



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 20, 2026 – 12:04 PM UTC

PDB ID : 1SR5 / pdb_00001sr5
Title : ANTITHROMBIN-ANHYDROTHROMBIN-HEPARIN TERNARY COMPLEX STRUCTURE
Authors : Dementiev, A.; Petitou, M.; Gettins, P.G.
Deposited on : 2004-03-22
Resolution : 3.10 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

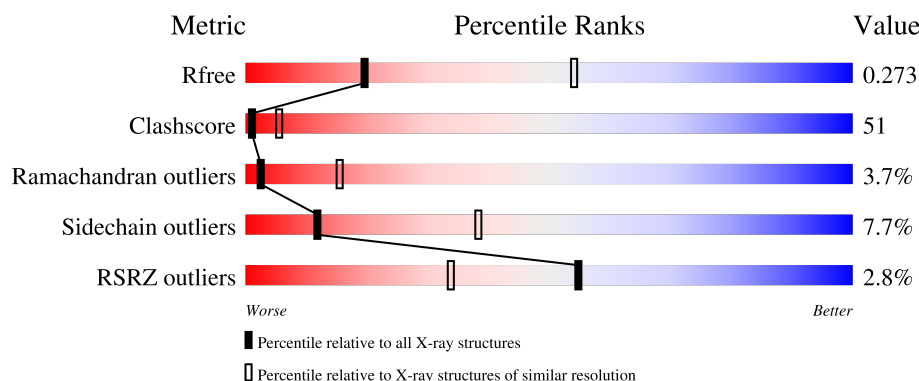
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.10 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	1456 (3.10-3.10)
Clashscore	190562	1539 (3.10-3.10)
Ramachandran outliers	187476	1467 (3.10-3.10)
Sidechain outliers	187428	1467 (3.10-3.10)
RSRZ outliers	180081	1456 (3.10-3.10)

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	432	4% 34% 51% 10% 5%
2	B	36	50% 33% 6% 11%
3	C	259	34% 49% 10% • •
4	D	7	43% 57%

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
4	U9D	D	7	X	-	-	-

2 Entry composition

There are 7 unique types of molecules in this entry. The entry contains 5534 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 Antithrombin-III.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	409	Total	C	N	O	S	0	0	0
			3085	1974	523	571	17			

- Molecule 2 is a protein called Prothrombin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	32	Total	C	N	O	S	0	0	0
			248	156	40	51	1			

- Molecule 3 is a protein called Prothrombin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	248	Total	C	N	O	S	0	0	0
			1960	1251	341	354	14			

- Molecule 4 is an oligosaccharide called 4-deoxy-2,3,6-tri-O-methyl-alpha-D-xylo-hexopyranose-(1-4)-2,3,6-tri-O-methyl-beta-D-glucopyranose-(1-4)-2,3-di-O-methyl-6-O-sulfo-alpha-D-glucopyranose-(1-4)-(2R,3R,4S,5S,6S)-6-(dihydroxymethyl)-3,4-dimethoxytetrahydro-2H-pyran-2,5-diol-(1-4)-2,3,6-tri-O-sulfo-alpha-D-glucopyranose-(1-4)-(2R,3R,4S,5S,6R)-6-(dihydroxymethyl)-3,4-dimethoxytetrahydro-2H-pyran-2,5-diol-(1-4)-1,5-anhydro-3-O-methyl-2,6-di-O-sulfo-D-glucitol.

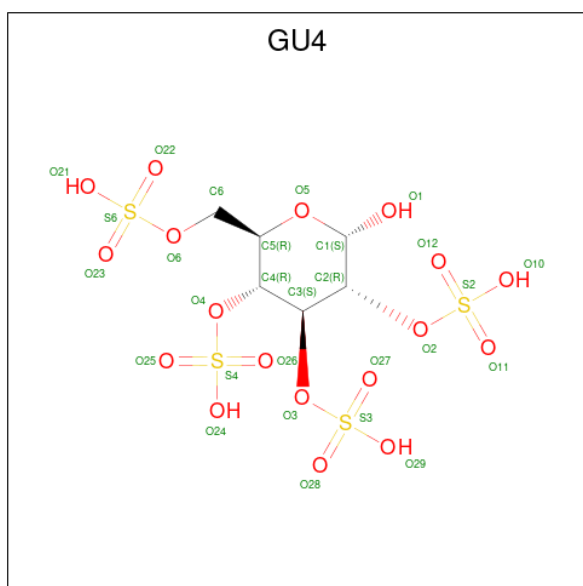
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	D	7	Total	C	O	S	0	0	0
			111	53	52	6			

- Molecule 5 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	A	1	Total	C	N	O	0	0
			14	8	1	5		
5	C	1	Total	C	N	O	0	0
			14	8	1	5		

- Molecule 6 is 2,3,4,6-tetra-O-sulfonato-alpha-D-glucopyranose (CCD ID: GU4) (formula: $C_6H_{12}O_{18}S_4$).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	C	1	Total	C	O	S	0	0
			13	6	6	1		

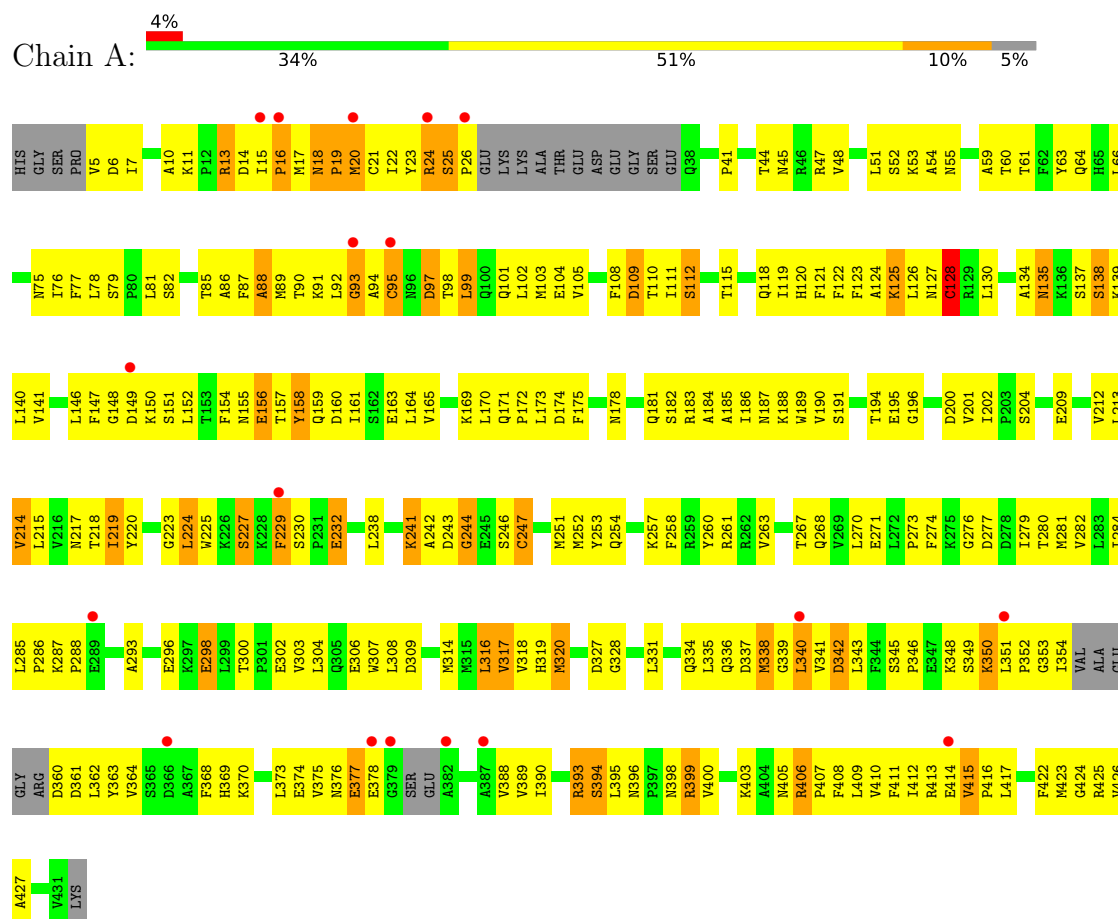
- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	37	Total	O	0	0
			37	37		
7	B	4	Total	O	0	0
			4	4		
7	C	34	Total	O	0	0
			34	34		

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: Antithrombin-III

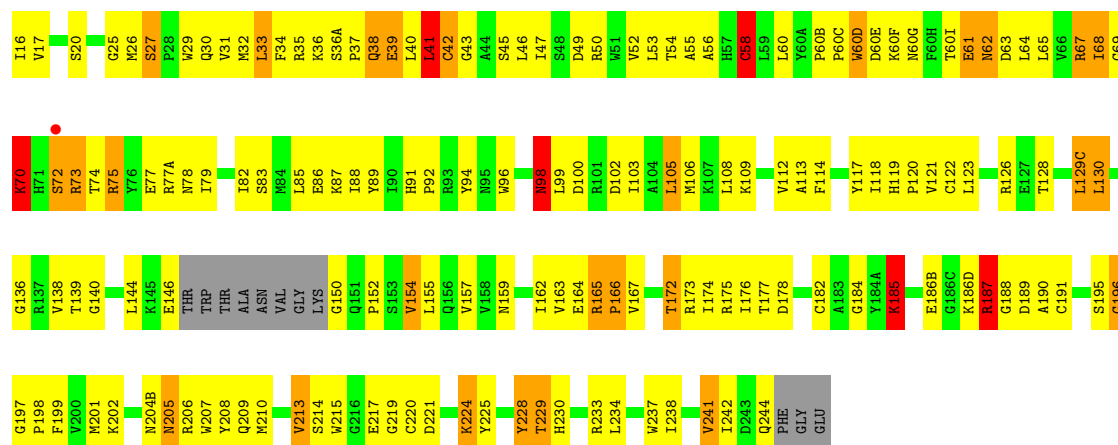


• Molecule 2: Prothrombin



• Molecule 3: Prothrombin





- Molecule 4: 4-deoxy-2,3,6-tri-O-methyl- α -D-xylo-hexopyranose-(1-4)-2,3,6-tri-O-methyl- β -D-glucopyranose-(1-4)-2,3-di-O-methyl-6-O-sulfo- α -D-glucopyranose-(1-4)-(2R,3R,4S,5S,6S)-6-(dihydroxymethyl)-3,4-dimethoxytetrahydro-2H-pyran-2,5-diol-(1-4)-2,3,6-tri-O-sulfo- α -D-glucopyranose-(1-4)-(2R,3R,4S,5S,6R)-6-(dihydroxymethyl)-3,4-dimethoxytetrahydro-2H-pyran-2,5-diol-(1-4)-1,5-anhydro-3-O-methyl-2,6-di-O-sulfo-D-glucitol

Chain D:



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	90.04Å 90.70Å 159.90Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 3.10 30.00 – 3.10	Depositor EDS
% Data completeness (in resolution range)	99.6 (30.00-3.10) 99.5 (30.00-3.10)	Depositor EDS
R_{merge}	0.12	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 3.11Å)	Xtriage
Refinement program	CNS	Depositor
R, R_{free}	0.227 , 0.278 0.230 , 0.273	Depositor DCC
R_{free} test set	2278 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	66.0	Xtriage
Anisotropy	0.879	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.27 , 64.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	0.027 for k,h,-l	Xtriage
F_o, F_c correlation	0.92	EDS
Total number of atoms	5534	wwPDB-VP
Average B, all atoms (Å ²)	62.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.17% 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: U9M, U9D, YYB, GU4, U9J, GU6, NAG, GU8, U9G

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	0.56	0/3149	1.15	23/4286 (0.5%)
2	B	0.52	0/251	1.02	3/335 (0.9%)
3	C	0.57	0/2011	1.09	16/2728 (0.6%)
All	All	0.56	0/5411	1.12	42/7349 (0.6%)

There are no bond length outliers.

