1	C	15	ASN
1	C	23	LEU
1	C	67	SER
1	C	166	TYR
1	C	195	LEU
1	C	288	TYR
2	D	202	ARG
2	D	215	ASN
2	D	262	LEU
2	D	365	GLU
2	D	432	ASP
3	H	213	ASP
4	L	143	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (13) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	372	ASN
1	A	444	GLN
2	B	141	GLN
2	B	342	GLN
1	C	78	ASN
1	C	158	ASN
1	C	333	GLN
1	C	444	GLN
2	D	82	GLN
2	D	450	ASN
4	F	93	GLN
3	H	177	GLN
4	L	37	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	0.48	0	17,19,21	0.75	0
5	NAG	G	2	5	14,14,15	0.61	0	17,19,21	0.91	0
5	BMA	G	3	5	11,11,12	0.62	0	15,15,17	0.83	0
5	MAN	G	4	5	11,11,12	0.57	0	15,15,17	0.68	0
5	MAN	G	5	5	11,11,12	0.63	0	15,15,17	0.60	0
6	NAG	I	1	6,2	14,14,15	0.59	0	17,19,21	0.80	0
6	NAG	I	2	6	14,14,15	0.51	0	17,19,21	0.67	0
7	NAG	J	1	7,2	14,14,15	0.59	0	17,19,21	0.77	0
7	NAG	J	2	7	14,14,15	0.66	0	17,19,21	1.11	1 (5%)
7	BMA	J	3	7	11,11,12	0.67	0	15,15,17	0.75	0
7	MAN	J	4	7	11,11,12	0.60	0	15,15,17	0.76	0
6	NAG	K	1	6,2	14,14,15	0.64	0	17,19,21	0.67	0
6	NAG	K	2	6	14,14,15	0.53	0	17,19,21	0.69	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	-	0/2/19/22	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	6,2	-	0/6/23/26	0/1/1/1

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

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	J	2	NAG	C4-C3-C2	2.93	115.31	111.02

There are no chirality outliers.

All (9) torsion outliers are listed below:

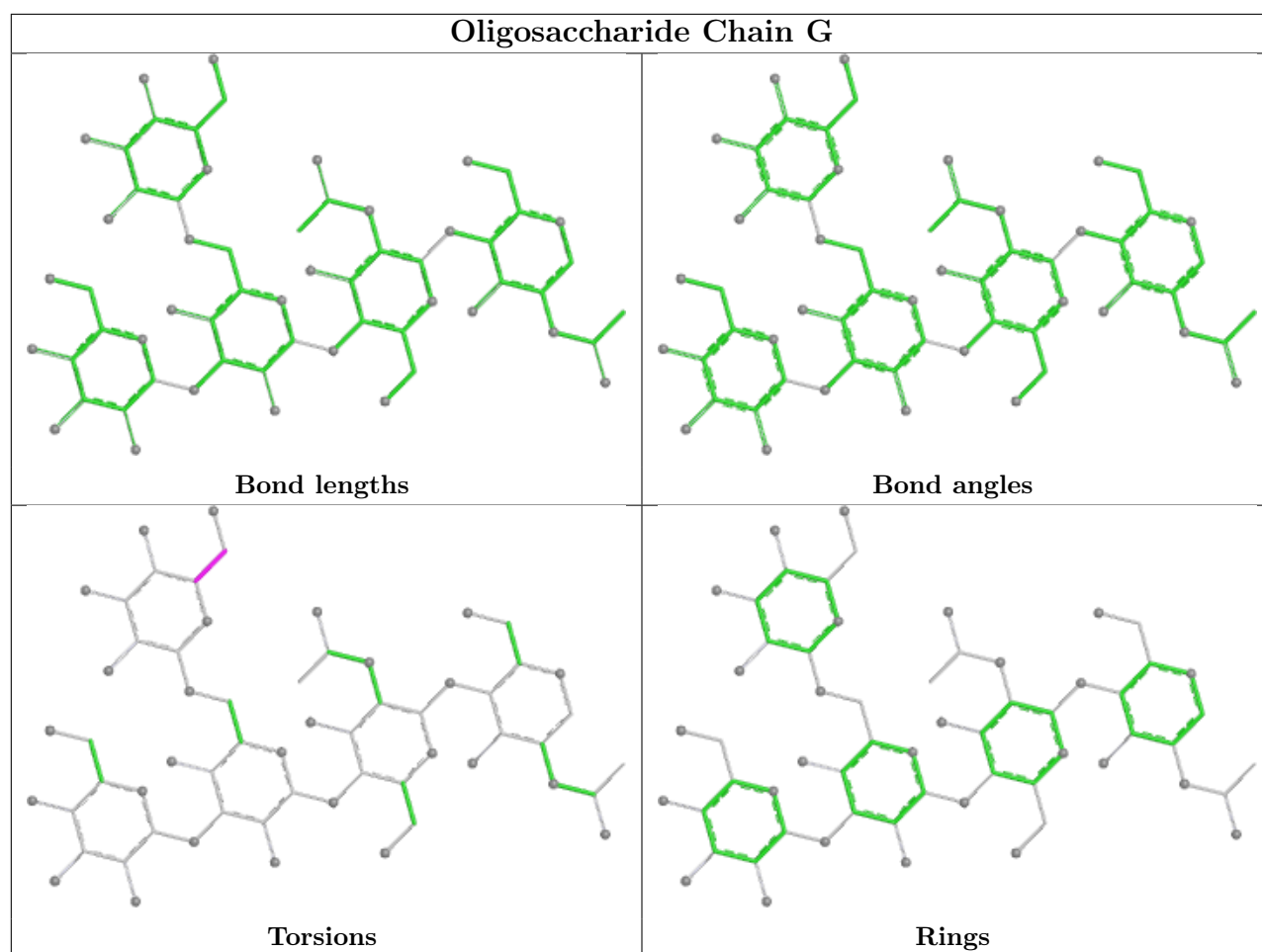
Mol	Chain	Res	Type	Atoms
6	I	2	NAG	C8-C7-N2-C2
6	I	2	NAG	O7-C7-N2-C2
6	K	2	NAG	C8-C7-N2-C2
6	K	2	NAG	O7-C7-N2-C2
6	I	2	NAG	O5-C5-C6-O6
5	G	5	MAN	O5-C5-C6-O6
7	J	1	NAG	C8-C7-N2-C2
7	J	1	NAG	O7-C7-N2-C2
6	I	2	NAG	C1-C2-N2-C7