All (42) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	229	PHE	O-C-N	-14.07	106.17	123.06
1	A	157	THR	N-CA-C	-10.95	99.75	113.55
1	A	388	VAL	N-CA-C	-9.26	103.34	113.43
1	A	18	ASN	CA-C-N	-8.37	109.37	119.84
1	A	18	ASN	C-N-CA	-8.37	109.37	119.84
1	A	94	ALA	N-CA-C	-8.38	92.96	110.80
1	A	317	VAL	N-CA-C	-8.24	95.85	107.80
1	A	93	GLY	N-CA-C	-7.82	94.65	113.18
1	A	94	ALA	N-CA-CB	7.72	123.54	110.49
3	C	70	LYS	CA-C-N	-6.95	110.41	122.36
3	C	70	LYS	C-N-CA	-6.95	110.41	122.36
3	C	196	GLY	N-CA-C	-6.86	106.92	115.08
1	A	88	ALA	N-CA-C	-6.61	104.70	112.89
3	C	58	CYS	N-CA-C	-6.39	104.41	111.82
1	A	158	TYR	N-CA-C	-6.28	104.13	110.97
1	A	415	VAL	N-CA-C	6.19	122.26	108.88
1	A	393	ARG	N-CA-C	6.13	119.71	112.72
3	C	129(C)	LEU	N-CA-C	6.09	120.73	113.12
3	C	27	SER	CA-C-N	6.06	127.41	119.84
3	C	27	SER	C-N-CA	6.06	127.41	119.84
1	A	406	ARG	N-CA-C	-6.05	100.31	108.11

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	128	CYS	CA-CB-SG	6.05	128.31	114.40
3	C	60	LEU	N-CA-C	6.02	118.74	108.02
1	A	138	SER	N-CA-C	6.01	118.28	110.53
3	C	98	ASN	N-CA-C	5.91	118.99	109.83
1	A	16	PRO	N-CA-CB	5.66	108.21	103.17
1	A	413	ARG	N-CA-C	5.66	117.78	109.24
3	C	75	ARG	CD-NE-CZ	-5.64	116.50	124.40
1	A	251	MET	N-CA-C	5.52	117.72	108.73
3	C	68	ILE	N-CA-C	5.49	117.48	108.97
1	A	63	TYR	N-CA-C	-5.48	105.20	111.07
3	C	185	LYS	CA-C-N	-5.40	114.19	119.64
3	C	185	LYS	C-N-CA	-5.40	114.19	119.64
1	A	394	SER	N-CA-C	-5.36	102.95	110.35
1	A	214	VAL	N-CA-C	5.35	115.98	108.17
3	C	60(D)	TRP	N-CA-C	-5.31	106.78	113.20
1	A	342	ASP	CB-CG-OD1	-5.22	106.39	118.40
2	B	4	ARG	CA-C-N	5.10	124.89	119.28
2	B	4	ARG	C-N-CA	5.10	124.89	119.28
3	C	187	ARG	CD-NE-CZ	-5.08	117.28	124.40
3	C	187	ARG	N-CA-C	5.08	114.99	108.34
2	B	14(B)	THR	N-CA-C	5.02	119.26	113.18

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	3085	0	2922	341	1
2	B	248	0	236	16	1
3	C	1960	0	1884	184	0
4	D	111	0	16	11	0
5	A	28	0	26	6	0
5	C	14	0	13	3	0
6	C	13	0	8	4	0
7	A	37	0	0	2	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
7	B	4	0	0	0	0
7	C	34	0	0	1	0
All	All	5534	0	5105	534	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 51.

All (534) 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)
4:D:6:GU8:C7	4:D:6:GU8:O2	1.63	1.43
4:D:2:U9J:O2	4:D:2:U9J:C2M	1.63	1.41
4:D:5:U9G:C3G	4:D:5:U9G:O2	1.65	1.39
4:D:6:GU8:O3	4:D:6:GU8:C8	1.67	1.39
1:A:95:CYS:O	1:A:99:LEU:HB3	1.29	1.24
1:A:5:VAL:HG11	1:A:15:ILE:HD11	1.24	1.16
1:A:7:ILE:CD1	1:A:164:LEU:O	1.94	1.15
1:A:15:ILE:HG23	1:A:16:PRO:HD2	1.25	1.13
1:A:23:TYR:HB2	1:A:99:LEU:HD21	1.11	1.10
1:A:95:CYS:O	1:A:99:LEU:CB	2.01	1.09
1:A:298:GLU:O	1:A:298:GLU:HG2	1.55	1.05
1:A:23:TYR:OH	1:A:25:SER:HB3	1.54	1.05
3:C:41:LEU:O	3:C:42:CYS:SG	2.15	1.04
1:A:7:ILE:HD11	1:A:164:LEU:O	1.57	1.01
1:A:254:GLN:NE2	1:A:258:PHE:HZ	1.58	1.01
1:A:90:THR:O	1:A:93:GLY:O	1.79	1.00
3:C:50:ARG:HA	3:C:108:LEU:HD12	1.42	0.99
1:A:23:TYR:O	1:A:24:ARG:HG3	1.62	0.98
1:A:7:ILE:HD13	1:A:164:LEU:O	1.61	0.98
3:C:61:GLU:HG2	3:C:87:LYS:HA	1.45	0.98
1:A:25:SER:HB2	1:A:26:PRO:HD2	1.47	0.97
1:A:254:GLN:HE21	1:A:258:PHE:HZ	0.97	0.95
1:A:23:TYR:HB2	1:A:99:LEU:CD2	1.94	0.95
3:C:62:ASN:HD22	3:C:62:ASN:H	1.06	0.94
1:A:15:ILE:CG2	1:A:16:PRO:HD2	1.98	0.93
1:A:334:GLN:O	1:A:337:ASP:OD1	1.87	0.93
3:C:72:SER:O	3:C:154:VAL:HA	1.69	0.91
1:A:170:LEU:HD23	1:A:171:GLN:N	1.87	0.90
1:A:229:PHE:HB2	1:A:377:GLU:HA	1.53	0.89
1:A:238:LEU:HD22	1:A:246:SER:HB3	1.52	0.89
1:A:252:MET:HE3	1:A:320:MET:HG2	1.55	0.88

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:1(G):PHE:HD1	3:C:242:ILE:HG21	1.38	0.87
3:C:62:ASN:H	3:C:62:ASN:ND2	1.67	0.86
1:A:81:LEU:HD21	1:A:127:ASN:HD21	1.40	0.86
1:A:23:TYR:CB	1:A:99:LEU:HD21	2.03	0.85
3:C:165:ARG:HH11	3:C:178:ASP:HA	1.40	0.84
4:D:2:U9J:C2M	4:D:2:U9J:C2	2.55	0.84
1:A:18:ASN:O	5:A:502:NAG:H61	1.75	0.84
1:A:102:LEU:HD23	1:A:340:LEU:HD11	1.60	0.83
2:B:6:LEU:HD12	3:C:25:GLY:HA3	1.61	0.83
3:C:36(A):SER:HA	3:C:38:GLN:N	1.96	0.81
1:A:229:PHE:CD2	1:A:252:MET:HB3	2.16	0.80
1:A:19:PRO:HB3	1:A:92:LEU:HD12	1.61	0.80
3:C:72:SER:O	3:C:73:ARG:HB2	1.82	0.80
1:A:282:VAL:HG21	1:A:308:LEU:HD21	1.64	0.80
1:A:316:LEU:HD23	1:A:400:VAL:HG13	1.63	0.80
1:A:412:ILE:HD12	1:A:422:PHE:CD2	2.16	0.80
1:A:20:MET:SD	1:A:353:GLY:HA2	2.22	0.79
1:A:284:ILE:HD13	1:A:307:TRP:CZ3	2.16	0.79
1:A:155:ASN:O	1:A:156:GLU:HB2	1.82	0.79
3:C:94:TYR:CZ	3:C:96:TRP:HB3	2.17	0.79
1:A:414:GLU:OE1	1:A:417:LEU:HB2	1.84	0.78
3:C:36(A):SER:HA	3:C:38:GLN:H	1.49	0.78
3:C:62:ASN:HD22	3:C:62:ASN:N	1.70	0.78
3:C:70:LYS:HG2	3:C:77:GLU:OE1	1.83	0.78
1:A:5:VAL:CG1	1:A:15:ILE:HD11	2.11	0.78
3:C:103:ILE:HD11	3:C:238:ILE:HD11	1.65	0.77
1:A:55:ASN:ND2	1:A:81:LEU:HA	2.00	0.77
1:A:23:TYR:OH	1:A:25:SER:CB	2.31	0.76
3:C:41:LEU:O	3:C:41:LEU:HD12	1.84	0.76
1:A:95:CYS:HB2	1:A:352:PRO:CG	2.15	0.76
1:A:187:ASN:ND2	1:A:200:ASP:HA	1.99	0.76
1:A:328:GLY:HA3	1:A:370:LYS:HD3	1.67	0.76
4:D:6:GU8:C7	4:D:6:GU8:C2	2.65	0.75
1:A:335:LEU:HB3	1:A:340:LEU:HD23	1.67	0.75
1:A:75:ASN:HB3	1:A:427:ALA:H	1.51	0.75
1:A:108:PHE:O	1:A:111:ILE:HG12	1.86	0.75
3:C:31:VAL:HG22	3:C:68:ILE:HG23	1.67	0.74
3:C:35:ARG:O	3:C:38:GLN:HA	1.87	0.74
3:C:62:ASN:ND2	3:C:62:ASN:N	2.32	0.74
3:C:29:TRP:CD2	3:C:121:VAL:HB	2.23	0.74
1:A:175:PHE:O	1:A:209:GLU:HA	1.88	0.73

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:258:PHE:HB2	1:A:316:LEU:CD1	2.18	0.73
3:C:60(G):ASN:HD21	5:C:503:NAG:C1	2.01	0.73
4:D:5:U9G:C3G	4:D:5:U9G:C2	2.67	0.72
1:A:78:LEU:HD23	1:A:78:LEU:N	2.04	0.72
1:A:229:PHE:HD2	1:A:252:MET:HB3	1.54	0.72
3:C:72:SER:OG	3:C:73:ARG:N	2.21	0.72
1:A:66:LEU:HA	1:A:334:GLN:NE2	2.05	0.71
1:A:253:TYR:HE2	1:A:317:VAL:HG12	1.55	0.71
1:A:66:LEU:HA	1:A:334:GLN:HE21	1.55	0.71
1:A:101:GLN:OE1	1:A:341:VAL:HG22	1.90	0.71
1:A:319:HIS:CD2	1:A:403:LYS:HG3	2.25	0.71
1:A:229:PHE:HB3	1:A:377:GLU:CG	2.21	0.70
1:A:284:ILE:CD1	1:A:307:TRP:CZ3	2.74	0.70
3:C:204(B):ASN:C	3:C:205:ASN:HD22	1.98	0.70
4:D:6:GU8:C8	4:D:6:GU8:C3	2.69	0.70
1:A:146:LEU:HD21	1:A:215:LEU:HG	1.74	0.70
1:A:101:GLN:HE22	1:A:342:ASP:H	1.38	0.69
1:A:328:GLY:CA	1:A:370:LYS:HD3	2.22	0.69
3:C:105:LEU:HD12	3:C:105:LEU:H	1.57	0.69
1:A:147:PHE:O	1:A:213:LEU:HD12	1.92	0.69
1:A:227:SER:HB3	1:A:254:GLN:HE22	1.55	0.69
2:B:1:CYS:C	3:C:122:CYS:SG	2.75	0.69
1:A:190:VAL:HG21	1:A:201:VAL:HG21	1.75	0.69
1:A:51:LEU:O	1:A:54:ALA:HB3	1.92	0.69
1:A:317:VAL:CG2	1:A:399:ARG:HD2	2.22	0.69
1:A:23:TYR:O	1:A:24:ARG:CG	2.40	0.68
1:A:95:CYS:HB2	1:A:352:PRO:HG3	1.76	0.68
1:A:253:TYR:HE2	1:A:317:VAL:CG1	2.06	0.68
3:C:129(C):LEU:HB2	3:C:210:MET:HE2	1.75	0.68
1:A:155:ASN:HD21	5:A:502:NAG:HN2	1.41	0.68
2:B:14(B):THR:HB	3:C:159:ASN:HD21	1.59	0.68
1:A:336:GLN:HA	1:A:340:LEU:O	1.94	0.68
3:C:87:LYS:HE2	7:C:632:HOH:O	1.94	0.68
1:A:89:MET:HE1	1:A:120:HIS:HB2	1.75	0.68
3:C:35:ARG:HG2	3:C:39:GLU:H	1.57	0.67
3:C:237:TRP:O	3:C:241:VAL:HG13	1.94	0.67
3:C:55:ALA:O	3:C:58:CYS:HB2	1.94	0.67
1:A:229:PHE:HB2	1:A:377:GLU:CA	2.25	0.67
1:A:339:GLY:O	1:A:340:LEU:C	2.37	0.67
1:A:213:LEU:HD23	1:A:364:VAL:HG22	1.78	0.66
3:C:86:GLU:HB2	3:C:109:LYS:HA	1.78	0.66

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:36(A):SER:CA	3:C:38:GLN:H	2.09	0.66
1:A:190:VAL:HG13	1:A:191:SER:N	2.12	0.65
3:C:98:ASN:HD22	3:C:98:ASN:H	1.42	0.65
1:A:351:LEU:HD12	1:A:362:LEU:HG	1.77	0.65
3:C:204(B):ASN:O	3:C:205:ASN:ND2	2.27	0.65
1:A:23:TYR:CZ	1:A:25:SER:HB3	2.30	0.65
1:A:15:ILE:CG2	1:A:16:PRO:CD	2.72	0.65
1:A:227:SER:CB	1:A:254:GLN:HE22	2.10	0.65
3:C:119:HIS:CD2	3:C:120:PRO:HD2	2.32	0.65
1:A:267:THR:HB	1:A:286:PRO:HA	1.79	0.65
1:A:254:GLN:NE2	1:A:258:PHE:CZ	2.47	0.65
1:A:300:THR:O	1:A:303:VAL:HG12	1.97	0.65
1:A:376:ASN:OD1	1:A:376:ASN:C	2.39	0.64
3:C:130:LEU:HD22	3:C:210:MET:HE3	1.77	0.64
2:B:1(G):PHE:CD1	3:C:242:ILE:HG21	2.26	0.64
1:A:23:TYR:HH	1:A:25:SER:HB3	1.62	0.64
1:A:85:THR:HG22	1:A:123:PHE:CD1	2.32	0.64
1:A:345:SER:O	1:A:349:SER:HB2	1.97	0.64
1:A:339:GLY:O	1:A:341:VAL:HG13	1.98	0.64
1:A:336:GLN:O	1:A:339:GLY:O	2.15	0.64
1:A:149:ASP:HA	1:A:173:LEU:O	1.98	0.63
3:C:60(I):THR:OG1	3:C:63:ASP:OD1	2.14	0.63
1:A:213:LEU:HB3	1:A:363:TYR:O	1.97	0.63
1:A:5:VAL:HG11	1:A:15:ILE:CD1	2.16	0.63
1:A:18:ASN:CB	5:A:502:NAG:O6	2.47	0.63
1:A:257:LYS:HA	1:A:314:MET:O	1.99	0.63
3:C:144:LEU:HD11	3:C:152:PRO:HB3	1.80	0.63
1:A:126:LEU:HD23	1:A:126:LEU:C	2.24	0.63
1:A:182:SER:C	1:A:184:ALA:H	2.06	0.62
3:C:34:PHE:HB2	3:C:65:LEU:CD1	2.28	0.62
1:A:202:ILE:HG23	1:A:368:PHE:CE2	2.35	0.62
3:C:56:ALA:HB3	3:C:102:ASP:OD1	1.98	0.62
1:A:306:GLU:O	1:A:309:ASP:HB2	1.99	0.62
1:A:163:GLU:HB2	1:A:169:LYS:HG2	1.82	0.62
1:A:258:PHE:HB2	1:A:316:LEU:HD11	1.82	0.62
3:C:228:TYR:CD1	3:C:228:TYR:N	2.68	0.62
3:C:98:ASN:HD22	3:C:98:ASN:N	1.97	0.61
1:A:25:SER:HB2	1:A:26:PRO:CD	2.25	0.61
1:A:119:ILE:HG23	1:A:120:HIS:N	2.13	0.61
1:A:252:MET:HE3	1:A:320:MET:CG	2.28	0.61
3:C:32:MET:CE	3:C:70:LYS:HD3	2.30	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:61:GLU:CG	3:C:87:LYS:HA	2.26	0.61
1:A:78:LEU:HD23	1:A:78:LEU:H	1.65	0.60
1:A:85:THR:O	1:A:88:ALA:HB3	2.01	0.60
3:C:32:MET:HE3	3:C:70:LYS:HD3	1.82	0.60
3:C:112:VAL:HG22	3:C:113:ALA:H	1.65	0.60
2:B:1(G):PHE:HA	3:C:242:ILE:CG2	2.32	0.60
3:C:233:ARG:HH21	3:C:233:ARG:HG3	1.67	0.60
3:C:165:ARG:HG2	6:C:602:GU4:H3	1.84	0.60
1:A:112:SER:OG	1:A:115:THR:CB	2.49	0.59
2:B:14(B):THR:HB	3:C:159:ASN:ND2	2.16	0.59
1:A:229:PHE:HB3	1:A:377:GLU:CB	2.32	0.59
3:C:34:PHE:HB2	3:C:65:LEU:HD12	1.84	0.59
3:C:165:ARG:HG2	3:C:165:ARG:HH21	1.67	0.59
1:A:95:CYS:O	1:A:99:LEU:HB2	2.00	0.59
1:A:395:LEU:HG	1:A:396:ASN:N	2.17	0.59
1:A:155:ASN:HB3	1:A:158:TYR:HB3	1.85	0.59
3:C:60(B):PRO:HG2	3:C:96:TRP:CZ2	2.38	0.59
1:A:119:ILE:CG2	1:A:120:HIS:N	2.64	0.59
1:A:190:VAL:HG11	1:A:201:VAL:CG2	2.33	0.59
1:A:139:LYS:HA	5:A:501:NAG:H83	1.85	0.58
1:A:350:LYS:C	1:A:352:PRO:HD3	2.29	0.58
3:C:46:LEU:O	3:C:120:PRO:HA	2.03	0.58
1:A:151:SER:O	1:A:152:LEU:HG	2.02	0.58
1:A:352:PRO:C	1:A:354:ILE:H	2.12	0.58
1:A:246:SER:O	1:A:247:CYS:HB2	2.02	0.58
3:C:112:VAL:HG22	3:C:113:ALA:N	2.18	0.58
1:A:134:ALA:HA	1:A:279:ILE:HD12	1.86	0.57
3:C:17:VAL:HG21	3:C:220:CYS:HB3	1.86	0.57
3:C:53:LEU:HD23	3:C:209:GLN:NE2	2.20	0.57
1:A:148:GLY:O	1:A:172:PRO:HA	2.03	0.57
1:A:159:GLN:O	1:A:169:LYS:HD2	2.04	0.57
3:C:163:VAL:HB	3:C:182:CYS:SG	2.45	0.57
3:C:202:LYS:NZ	3:C:205:ASN:HB2	2.19	0.57
1:A:190:VAL:HG21	1:A:218:THR:HG21	1.86	0.57
1:A:45:ASN:CB	1:A:125:LYS:HZ1	2.18	0.57
3:C:43:GLY:O	3:C:196:GLY:HA3	2.04	0.57
1:A:346:PRO:HG3	1:A:363:TYR:CE2	2.39	0.57
3:C:176:ILE:HG22	3:C:177:THR:N	2.20	0.56
1:A:187:ASN:HD22	1:A:200:ASP:HA	1.66	0.56
3:C:35:ARG:HG2	3:C:39:GLU:N	2.19	0.56
2:B:2:GLY:O	2:B:3:LEU:HD23	2.06	0.56