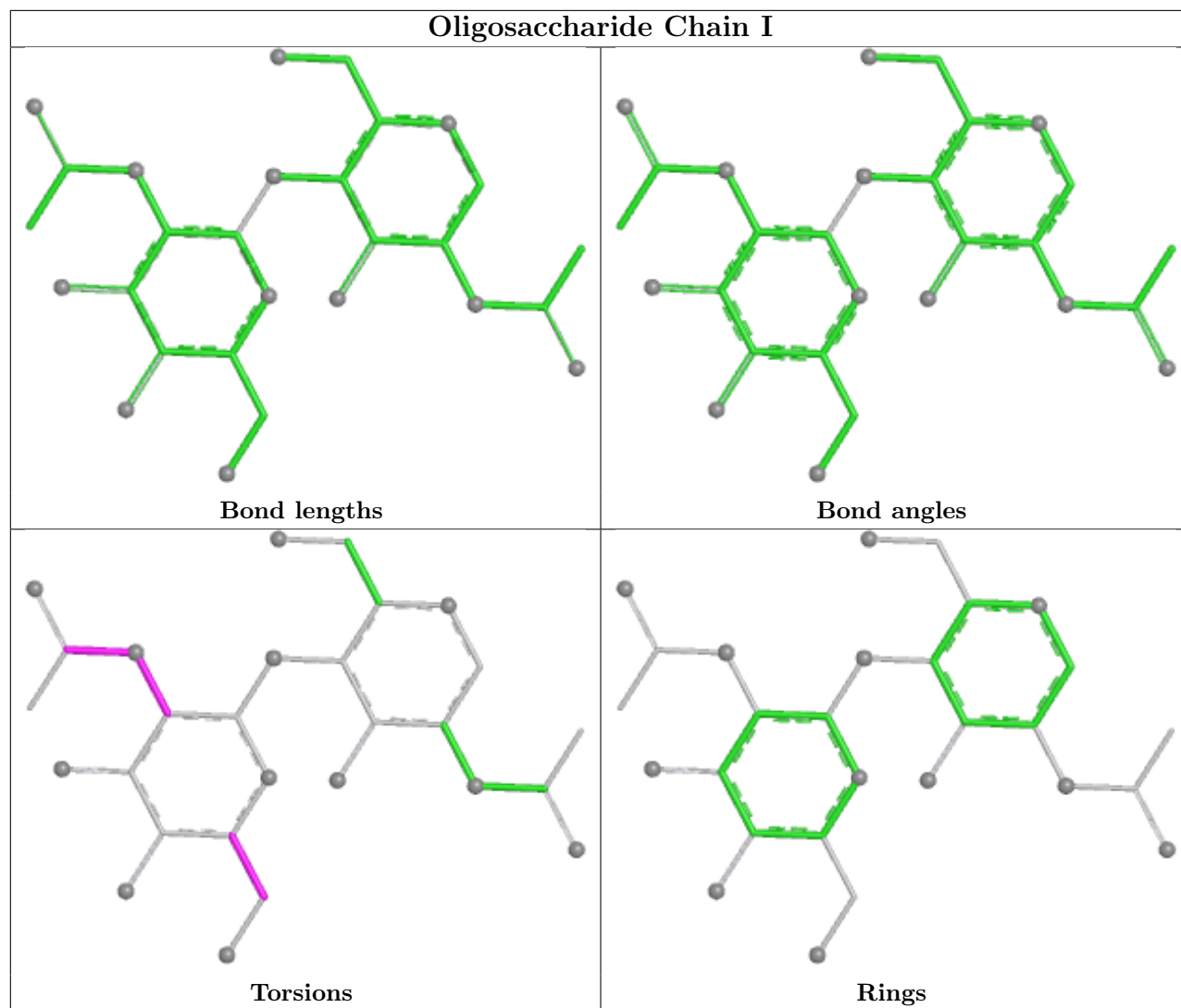
There are no ring outliers.

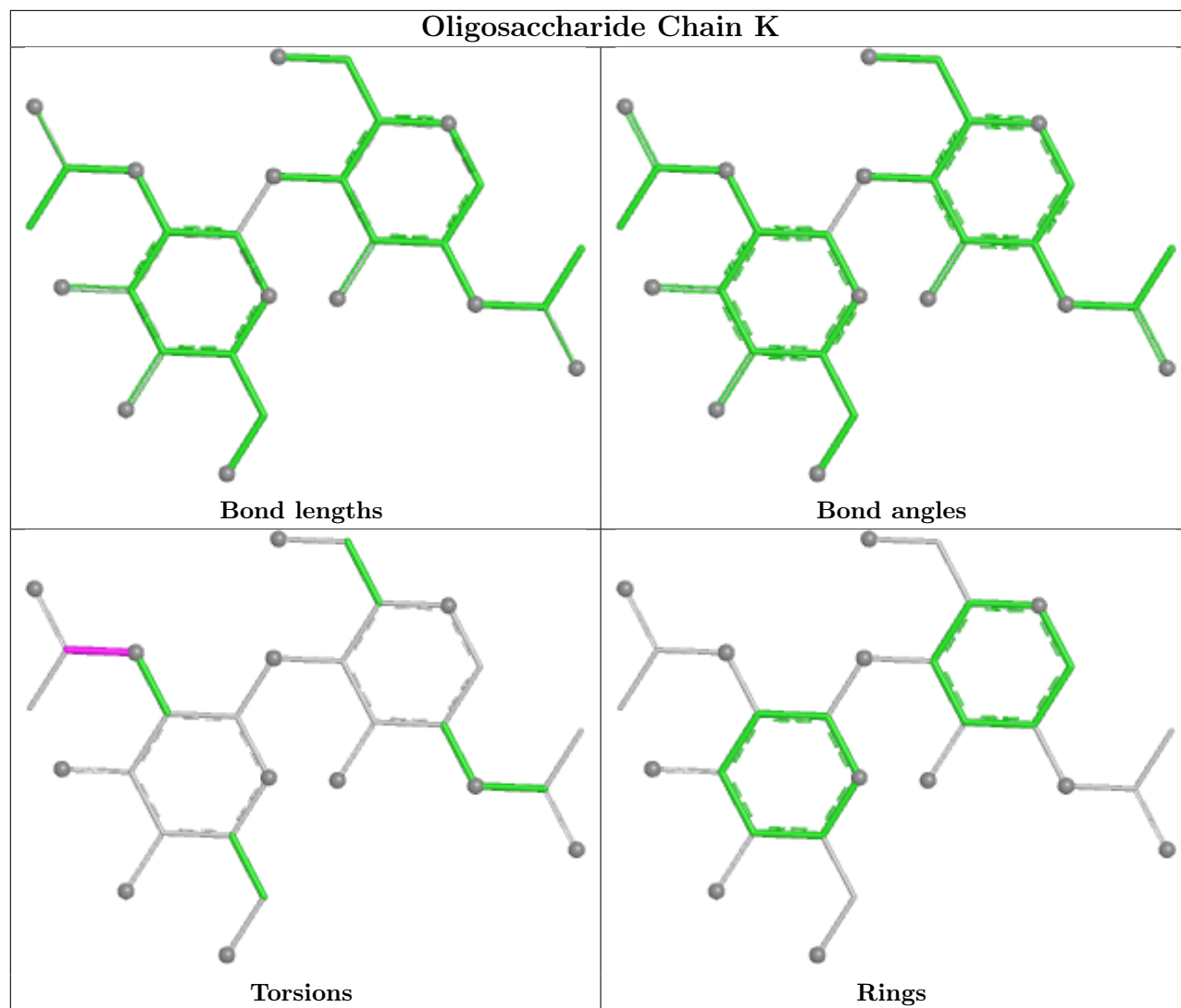
1 monomer is involved in 2 short contacts:

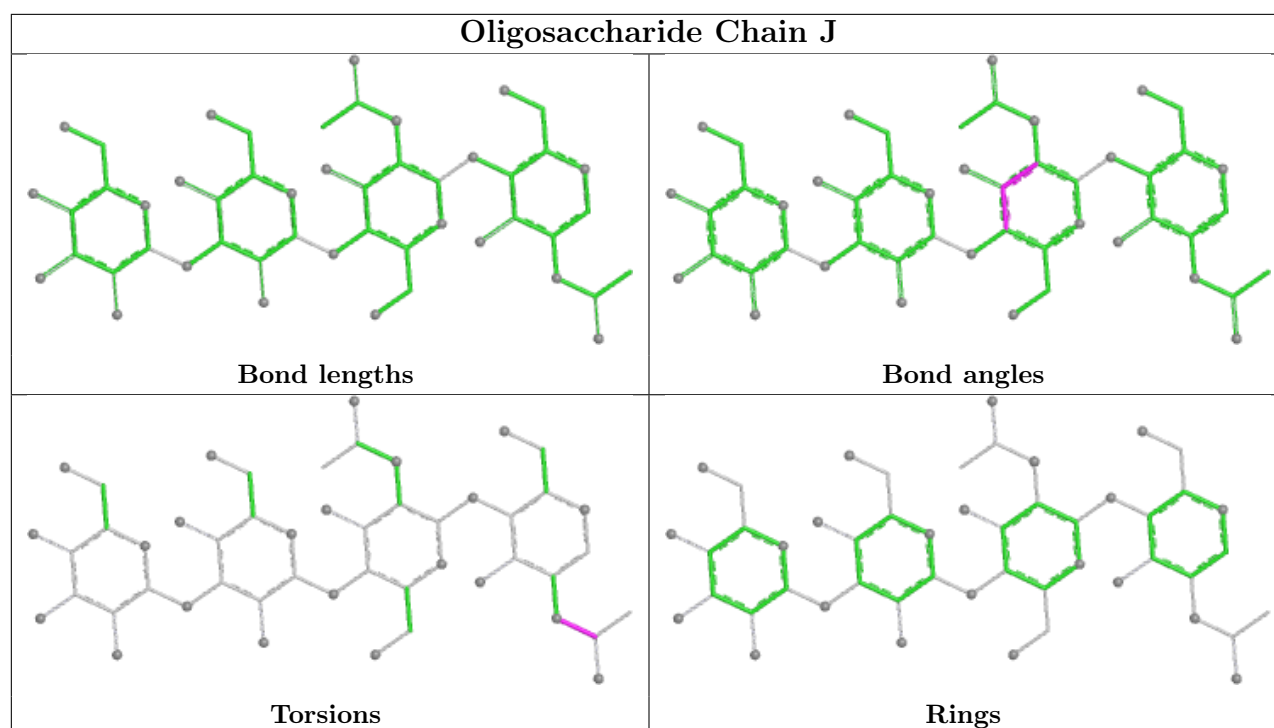
Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	K	1	NAG	2	0