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:13:ARG:CZ	4:D:3:GU6:O15	2.53	0.56
1:A:17:MET:CB	1:A:118:GLN:NE2	2.69	0.56
1:A:317:VAL:HG22	1:A:399:ARG:HD2	1.86	0.56
3:C:69:GLY:HA3	3:C:118:ILE:HD13	1.87	0.56
1:A:190:VAL:HG13	1:A:191:SER:H	1.71	0.56
1:A:18:ASN:O	5:A:502:NAG:C6	2.51	0.56
3:C:65:LEU:HD12	3:C:65:LEU:C	2.31	0.56
1:A:229:PHE:CB	1:A:377:GLU:HB3	2.36	0.56
1:A:229:PHE:CB	1:A:377:GLU:CB	2.84	0.56
1:A:320:MET:HE2	1:A:375:VAL:HG11	1.87	0.56
1:A:337:ASP:OD1	1:A:337:ASP:N	2.32	0.56
1:A:13:ARG:HG2	1:A:14:ASP:N	2.20	0.55
1:A:171:GLN:NE2	1:A:172:PRO:HD2	2.22	0.55
1:A:230:SER:HB2	1:A:232:GLU:OE1	2.07	0.55
3:C:67:ARG:HH21	3:C:70:LYS:HZ1	1.55	0.55
1:A:281:MET:HE2	1:A:410:VAL:HG13	1.88	0.55
1:A:202:ILE:HG12	1:A:368:PHE:CD2	2.41	0.55
1:A:253:TYR:CE2	1:A:317:VAL:HG12	2.40	0.55
3:C:98:ASN:N	3:C:98:ASN:ND2	2.54	0.55
3:C:165:ARG:HG2	3:C:165:ARG:NH2	2.22	0.55
1:A:102:LEU:HD23	1:A:340:LEU:CD1	2.34	0.55
1:A:147:PHE:CE1	1:A:171:GLN:HB3	2.42	0.55
1:A:219:ILE:HD13	1:A:422:PHE:CE1	2.42	0.55
1:A:229:PHE:CE2	1:A:252:MET:HB3	2.41	0.55
3:C:186(D):LYS:HB2	3:C:186(D):LYS:NZ	2.22	0.55
1:A:48:VAL:HG21	1:A:125:LYS:CE	2.37	0.55
3:C:41:LEU:O	3:C:42:CYS:CB	2.55	0.55
3:C:20:SER:O	3:C:157:VAL:HG12	2.06	0.54
1:A:147:PHE:HB2	1:A:214:VAL:HG23	1.89	0.54
1:A:48:VAL:HG21	1:A:125:LYS:HE3	1.90	0.54
3:C:40:LEU:HG	3:C:41:LEU:N	2.23	0.54
3:C:67:ARG:HH21	3:C:70:LYS:NZ	2.05	0.54
3:C:138:VAL:HG11	3:C:190:ALA:HB2	1.90	0.54
1:A:90:THR:O	1:A:93:GLY:C	2.49	0.54
1:A:284:ILE:CD1	1:A:307:TRP:HZ3	2.20	0.54
1:A:135:ASN:OD1	1:A:140:LEU:HB3	2.08	0.53
1:A:146:LEU:HD23	1:A:215:LEU:HA	1.90	0.53
1:A:147:PHE:CD1	1:A:171:GLN:HB3	2.44	0.53
3:C:202:LYS:HZ1	3:C:205:ASN:HB2	1.72	0.53
1:A:155:ASN:O	1:A:156:GLU:CB	2.55	0.53
3:C:202:LYS:HD2	3:C:207:TRP:CZ2	2.43	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:44:THR:HG21	1:A:417:LEU:HD21	1.90	0.53
1:A:81:LEU:C	1:A:81:LEU:HD23	2.34	0.53
1:A:258:PHE:HB2	1:A:316:LEU:HD12	1.91	0.53
1:A:407:PRO:HA	1:A:426:VAL:O	2.07	0.53
3:C:16:ILE:HD11	3:C:139:THR:C	2.33	0.53
3:C:172:THR:HB	3:C:217:GLU:OE1	2.08	0.53
3:C:177:THR:HG22	3:C:178:ASP:N	2.23	0.53
3:C:201:MET:SD	3:C:210:MET:HG3	2.49	0.53
3:C:165:ARG:CG	6:C:602:GU4:H3	2.39	0.53
1:A:389:VAL:HG23	1:A:390:ILE:HG23	1.91	0.53
3:C:29:TRP:O	3:C:31:VAL:HG23	2.08	0.53
3:C:91:HIS:CG	3:C:92:PRO:HD2	2.44	0.53
1:A:47:ARG:HD2	1:A:122:PHE:CZ	2.43	0.53
3:C:45:SER:O	3:C:52:VAL:HG13	2.09	0.52
3:C:87:LYS:HB3	3:C:89:TYR:CE2	2.44	0.52
1:A:41:PRO:HG3	1:A:417:LEU:HD23	1.91	0.52
1:A:93:GLY:CA	1:A:353:GLY:HA3	2.39	0.52
1:A:335:LEU:HB3	1:A:340:LEU:CD2	2.37	0.52
3:C:67:ARG:NH2	3:C:70:LYS:NZ	2.57	0.52
1:A:335:LEU:O	1:A:338:MET:HG3	2.10	0.52
2:B:6:LEU:CD1	3:C:25:GLY:HA3	2.38	0.52
3:C:36:LYS:HB2	3:C:63:ASP:O	2.10	0.52
1:A:78:LEU:HD23	1:A:423:MET:O	2.09	0.51
3:C:188:GLY:O	3:C:189:ASP:HB2	2.10	0.51
1:A:273:PRO:HA	1:A:280:THR:HA	1.90	0.51
3:C:47:ILE:HG21	3:C:123:LEU:HD21	1.92	0.51
1:A:76:ILE:HG22	1:A:77:PHE:N	2.24	0.51
1:A:78:LEU:N	1:A:78:LEU:CD2	2.73	0.51
1:A:170:LEU:HD23	1:A:170:LEU:C	2.35	0.51
1:A:411:PHE:CE1	1:A:423:MET:HE3	2.44	0.51
1:A:112:SER:OG	1:A:115:THR:OG1	1.93	0.51
1:A:287:LYS:HG2	1:A:288:PRO:HD2	1.92	0.51
3:C:144:LEU:CD1	3:C:152:PRO:HD3	2.40	0.51
1:A:17:MET:CB	1:A:118:GLN:HE22	2.23	0.51
1:A:335:LEU:HD13	1:A:340:LEU:CD2	2.40	0.51
1:A:352:PRO:C	1:A:354:ILE:N	2.67	0.51
1:A:81:LEU:HD21	1:A:127:ASN:ND2	2.18	0.51
1:A:146:LEU:HD21	1:A:215:LEU:CG	2.40	0.51
1:A:190:VAL:HG21	1:A:201:VAL:CG2	2.40	0.51
3:C:37:PRO:O	3:C:38:GLN:O	2.29	0.51
3:C:187:ARG:NH1	3:C:221:ASP:OD2	2.44	0.51

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:67:ARG:NH2	3:C:70:LYS:HZ1	2.07	0.51
1:A:182:SER:C	1:A:184:ALA:N	2.67	0.51
1:A:331:LEU:HD11	1:A:369:HIS:HB2	1.92	0.51
1:A:61:THR:O	1:A:64:GLN:HB2	2.09	0.50
1:A:118:GLN:O	1:A:119:ILE:C	2.54	0.50
1:A:181:GLN:O	1:A:185:ALA:HB2	2.10	0.50
1:A:393:ARG:NH2	3:C:189:ASP:OD2	2.38	0.50
3:C:73:ARG:HD3	3:C:152:PRO:O	2.12	0.50
1:A:66:LEU:CD2	1:A:78:LEU:HD13	2.42	0.50
1:A:126:LEU:HD21	1:A:130:LEU:HD11	1.94	0.50
1:A:186:ILE:HG21	1:A:202:ILE:CD1	2.42	0.50
1:A:319:HIS:HB2	1:A:403:LYS:HA	1.91	0.50
3:C:36:LYS:H	3:C:64:LEU:HA	1.77	0.50
2:B:1:CYS:O	3:C:122:CYS:SG	2.69	0.50
3:C:174:ILE:HD12	3:C:215:TRP:CZ3	2.46	0.50
3:C:204(B):ASN:C	3:C:205:ASN:ND2	2.67	0.50
1:A:89:MET:HE1	1:A:120:HIS:CB	2.41	0.50
1:A:161:ILE:HG22	1:A:165:VAL:HG12	1.94	0.50
1:A:48:VAL:HG21	4:D:5:U9G:O3A	2.11	0.50
1:A:412:ILE:HD12	1:A:422:PHE:CG	2.45	0.50
3:C:91:HIS:ND1	3:C:92:PRO:HD2	2.26	0.50
3:C:102:ASP:HB3	3:C:229:THR:HG23	1.93	0.50
1:A:352:PRO:O	1:A:354:ILE:N	2.45	0.50
2:B:4:ARG:NH2	2:B:8:GLU:OE2	2.41	0.50
1:A:55:ASN:HD21	1:A:81:LEU:HA	1.72	0.50
1:A:335:LEU:O	1:A:336:GLN:C	2.54	0.50
2:B:3:LEU:HD21	3:C:206:ARG:HG2	1.92	0.50
3:C:17:VAL:HG11	3:C:221:ASP:CB	2.42	0.50
1:A:41:PRO:O	1:A:44:THR:HB	2.12	0.49
1:A:59:ALA:O	1:A:60:THR:C	2.54	0.49
3:C:60(G):ASN:ND2	5:C:503:NAG:H83	2.26	0.49
3:C:33:LEU:HD21	3:C:64:LEU:HD22	1.93	0.49
3:C:165:ARG:CB	3:C:166:PRO:HD3	2.41	0.49
1:A:66:LEU:HD12	1:A:334:GLN:HE21	1.76	0.49
1:A:101:GLN:NE2	1:A:342:ASP:OD1	2.45	0.49
1:A:343:LEU:HG	1:A:364:VAL:CG2	2.42	0.49
1:A:263:VAL:HG11	1:A:307:TRP:CD1	2.47	0.49
1:A:394:SER:OG	3:C:60(F):LYS:NZ	2.45	0.49
3:C:88:ILE:HG22	3:C:89:TYR:N	2.26	0.49
3:C:128:THR:HG21	3:C:208:TYR:CD2	2.47	0.49
3:C:146:GLU:OE2	3:C:219:GLY:HA3	2.12	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:115:THR:HA	1:A:122:PHE:CE2	2.47	0.49
1:A:182:SER:O	1:A:184:ALA:N	2.46	0.49
3:C:49:ASP:O	3:C:112:VAL:HG12	2.13	0.49
3:C:129(C):LEU:HB2	3:C:210:MET:CE	2.42	0.49
1:A:18:ASN:CB	5:A:502:NAG:C6	2.90	0.49
1:A:154:PHE:HD1	1:A:354:ILE:HG22	1.77	0.49
1:A:217:ASN:O	1:A:369:HIS:HA	2.13	0.49
1:A:327:ASP:O	1:A:370:LYS:HA	2.13	0.49
3:C:60(B):PRO:HG2	3:C:96:TRP:CE2	2.47	0.49
1:A:118:GLN:HE21	1:A:118:GLN:HA	1.77	0.49
1:A:229:PHE:CD2	1:A:252:MET:SD	3.06	0.49
3:C:195:SER:HA	3:C:213:VAL:HB	1.94	0.49
1:A:351:LEU:CD1	1:A:362:LEU:HG	2.42	0.49
1:A:412:ILE:HB	1:A:422:PHE:HB2	1.95	0.49
3:C:100:ASP:OD1	3:C:177:THR:HG21	2.13	0.49
1:A:19:PRO:O	1:A:20:MET:HB2	2.13	0.48
1:A:194:THR:O	1:A:196:GLY:N	2.46	0.48
1:A:190:VAL:HG11	1:A:201:VAL:HG23	1.94	0.48
1:A:75:ASN:HB2	1:A:425:ARG:O	2.14	0.48
1:A:101:GLN:NE2	1:A:342:ASP:HB2	2.27	0.48
1:A:270:LEU:HD12	1:A:271:GLU:H	1.78	0.48
1:A:298:GLU:O	1:A:298:GLU:CG	2.38	0.48
3:C:88:ILE:HD13	3:C:106:MET:HB3	1.96	0.48
1:A:393:ARG:HB2	3:C:214:SER:O	2.13	0.48
1:A:270:LEU:HD12	1:A:271:GLU:N	2.29	0.48
1:A:350:LYS:C	1:A:352:PRO:CD	2.87	0.48
1:A:346:PRO:HG3	1:A:363:TYR:CZ	2.49	0.48
1:A:396:ASN:ND2	1:A:398:ASN:H	2.12	0.48
3:C:166:PRO:O	3:C:167:VAL:C	2.56	0.48
1:A:316:LEU:HD23	1:A:400:VAL:CG1	2.40	0.47
3:C:136:GLY:HA3	3:C:199:PHE:CZ	2.48	0.47
6:C:602:GU4:S4	6:C:602:GU4:O3	2.72	0.47
1:A:212:VAL:HG23	1:A:213:LEU:N	2.28	0.47
1:A:258:PHE:CD2	1:A:316:LEU:HD12	2.49	0.47
1:A:45:ASN:HB2	1:A:125:LYS:NZ	2.29	0.47
1:A:101:GLN:O	1:A:102:LEU:C	2.55	0.47
1:A:118:GLN:NE2	1:A:118:GLN:HA	2.29	0.47
3:C:72:SER:C	3:C:154:VAL:HA	2.38	0.47
3:C:34:PHE:HB2	3:C:65:LEU:HD11	1.95	0.47
1:A:158:TYR:C	1:A:160:ASP:H	2.22	0.47
1:A:335:LEU:CB	1:A:340:LEU:HD23	2.42	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:360:ASP:CG	1:A:361:ASP:H	2.21	0.47
1:A:174:ASP:OD2	1:A:178:ASN:ND2	2.47	0.47
1:A:190:VAL:CG1	1:A:191:SER:N	2.78	0.47
1:A:229:PHE:CB	1:A:377:GLU:HA	2.35	0.47
3:C:74:THR:O	3:C:75:ARG:C	2.58	0.47
3:C:114:PHE:HA	3:C:118:ILE:HB	1.96	0.47
1:A:47:ARG:HH11	1:A:47:ARG:HG2	1.78	0.47
1:A:146:LEU:HD21	1:A:215:LEU:CD1	2.45	0.47
1:A:229:PHE:HB3	1:A:377:GLU:HB3	1.97	0.47
1:A:394:SER:HB2	3:C:42:CYS:SG	2.55	0.47
3:C:60(B):PRO:HB2	3:C:60(C):PRO:HD3	1.96	0.47
3:C:221:ASP:CG	3:C:221:ASP:O	2.58	0.47
1:A:121:PHE:O	1:A:124:ALA:HB3	2.14	0.47
1:A:141:VAL:HG13	1:A:220:TYR:HB3	1.98	0.46
1:A:102:LEU:CD2	1:A:340:LEU:HD11	2.38	0.46
1:A:241:LYS:HE3	1:A:243:ASP:OD2	2.15	0.46
3:C:186(D):LYS:NZ	3:C:186(D):LYS:CB	2.78	0.46
1:A:190:VAL:HG11	1:A:201:VAL:HG21	1.96	0.46
3:C:29:TRP:CG	3:C:121:VAL:HB	2.50	0.46
3:C:144:LEU:HD11	3:C:152:PRO:CB	2.45	0.46
1:A:138:SER:HB3	1:A:224:LEU:H	1.79	0.46
1:A:412:ILE:CD1	1:A:422:PHE:CD2	2.93	0.46
3:C:184:GLY:HA3	3:C:225:TYR:HD2	1.79	0.46
1:A:189:TRP:O	1:A:190:VAL:C	2.59	0.46
3:C:30:GLN:HG2	3:C:155:LEU:CD1	2.46	0.46
1:A:77:PHE:CE2	1:A:373:LEU:HB2	2.51	0.46
1:A:349:SER:OG	1:A:350:LYS:N	2.48	0.46
1:A:373:LEU:HD12	1:A:374:GLU:H	1.80	0.46
1:A:45:ASN:CB	1:A:125:LYS:NZ	2.79	0.46
1:A:276:GLY:O	1:A:277:ASP:HB2	2.14	0.46
1:A:353:GLY:C	1:A:354:ILE:HG13	2.40	0.46
3:C:130:LEU:HD12	3:C:162:ILE:HD13	1.96	0.46
1:A:15:ILE:HG22	1:A:16:PRO:N	2.31	0.46
3:C:195:SER:HA	3:C:213:VAL:CG1	2.46	0.46
1:A:303:VAL:HG13	1:A:304:LEU:N	2.31	0.45
1:A:303:VAL:CG1	1:A:304:LEU:N	2.79	0.45
1:A:260:TYR:HE1	1:A:268:GLN:HB3	1.80	0.45
1:A:284:ILE:HD11	1:A:307:TRP:CZ3	2.51	0.45
3:C:174:ILE:HG22	3:C:175:ARG:N	2.30	0.45
1:A:86:ALA:O	1:A:89:MET:HB2	2.15	0.45
3:C:65:LEU:CD1	3:C:65:LEU:C	2.89	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:103:ILE:CG2	3:C:234:LEU:HD23	2.47	0.45
1:A:410:VAL:N	1:A:424:GLY:O	2.46	0.45
1:A:48:VAL:CG2	1:A:125:LYS:CE	2.95	0.45
1:A:186:ILE:C	1:A:188:LYS:N	2.73	0.45
3:C:64:LEU:C	3:C:64:LEU:HD12	2.42	0.45
3:C:98:ASN:H	3:C:98:ASN:ND2	2.12	0.45
1:A:81:LEU:HD11	1:A:126:LEU:CD2	2.47	0.45
1:A:93:GLY:HA3	1:A:353:GLY:HA3	1.98	0.45
1:A:119:ILE:CG2	1:A:120:HIS:H	2.28	0.45
3:C:114:PHE:N	3:C:114:PHE:CD1	2.85	0.45
1:A:319:HIS:CG	1:A:403:LYS:HG3	2.52	0.45
1:A:93:GLY:HA2	1:A:353:GLY:HA3	1.99	0.45
1:A:258:PHE:HD2	1:A:316:LEU:HD12	1.80	0.45
3:C:186(B):GLU:O	3:C:186(D):LYS:N	2.48	0.45
3:C:98:ASN:O	3:C:99:LEU:C	2.59	0.44
3:C:202:LYS:HD2	3:C:207:TRP:CE2	2.52	0.44
3:C:30:GLN:HG2	3:C:155:LEU:HD13	1.97	0.44
3:C:103:ILE:CD1	3:C:238:ILE:HD11	2.43	0.44
3:C:105:LEU:HD12	3:C:105:LEU:N	2.28	0.44
1:A:21:CYS:C	1:A:22:ILE:HG13	2.43	0.44
1:A:204:SER:HA	7:A:605:HOH:O	2.16	0.44
3:C:35:ARG:O	3:C:35:ARG:HG3	2.18	0.44
1:A:52:SER:C	1:A:54:ALA:N	2.71	0.44
1:A:82:SER:HA	7:A:616:HOH:O	2.17	0.44
3:C:33:LEU:C	3:C:33:LEU:CD2	2.91	0.44
3:C:56:ALA:HB3	3:C:102:ASP:HA	1.99	0.44
1:A:127:ASN:O	1:A:128:CYS:C	2.60	0.44
1:A:284:ILE:O	1:A:408:PHE:HB2	2.17	0.44
1:A:150:LYS:C	1:A:152:LEU:H	2.26	0.44
1:A:154:PHE:O	1:A:155:ASN:C	2.60	0.44
2:B:14:ASP:HB2	3:C:26:MET:HE3	2.00	0.44
3:C:103:ILE:HG21	3:C:234:LEU:HD23	2.00	0.44
1:A:105:VAL:HG22	1:A:338:MET:O	2.18	0.44
1:A:137:SER:OG	1:A:138:SER:N	2.51	0.44
1:A:229:PHE:CE2	1:A:252:MET:CB	3.01	0.44
1:A:229:PHE:O	1:A:377:GLU:HB3	2.17	0.43
1:A:253:TYR:HA	1:A:318:VAL:O	2.18	0.43
3:C:54:THR:OG1	3:C:55:ALA:N	2.51	0.43
3:C:176:ILE:CG2	3:C:177:THR:N	2.81	0.43
1:A:99:LEU:C	1:A:101:GLN:H	2.26	0.43
1:A:99:LEU:C	1:A:101:GLN:N	2.76	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:242:ALA:C	1:A:244:GLY:H	2.27	0.43
1:A:351:LEU:HD12	1:A:362:LEU:C	2.43	0.43
1:A:81:LEU:HD11	1:A:126:LEU:HD21	2.01	0.43
1:A:241:LYS:HE3	1:A:241:LYS:HB2	1.88	0.43
3:C:32:MET:HE3	3:C:70:LYS:HB3	2.01	0.43
1:A:345:SER:HA	1:A:346:PRO:HD3	1.86	0.43
3:C:60(G):ASN:HD22	5:C:503:NAG:H83	1.84	0.43
6:C:602:GU4:S4	6:C:602:GU4:H61	2.58	0.43
1:A:6:ASP:O	1:A:10:ALA:HB2	2.19	0.43
1:A:52:SER:O	1:A:53:LYS:C	2.61	0.43
1:A:112:SER:OG	1:A:115:THR:HB	2.17	0.43
1:A:341:VAL:HG23	1:A:342:ASP:N	2.32	0.43
3:C:98:ASN:ND2	3:C:100:ASP:HB2	2.34	0.43
1:A:11:LYS:O	1:A:14:ASP:N	2.52	0.43
1:A:260:TYR:CG	1:A:261:ARG:N	2.87	0.43
2:B:4:ARG:HB2	2:B:7:PHE:HB2	2.01	0.43
3:C:72:SER:O	3:C:154:VAL:CA	2.55	0.43
1:A:223:GLY:HA3	1:A:274:PHE:CE1	2.54	0.42
1:A:304:LEU:HD12	1:A:304:LEU:O	2.19	0.42
1:A:186:ILE:HG21	1:A:202:ILE:HD12	2.01	0.42
3:C:60(C):PRO:C	3:C:60(E):ASP:H	2.26	0.42
1:A:97:ASP:O	1:A:98:THR:C	2.60	0.42
1:A:296:GLU:C	1:A:298:GLU:H	2.28	0.42
1:A:274:PHE:HD2	1:A:279:ILE:HG22	1.85	0.42
1:A:87:PHE:CZ	1:A:335:LEU:CD1	3.03	0.42
1:A:171:GLN:HA	1:A:172:PRO:HD3	1.75	0.42
3:C:17:VAL:HG11	3:C:221:ASP:HB3	2.01	0.42
1:A:120:HIS:O	1:A:121:PHE:C	2.62	0.42
1:A:350:LYS:O	1:A:352:PRO:HD2	2.19	0.42
3:C:102:ASP:HB3	3:C:229:THR:CG2	2.50	0.42
1:A:412:ILE:HD12	1:A:422:PHE:HB2	2.01	0.42
3:C:88:ILE:CG2	3:C:89:TYR:N	2.83	0.42
1:A:15:ILE:CG2	1:A:16:PRO:N	2.83	0.42
1:A:79:SER:OG	1:A:82:SER:HB2	2.20	0.42
1:A:293:ALA:HA	1:A:296:GLU:OE1	2.19	0.42
1:A:101:GLN:O	1:A:104:GLU:N	2.52	0.42
1:A:218:THR:O	1:A:219:ILE:HB	2.20	0.42
3:C:35:ARG:O	3:C:36:LYS:C	2.62	0.42
3:C:195:SER:C	3:C:197:GLY:H	2.27	0.42
1:A:154:PHE:HD1	1:A:354:ILE:CG2	2.33	0.41
1:A:343:LEU:HD12	1:A:351:LEU:HD21	2.02	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:405:ASN:OD1	1:A:405:ASN:N	2.53	0.41
3:C:36:LYS:N	3:C:64:LEU:HA	2.35	0.41
3:C:79:ILE:HG23	3:C:117:TYR:CD2	2.55	0.41
3:C:144:LEU:HD13	3:C:150:GLY:O	2.20	0.41
1:A:45:ASN:CG	1:A:125:LYS:HZ1	2.27	0.41
1:A:285:LEU:HA	1:A:286:PRO:HD2	1.93	0.41
1:A:342:ASP:OD2	1:A:348:LYS:O	2.38	0.41
1:A:66:LEU:HD22	1:A:78:LEU:HD13	2.00	0.41
1:A:158:TYR:C	1:A:160:ASP:N	2.77	0.41
1:A:186:ILE:C	1:A:188:LYS:H	2.28	0.41
3:C:32:MET:HE3	3:C:70:LYS:CB	2.51	0.41
3:C:172:THR:OG1	3:C:173:ARG:N	2.53	0.41
1:A:51:LEU:HD11	1:A:119:ILE:HG13	2.02	0.41
1:A:66:LEU:HA	1:A:66:LEU:HD12	1.89	0.41
1:A:118:GLN:HA	1:A:120:HIS:CE1	2.55	0.41
1:A:284:ILE:HB	1:A:409:LEU:HB2	2.02	0.41
1:A:406:ARG:O	1:A:407:PRO:C	2.62	0.41
1:A:412:ILE:HD12	1:A:422:PHE:CB	2.50	0.41
1:A:415:VAL:HB	1:A:416:PRO:HD3	2.03	0.41
1:A:425:ARG:HD3	1:A:427:ALA:HB2	2.01	0.41
2:B:2:GLY:O	3:C:206:ARG:HA	2.21	0.41
3:C:178:ASP:HB3	3:C:233:ARG:NH1	2.36	0.41
3:C:16:ILE:HD11	3:C:140:GLY:N	2.36	0.41
3:C:230:HIS:CG	3:C:233:ARG:HB2	2.56	0.41
1:A:281:MET:CE	1:A:410:VAL:HG13	2.51	0.41
1:A:343:LEU:HG	1:A:364:VAL:HG23	2.03	0.41
1:A:47:ARG:HG2	1:A:47:ARG:NH1	2.36	0.41
1:A:108:PHE:C	1:A:110:THR:H	2.29	0.41
1:A:229:PHE:HB3	1:A:377:GLU:HG3	2.01	0.41
1:A:393:ARG:HD3	3:C:191:CYS:O	2.20	0.41
3:C:77(A):ARG:O	3:C:78:ASN:HB2	2.21	0.41
3:C:82:ILE:CG2	3:C:83:SER:N	2.84	0.41
1:A:161:ILE:HG22	1:A:165:VAL:CG1	2.51	0.41
3:C:60(D):TRP:CD1	3:C:60(D):TRP:N	2.88	0.41
1:A:91:LYS:C	1:A:91:LYS:HD3	2.45	0.40
1:A:95:CYS:CB	1:A:352:PRO:HG3	2.49	0.40
1:A:300:THR:H	1:A:303:VAL:HG12	1.85	0.40
3:C:17:VAL:HG23	3:C:191:CYS:HB2	2.03	0.40
3:C:164:GLU:OE2	3:C:164:GLU:N	2.30	0.40
3:C:224:LYS:NZ	3:C:224:LYS:HB3	2.36	0.40
1:A:160:ASP:O	1:A:163:GLU:HB3	2.21	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:185:LYS:HG3	3:C:225:TYR:OH	2.22	0.40
1:A:103:MET:O	1:A:109:ASP:HB3	2.21	0.40
1:A:115:THR:O	1:A:119:ILE:N	2.55	0.40
2:B:4:ARG:HA	2:B:5:PRO:HD3	1.83	0.40
3:C:85:LEU:HD13	3:C:106:MET:HB3	2.04	0.40
1:A:125:LYS:NZ	4:D:5:U9G:O3A	2.52	0.40
1:A:186:ILE:HG21	1:A:202:ILE:HD11	2.03	0.40
1:A:147:PHE:HB2	1:A:214:VAL:CG2	2.51	0.40
1:A:194:THR:C	1:A:196:GLY:N	2.80	0.40
1:A:229:PHE:HB2	1:A:377:GLU:CB	2.51	0.40
3:C:165:ARG:NH1	3:C:178:ASP:HA	2.22	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:378:GLU:O	2:B:11:SER:OG[4_445]	1.94	0.26