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 28 ligands modelled in this entry, 18 are monoatomic - leaving 10 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	458	-	4,4,4	0.24	0	6,6,6	0.09	0
13	NAG	B	3099	2	14,14,15	0.56	0	17,19,21	0.84	1 (5%)
8	SO4	L	215	-	4,4,4	0.24	0	6,6,6	0.07	0
8	SO4	C	460	-	4,4,4	0.24	0	6,6,6	0.12	0
8	SO4	C	458	-	4,4,4	0.28	0	6,6,6	0.14	0
9	GOL	A	461	-	5,5,5	0.36	0	5,5,5	0.32	0
8	SO4	C	459	-	4,4,4	0.26	0	6,6,6	0.08	0
13	NAG	D	3099	2	14,14,15	0.50	0	17,19,21	0.74	0
8	SO4	A	460	-	4,4,4	0.20	0	6,6,6	0.16	0
8	SO4	A	459	-	4,4,4	0.27	0	6,6,6	0.17	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
13	NAG	D	3099	2	-	0/6/23/26	0/1/1/1
9	GOL	A	461	-	-	2/4/4/4	-
13	NAG	B	3099	2	-	0/6/23/26	0/1/1/1

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
13	B	3099	NAG	C1-O5-C5	2.49	115.52	112.19

There are no chirality outliers.

All (2) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
9	A	461	GOL	O1-C1-C2-C3
9	A	461	GOL	O1-C1-C2-O2

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
8	A	460	SO4	1	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data

6.1 Protein, DNA and RNA chains

In the following table, the column labelled ‘#RSRZ > 2’ contains the number (and percentage) of RSRZ outliers, followed by percent RSRZ outliers for the chain as percentile scores relative to all X-ray entries and entries of similar resolution. The OWAB column contains the minimum, median, 95th percentile and maximum values of the occupancy-weighted average B-factor per residue. The column labelled ‘Q < 0.9’ lists the number of (and percentage) of residues with an average occupancy less than 0.9.

Mol	Chain	Analysed	<RSRZ>	#RSRZ>2	OWAB(Å ²)	Q<0.9
1	A	454/457 (99%)	-0.95	5 (1%) 77 75	3, 10, 34, 73	8 (1%)
1	C	453/457 (99%)	-0.59	6 (1%) 74 71	9, 23, 50, 77	4 (0%)
2	B	466/472 (98%)	-0.20	19 (4%) 42 38	2, 32, 90, 112	8 (1%)
2	D	471/472 (99%)	-0.21	17 (3%) 46 43	11, 33, 78, 142	3 (0%)
3	E	214/221 (96%)	1.52	73 (34%) 1 1	33, 85, 137, 155	0
3	H	216/221 (97%)	0.47	16 (7%) 22 20	16, 59, 103, 118	0
4	F	214/214 (100%)	0.99	45 (21%) 3 2	33, 81, 134, 157	1 (0%)
4	L	214/214 (100%)	0.01	2 (0%) 81 78	20, 44, 70, 95	1 (0%)
All	All	2702/2728 (99%)	-0.09	183 (6%) 25 22	2, 34, 109, 157	25 (0%)

All (183) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
3	E	212	VAL	7.3
3	E	165	LEU	7.2
1	A	454	VAL	5.2
2	B	36	PRO	5.1
3	E	147	LEU	5.0
3	E	187	VAL	4.7
3	E	134	CYS	4.7
2	B	33	LEU	4.7
3	E	127	VAL	4.6
3	E	144	LEU	4.5
3	E	142	VAL	4.5
3	E	199	ILE	4.4
2	D	471	CYS	4.4
3	E	214	LYS	4.3
3	E	160	TRP	4.2
3	E	201	CYS	4.1