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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	401/432 (93%)	310 (77%)	74 (18%)	17 (4%)	2	13
2	B	30/36 (83%)	25 (83%)	4 (13%)	1 (3%)	3	17
3	C	244/259 (94%)	197 (81%)	40 (16%)	7 (3%)	3	19
All	All	675/727 (93%)	532 (79%)	118 (18%)	25 (4%)	2	15

All (25) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	19	PRO

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Mol	Chain	Res	Type
3	C	38	GLN
1	A	20	MET
1	A	25	SER
1	A	183	ARG
1	A	195	GLU
1	A	219	ILE
1	A	350	LYS
1	A	377	GLU
3	C	73	ARG
1	A	24	ARG
1	A	225	TRP
1	A	298	GLU
3	C	126	ARG
1	A	241	LYS
1	A	247	CYS
1	A	340	LEU
2	B	14(A)	LYS
3	C	41	LEU
3	C	42	CYS
1	A	109	ASP
1	A	232	GLU
3	C	213	VAL
1	A	244	GLY
3	C	166	PRO

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	316/383 (82%)	300 (95%)	16 (5%)	21	52
2	B	26/31 (84%)	25 (96%)	1 (4%)	29	60
3	C	206/225 (92%)	181 (88%)	25 (12%)	5	20
All	All	548/639 (86%)	506 (92%)	42 (8%)	12	38

All (42) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	13	ARG
1	A	95	CYS
1	A	97	ASP
1	A	99	LEU
1	A	112	SER
1	A	125	LYS
1	A	128	CYS
1	A	135	ASN
1	A	156	GLU
1	A	224	LEU
1	A	227	SER
1	A	302	GLU
1	A	316	LEU
1	A	320	MET
1	A	338	MET
1	A	399	ARG
2	B	12	LEU
3	C	27	SER
3	C	33	LEU
3	C	39	GLU
3	C	41	LEU
3	C	58	CYS
3	C	61	GLU
3	C	62	ASN
3	C	67	ARG
3	C	70	LYS
3	C	72	SER
3	C	98	ASN
3	C	105	LEU
3	C	130	LEU
3	C	154	VAL
3	C	165	ARG
3	C	172	THR
3	C	185	LYS
3	C	187	ARG
3	C	198	PRO
3	C	205	ASN
3	C	224	LYS
3	C	228	TYR
3	C	229	THR
3	C	241	VAL
3	C	244	GLN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (18)

such sidechains are listed below:

Mol	Chain	Res	Type
1	A	55	ASN
1	A	118	GLN
1	A	127	ASN
1	A	171	GLN
1	A	178	ASN
1	A	319	HIS
1	A	334	GLN
1	A	396	ASN
3	C	38	GLN
3	C	60(G)	ASN
3	C	62	ASN
3	C	78	ASN
3	C	95	ASN
3	C	98	ASN
3	C	143	ASN
3	C	156	GLN
3	C	205	ASN
3	C	244	GLN

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

7 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
4	YYB	D	1	4	20,20,20	1.40	5 (25%)	25,30,30	1.13	2 (8%)
4	U9J	D	2	4	14,14,15	3.29	7 (50%)	16,19,21	2.07	3 (18%)
4	GU6	D	3	4	23,23,24	2.16	7 (30%)	28,36,38	1.37	3 (10%)
4	U9M	D	4	4	14,14,15	3.72	9 (64%)	16,19,21	1.87	4 (25%)
4	U9G	D	5	4	17,17,18	3.37	7 (41%)	23,24,26	2.28	8 (34%)
4	GU8	D	6	4	12,12,15	5.32	10 (83%)	16,16,20	4.21	9 (56%)
4	U9D	D	7	4	11,11,14	3.81	7 (63%)	14,14,18	1.12	1 (7%)

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
4	YYB	D	1	4	-	6/13/30/30	0/1/1/1
4	U9J	D	2	4	-	3/8/25/28	0/1/1/1
4	GU6	D	3	4	-	6/16/33/36	0/1/1/1
4	U9M	D	4	4	-	4/8/25/28	0/1/1/1
4	U9G	D	5	4	-	8/10/27/30	0/1/1/1
4	GU8	D	6	4	-	0/4/21/27	0/1/1/1
4	U9D	D	7	4	1/1/3/4	1/4/17/23	0/1/1/1

All (52) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	6	GU8	O5-C1	8.28	1.57	1.43
4	D	6	GU8	C3-C2	7.47	1.73	1.52
4	D	6	GU8	O3-C8	7.45	1.67	1.42
4	D	6	GU8	C4-C5	6.92	1.68	1.52
4	D	5	U9G	O4-C4	6.90	1.60	1.43
4	D	5	U9G	O2-C3G	6.81	1.65	1.42
4	D	2	U9J	O6A-C6	-6.46	1.26	1.40
4	D	4	U9M	C6-C5	6.41	1.60	1.52
4	D	2	U9J	O2-C2M	6.29	1.63	1.42
4	D	6	GU8	C1-C2	6.25	1.61	1.51
4	D	6	GU8	O2-C7	6.25	1.63	1.42
4	D	7	U9D	O5-C5	5.89	1.49	1.44
4	D	3	GU6	O2-C2	-5.88	1.38	1.47
4	D	7	U9D	O3-C3M	5.75	1.62	1.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	D	7	U9D	C4-C5	5.54	1.61	1.52
4	D	5	U9G	C3-C2	5.52	1.67	1.52
4	D	2	U9J	O6B-C6	-5.44	1.28	1.40
4	D	4	U9M	C4-C3	5.40	1.67	1.52
4	D	4	U9M	C4-C5	5.15	1.66	1.52
4	D	4	U9M	O6-C6	-4.99	1.29	1.40
4	D	4	U9M	O6B-C6	-4.81	1.30	1.40
4	D	5	U9G	C4-C3	4.53	1.64	1.52
4	D	7	U9D	C2-C3	4.45	1.59	1.52
4	D	5	U9G	C1-C2	4.23	1.58	1.51
4	D	3	GU6	C4-C5	4.05	1.61	1.53
4	D	7	U9D	O2-C2M	3.82	1.55	1.42
4	D	2	U9J	C4-C5	3.63	1.62	1.52
4	D	7	U9D	O5-C1	3.51	1.49	1.43
4	D	6	GU8	O4-C4	3.42	1.51	1.43
4	D	4	U9M	O3-C3	3.39	1.51	1.42
4	D	4	U9M	C1-C2	3.34	1.57	1.51
4	D	5	U9G	O5-C5	3.32	1.49	1.43
4	D	2	U9J	C4-C3	3.29	1.61	1.52
4	D	4	U9M	O4-C4	3.11	1.50	1.43
4	D	6	GU8	O5-C5	3.10	1.49	1.43
4	D	3	GU6	O5-C5	3.05	1.49	1.43
4	D	3	GU6	O5-C1	3.02	1.48	1.43
4	D	4	U9M	C3-C2	2.89	1.60	1.52
4	D	3	GU6	C3-C2	2.85	1.60	1.52
4	D	3	GU6	O16-S3	-2.69	1.33	1.45
4	D	5	U9G	C4-C5	2.61	1.58	1.53
4	D	7	U9D	C1-C2	2.59	1.55	1.51
4	D	1	YYB	O3-C3	2.58	1.49	1.42
4	D	1	YYB	O6-C6	-2.54	1.37	1.46
4	D	1	YYB	C4-C5	2.47	1.58	1.53
4	D	2	U9J	C1-C2	2.36	1.55	1.51
4	D	6	GU8	C4-C3	2.35	1.58	1.52
4	D	3	GU6	O3-C3	-2.28	1.41	1.46
4	D	1	YYB	C1-C2	2.18	1.55	1.51
4	D	6	GU8	C6-C5	2.15	1.56	1.51
4	D	1	YYB	O3-C3M	2.08	1.49	1.42
4	D	2	U9J	C6-C5	2.04	1.55	1.52

All (30) bond angle outliers are listed below:

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	D	6	GU8	O5-C5-C4	-7.87	95.39	109.55
4	D	6	GU8	O4-C4-C3	-7.52	90.66	109.94
4	D	5	U9G	C1-O5-C5	6.77	121.26	112.19
4	D	6	GU8	C6-C5-C4	-6.51	101.17	113.08
4	D	6	GU8	O4-C4-C5	6.44	123.94	109.74
4	D	6	GU8	O5-C1-C2	-5.78	97.81	109.51
4	D	2	U9J	O6B-C6-O6A	5.35	120.48	111.26
4	D	6	GU8	O5-C5-C6	4.28	116.70	107.40
4	D	2	U9J	C1-O5-C5	4.26	118.46	111.48
4	D	1	YYB	O2-C2-C3	4.17	111.27	106.65
4	D	4	U9M	O6B-C6-O6	4.06	118.26	111.26
4	D	2	U9J	O5-C1-C2	3.61	116.82	109.51
4	D	3	GU6	O2-C2-C3	3.54	110.58	106.65
4	D	5	U9G	C6-C5-C4	-3.38	104.97	112.07
4	D	4	U9M	C3M-O3-C3	3.22	122.75	114.47
4	D	4	U9M	O5-C1-C2	3.18	115.96	109.51
4	D	5	U9G	O5-C5-C6	3.00	114.07	107.59
4	D	3	GU6	O13-S2-O2	-2.97	99.54	106.37
4	D	5	U9G	O38-S37-O6	-2.81	99.91	106.37
4	D	5	U9G	O2-C2-C3	2.72	116.22	109.01
4	D	5	U9G	O4-C4-C3	2.65	116.73	109.94
4	D	3	GU6	O13-S2-O15	2.63	117.75	108.56
4	D	5	U9G	C3D-O3-C3	2.61	121.18	114.47
4	D	6	GU8	C1-C2-C3	-2.53	105.61	109.40
4	D	1	YYB	C3M-O3-C3	2.40	120.63	114.47
4	D	4	U9M	C1-O5-C5	2.38	115.37	111.48
4	D	6	GU8	C3-C4-C5	2.37	115.28	110.12
4	D	5	U9G	O6-C6-C5	-2.24	103.57	107.57
4	D	7	U9D	C2M-O2-C2	2.19	119.77	114.01
4	D	6	GU8	O2-C2-C1	2.03	115.16	107.45

All (1) chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
4	D	7	U9D	C1

All (28) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1	YYB	C6-O6-S6-O2S6

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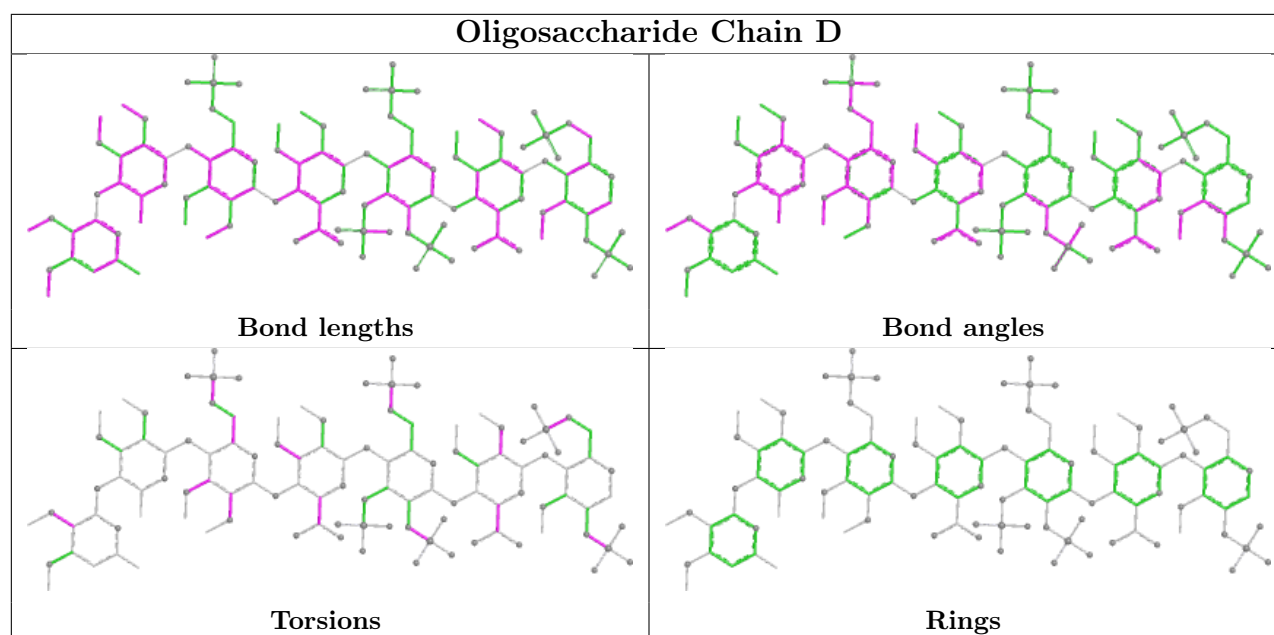
Mol	Chain	Res	Type	Atoms
4	D	1	YYB	C6-O6-S6-O3S6
4	D	2	U9J	C4-C5-C6-O6A
4	D	2	U9J	O5-C5-C6-O6A
4	D	3	GU6	C6-O6-S6-O20
4	D	3	GU6	C6-O6-S6-O21
4	D	4	U9M	C4-C5-C6-O6B
4	D	4	U9M	O5-C5-C6-O6B
4	D	5	U9G	C4-C5-C6-O6
4	D	5	U9G	O5-C5-C6-O6
4	D	5	U9G	C6-O6-S37-O39
4	D	5	U9G	C6-O6-S37-O3A
4	D	4	U9M	C2-C3-O3-C3M
4	D	1	YYB	C2-O2-S2-O2S2
4	D	1	YYB	C2-O2-S2-O3S2
4	D	3	GU6	C2-O2-S2-O14
4	D	3	GU6	C2-O2-S2-O15
4	D	1	YYB	C6-O6-S6-O1S6
4	D	3	GU6	C6-O6-S6-O19
4	D	5	U9G	C6-O6-S37-O38
4	D	5	U9G	C2-C3-O3-C3D
4	D	5	U9G	C3-C2-O2-C3G
4	D	1	YYB	C2-O2-S2-O1S2
4	D	3	GU6	C2-O2-S2-O13
4	D	4	U9M	C4-C3-O3-C3M
4	D	5	U9G	C4-C3-O3-C3D
4	D	7	U9D	C1-C2-O2-C2M
4	D	2	U9J	C1-C2-O2-C2M

There are no ring outliers.

4 monomers are involved in 11 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
4	D	6	GU8	4	0
4	D	3	GU6	1	0
4	D	2	U9J	2	0
4	D	5	U9G	4	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](#)

4 ligands 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	A	502	-	14,14,15	3.07	7 (50%)	17,19,21	2.53	6 (35%)
5	NAG	C	503	-	14,14,15	2.73	7 (50%)	17,19,21	2.89	7 (41%)
5	NAG	A	501	1	14,14,15	2.63	6 (42%)	17,19,21	2.80	7 (41%)
6	GU4	C	602	-	11,13,28	2.03	4 (36%)	17,18,45	3.65	9 (52%)

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	A	502	-	-	4/6/23/26	0/1/1/1
5	NAG	C	503	-	-	4/6/23/26	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	NAG	A	501	1	-	4/6/23/26	0/1/1/1
6	GU4	C	602	-	-	2/2/24/41	0/1/1/1

All (24) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	A	501	NAG	C4-C5	6.49	1.66	1.53
5	A	502	NAG	C1-C2	6.08	1.60	1.52
5	A	502	NAG	C4-C5	5.59	1.64	1.53
5	C	503	NAG	C4-C5	5.32	1.64	1.53
5	A	502	NAG	C4-C3	4.96	1.65	1.52
6	C	602	GU4	C1-C2	4.03	1.61	1.52
5	C	503	NAG	C1-C2	3.89	1.57	1.52
5	C	503	NAG	C3-C2	3.85	1.60	1.52
5	A	501	NAG	C3-C2	3.58	1.60	1.52
6	C	602	GU4	O5-C1	3.46	1.51	1.42
5	C	503	NAG	C4-C3	3.45	1.61	1.52
5	A	502	NAG	O5-C5	3.15	1.49	1.43
5	A	501	NAG	C4-C3	3.05	1.60	1.52
5	C	503	NAG	O5-C5	2.97	1.49	1.43
5	A	502	NAG	C2-N2	2.83	1.50	1.46
5	A	501	NAG	C8-C7	2.71	1.56	1.50
5	C	503	NAG	C8-C7	2.59	1.55	1.50
5	A	501	NAG	O5-C5	2.58	1.48	1.43
5	C	503	NAG	O5-C1	2.48	1.47	1.43
5	A	501	NAG	O5-C1	2.39	1.47	1.43
5	A	502	NAG	O4-C4	2.31	1.48	1.43
6	C	602	GU4	C6-C5	2.29	1.59	1.51
6	C	602	GU4	C4-C5	2.24	1.59	1.52
5	A	502	NAG	C8-C7	2.22	1.55	1.50

All (29) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	602	GU4	O3-C3-C4	-8.69	87.65	109.94
5	C	503	NAG	C1-O5-C5	7.82	122.66	112.19
5	A	501	NAG	C1-O5-C5	7.62	122.40	112.19
5	A	502	NAG	C2-N2-C7	6.07	131.03	122.90
6	C	602	GU4	O5-C1-C2	5.80	120.49	110.30
5	A	502	NAG	C1-O5-C5	5.39	119.41	112.19
6	C	602	GU4	O2-C2-C3	5.31	122.89	110.38
5	C	503	NAG	O5-C1-C2	-5.14	103.34	111.29