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Mol	Chain	Res	Type	RSRZ
3	E	168	GLY	4.0
3	E	203	VAL	4.0
4	F	126	THR	4.0
3	E	133	VAL	3.9
3	E	189	VAL	3.9
4	F	130	ALA	3.9
3	E	163	GLY	3.8
3	H	134	CYS	3.8
3	E	216	ILE	3.7
4	F	150	ILE	3.7
4	F	125	LEU	3.7
3	E	129	PRO	3.6
3	E	145	GLY	3.6
2	B	10	VAL	3.6
3	E	128	TYR	3.6
4	F	134	CYS	3.6
4	F	197	THR	3.6
3	E	131	ALA	3.6
1	C	336	GLY	3.5
3	H	189	VAL	3.5
2	B	375	LEU	3.5
3	E	174	ALA	3.5
4	F	204	PRO	3.5
4	F	135	PHE	3.5
3	E	159	THR	3.4
3	H	177	GLN	3.4
3	E	176	LEU	3.4
3	E	194	TRP	3.4
3	E	167	SER	3.4
3	H	138	THR	3.3
1	C	1	LEU	3.3
2	D	469	SER	3.3
3	H	168	GLY	3.3
4	F	210	ASN	3.3
2	B	466	TRP	3.3
3	E	219	ARG	3.2
4	F	209	PHE	3.2
2	B	32	PRO	3.2
2	B	77	SER	3.2
1	C	453	VAL	3.2
3	E	183	LEU	3.0
4	F	152	GLY	3.0

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Mol	Chain	Res	Type	RSRZ
4	F	179	LEU	3.0
4	F	214	CYS	3.0
3	E	162	SER	3.0
3	E	16	ALA	3.0
2	D	375	LEU	3.0
3	E	148	VAL	3.0
3	E	204	ALA	3.0
4	F	117	ILE	2.9
3	H	198	SER	2.9
2	B	44	LEU	2.9
2	D	129[A]	TRP	2.9
3	E	169	VAL	2.9
3	E	149	LYS	2.9
3	E	143	THR	2.9
2	B	4	ILE	2.9
4	F	142	LYS	2.8
2	D	404	ARG	2.8
4	F	181	LEU	2.8
1	A	45	PRO	2.8
2	D	2	PRO	2.8
4	F	169	LYS	2.8
4	F	213	GLU	2.8
3	E	195	PRO	2.8
4	L	214	CYS	2.8
4	F	202	THR	2.8
2	B	31	LEU	2.8
4	L	212	ASN	2.8
2	B	2	PRO	2.7
3	H	195	PRO	2.7
3	E	120	ALA	2.7
1	A	338	HIS	2.7
3	H	133	VAL	2.7
3	E	83	LEU	2.7
3	E	130	LEU	2.7
4	F	212	ASN	2.7
1	A	339	ALA	2.7
4	F	180	THR	2.7
3	E	164	SER	2.6
3	E	186	SER	2.6
3	E	121	LYS	2.6
1	C	339	ALA	2.6
3	E	157	THR	2.6

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Mol	Chain	Res	Type	RSRZ
3	E	188	THR	2.6
2	D	406	CYS	2.6
3	H	178	SER	2.6
3	E	211	LYS	2.6
2	D	1	GLY	2.6
3	E	196	SER	2.6
3	E	166	SER	2.5
3	E	191	SER	2.5
2	B	181	LYS	2.5
4	F	199	LYS	2.5
4	F	144	ILE	2.5
4	F	116	SER	2.5
2	B	46	LYS	2.5
3	H	219	ARG	2.5
3	E	141	SER	2.5
3	E	170	HIS	2.5
2	D	178	TYR	2.4
4	F	122	SER	2.4
3	E	124	ALA	2.4
3	H	142	VAL	2.4
3	E	210	THR	2.4
2	D	77	SER	2.4
2	B	39	ASP	2.4
3	E	207	ALA	2.4
1	A	337	PRO	2.4
3	E	153	PRO	2.4
3	E	192	SER	2.4
4	F	159	VAL	2.4
3	E	123	THR	2.4
3	E	171	THR	2.4
3	E	146	CYS	2.4
3	E	18	VAL	2.3
3	E	198	SER	2.3
4	F	196	ALA	2.3
2	B	22	MET	2.3
4	F	193	THR	2.3
4	F	190	ASN	2.3
4	F	178	THR	2.3
4	F	182	THR	2.3
4	F	163	TRP	2.3
4	F	115	VAL	2.3
4	F	177	SER	2.3

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Mol	Chain	Res	Type	RSRZ
4	F	160	LEU	2.2
3	E	190	THR	2.2
3	E	29	ILE	2.2
2	D	42	GLU	2.2
2	D	467	LEU	2.2
4	F	136	LEU	2.2
3	E	193	THR	2.2
4	F	132	VAL	2.2
3	E	184	SER	2.2
1	C	335	ARG	2.2
3	E	11	LEU	2.2
3	E	132	PRO	2.2
3	E	200	THR	2.2
3	E	213	ASP	2.2
2	D	234	GLU	2.2
3	H	11	LEU	2.2
4	F	153	SER	2.1
2	D	67	ARG	2.1
2	D	450	ASN	2.1
4	F	146	VAL	2.1
2	D	468	GLY	2.1
3	E	119	SER	2.1
3	E	126	SER	2.1
1	C	47	GLN	2.1
3	H	67	LYS	2.1
2	B	30	ALA	2.1
2	D	387	MET	2.1
4	F	206	VAL	2.1
2	B	34	GLY	2.1
3	E	85	SER	2.1
2	B	462	CYS	2.1
2	B	50	ALA	2.1
4	F	123	GLU	2.0
3	E	156	VAL	2.0
3	H	212	VAL	2.0
3	H	160	TRP	2.0
3	H	187	VAL	2.0
4	F	186	TYR	2.0
4	F	192	TYR	2.0
4	F	205	ILE	2.0
4	F	194	CYS	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](#)

SUGAR-RSR INFOmissingINFO

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(\AA^2)	Q<0.9
13	NAG	D	3099	14/15	0.72	0.16	61,76,81,81	0
13	NAG	B	3099	14/15	0.73	0.15	75,90,97,102	0
8	SO4	C	460	5/5	0.77	0.21	42,44,45,63	5
8	SO4	C	459	5/5	0.78	0.15	85,97,101,104	0
8	SO4	C	458	5/5	0.80	0.17	63,79,88,91	0
8	SO4	A	458	5/5	0.83	0.16	86,97,100,104	0
9	GOL	A	461	6/6	0.85	0.15	38,52,57,64	0
8	SO4	L	215	5/5	0.86	0.10	79,80,86,89	0
11	CL	C	462	1/1	0.91	0.15	57,57,57,57	0
8	SO4	A	459	5/5	0.92	0.20	34,51,66,77	0
12	MG	D	2001	1/1	0.93	0.06	7,7,7,7	1
8	SO4	A	460	5/5	0.94	0.13	40,46,55,60	0
11	CL	C	461	1/1	0.95	0.06	42,42,42,42	0
10	CA	C	2005	1/1	0.96	0.04	29,29,29,29	0
10	CA	C	2007	1/1	0.97	0.03	25,25,25,25	0
10	CA	C	2004	1/1	0.97	0.06	34,34,34,34	0
10	CA	D	2003	1/1	0.98	0.02	13,13,13,13	0
10	CA	B	2002	1/1	0.98	0.05	14,14,14,14	0
11	CL	B	473	1/1	0.99	0.09	13,13,13,13	0
10	CA	A	2006	1/1	0.99	0.06	0,0,0,0	0
10	CA	C	2006	1/1	0.99	0.02	24,24,24,24	0
11	CL	D	473	1/1	0.99	0.07	22,22,22,22	0
12	MG	B	2001	1/1	0.99	0.01	0,0,0,0	1
10	CA	A	2004	1/1	0.99	0.06	11,11,11,11	0
10	CA	D	2002	1/1	0.99	0.04	17,17,17,17	0
10	CA	A	2005	1/1	0.99	0.06	3,3,3,3	0
10	CA	A	2007	1/1	1.00	0.08	1,1,1,1	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
10	CA	B	2003	1/1	1.00	0.05	0,0,0,0	0

6.5 Other polymers [i](#)

There are no such residues in this entry.