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	C	602	GU4	C6-C5-C4	-4.99	99.36	113.38
5	A	501	NAG	O5-C1-C2	-4.93	103.66	111.29
6	C	602	GU4	C3-C4-C5	4.32	120.50	110.93
5	C	503	NAG	C8-C7-N2	4.13	122.96	116.12
5	A	501	NAG	C8-C7-N2	3.94	122.65	116.12
6	C	602	GU4	C1-O5-C5	3.71	120.83	113.65
5	A	502	NAG	C8-C7-N2	3.48	121.88	116.12
6	C	602	GU4	C2-C3-C4	-3.46	101.84	109.68
5	C	503	NAG	C2-N2-C7	3.38	127.43	122.90
5	C	503	NAG	O7-C7-C8	-3.35	116.09	122.05
5	A	501	NAG	O7-C7-C8	-3.21	116.33	122.05
5	A	502	NAG	O7-C7-C8	-3.10	116.53	122.05
6	C	602	GU4	C1-C2-C3	3.07	116.61	110.36
5	A	501	NAG	C2-N2-C7	2.91	126.81	122.90
5	A	502	NAG	C3-C4-C5	-2.73	105.28	110.23
6	C	602	GU4	O5-C5-C6	2.71	113.15	106.44
5	A	502	NAG	O4-C4-C3	-2.57	104.32	110.38
5	A	501	NAG	O4-C4-C3	-2.30	104.96	110.38
5	A	501	NAG	C4-C3-C2	2.29	114.38	111.02
5	C	503	NAG	C4-C3-C2	2.18	114.22	111.02
5	C	503	NAG	O4-C4-C3	-2.11	105.41	110.38

There are no chirality outliers.

All (14) torsion outliers are listed below:

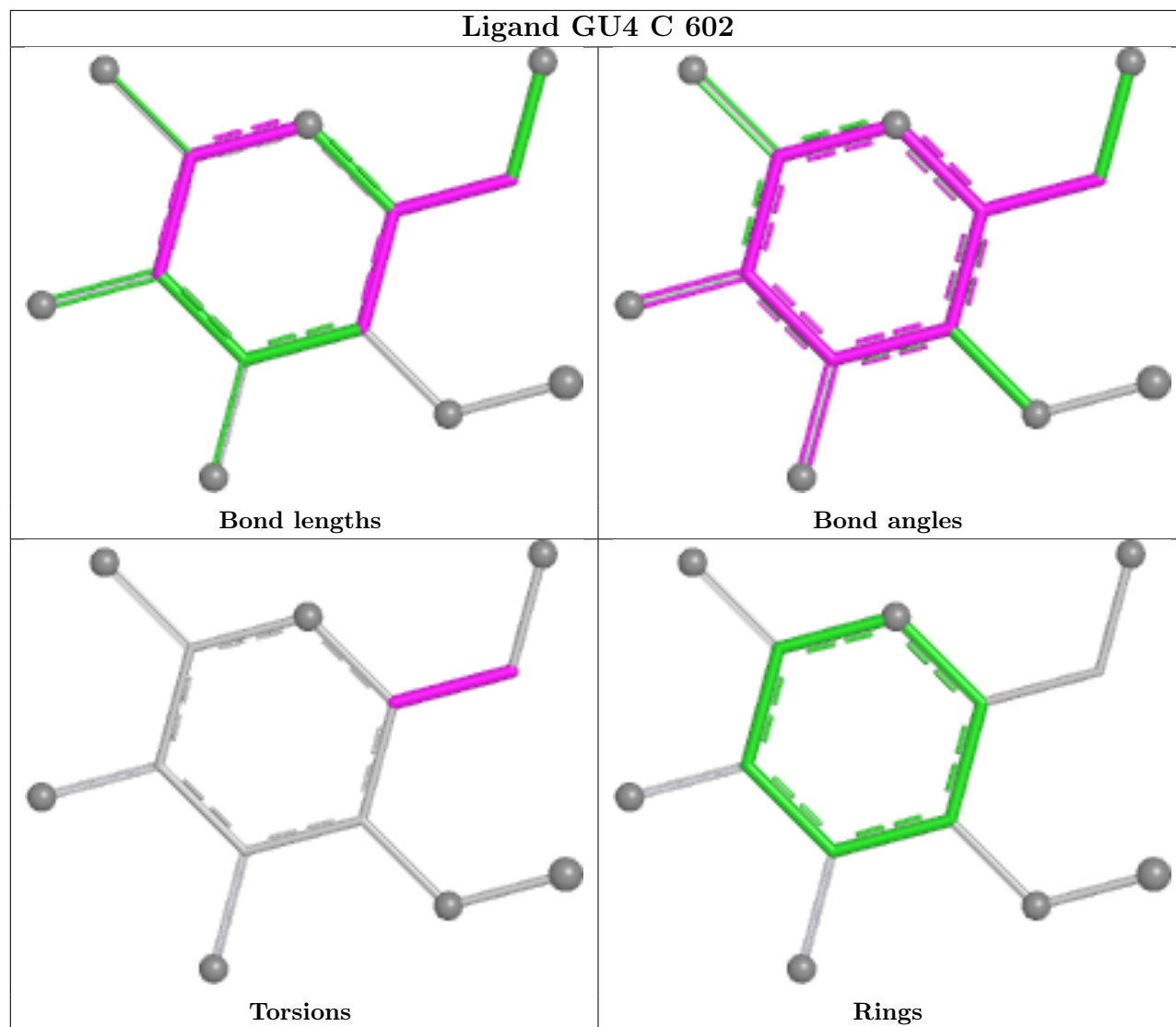
Mol	Chain	Res	Type	Atoms
5	A	501	NAG	O5-C5-C6-O6
5	C	503	NAG	O5-C5-C6-O6
5	A	501	NAG	C4-C5-C6-O6
5	C	503	NAG	C4-C5-C6-O6
5	A	502	NAG	O5-C5-C6-O6
6	C	602	GU4	O5-C5-C6-O6
5	A	502	NAG	C4-C5-C6-O6
5	A	501	NAG	C8-C7-N2-C2
5	A	501	NAG	O7-C7-N2-C2
5	C	503	NAG	C8-C7-N2-C2
5	C	503	NAG	O7-C7-N2-C2
6	C	602	GU4	C4-C5-C6-O6
5	A	502	NAG	C1-C2-N2-C7
5	A	502	NAG	C3-C2-N2-C7

There are no ring outliers.

4 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	502	NAG	5	0
5	C	503	NAG	3	0
5	A	501	NAG	1	0
6	C	602	GU4	4	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 [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	409/432 (94%)	0.19	18 (4%) 39 21	34, 67, 98, 116	0
2	B	32/36 (88%)	-0.17	0 100 100	37, 50, 74, 76	0
3	C	248/259 (95%)	-0.22	1 (0%) 88 76	15, 50, 69, 86	0
All	All	689/727 (94%)	0.02	19 (2%) 55 34	15, 59, 95, 116	0

All (19) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	378	GLU	6.4
1	A	382	ALA	4.3
1	A	93	GLY	3.5
1	A	366	ASP	3.3
3	C	72	SER	3.2
1	A	387	ALA	3.0
1	A	379	GLY	3.0
1	A	229	PHE	2.9
1	A	20	MET	2.4
1	A	95	CYS	2.4
1	A	289	GLU	2.4
1	A	26	PRO	2.2
1	A	351	LEU	2.2
1	A	340	LEU	2.2
1	A	149	ASP	2.2
1	A	15	ILE	2.1
1	A	16	PRO	2.1
1	A	24	ARG	2.0
1	A	414	GLU	2.0

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

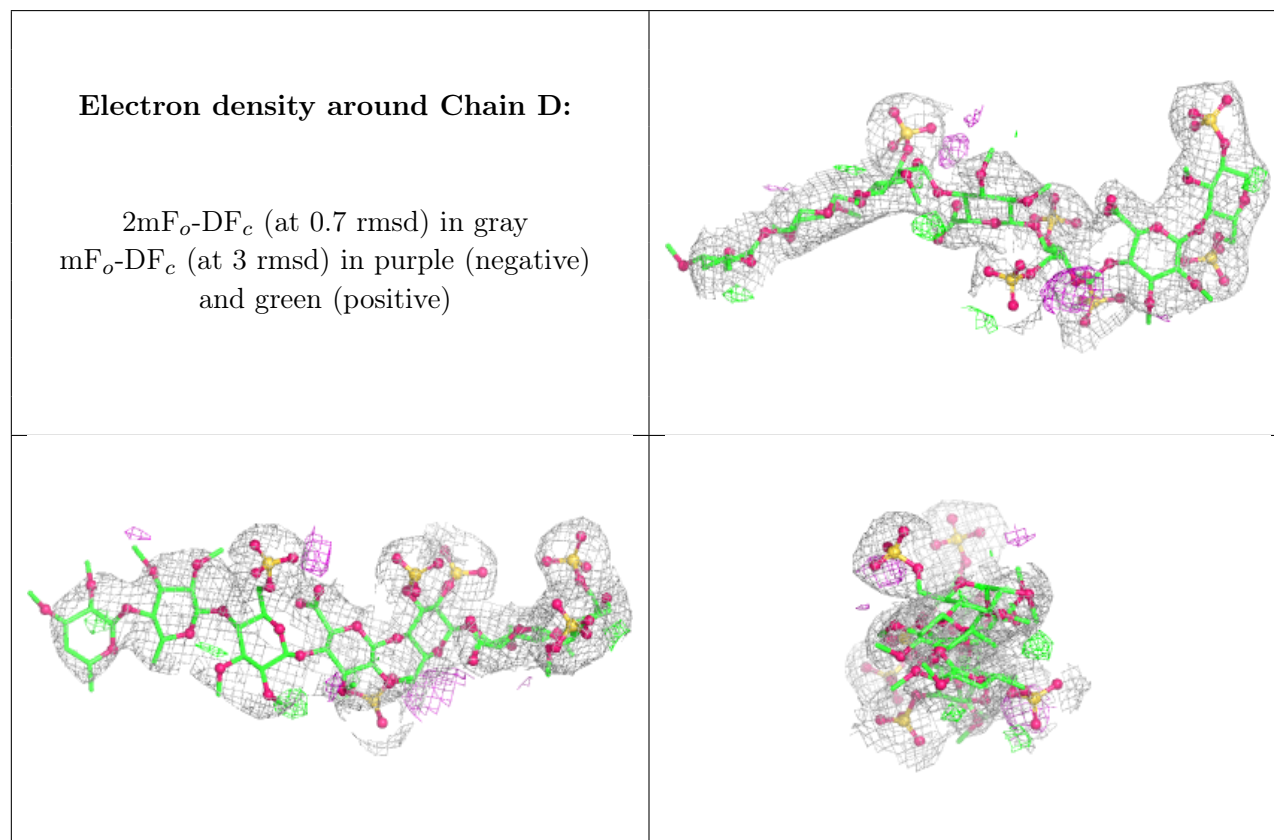
There are no non-standard protein/DNA/RNA residues in this entry.

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(Å ²)	Q<0.9
4	U9D	D	7	11/14	0.76	0.25	111,114,116,116	0
4	GU8	D	6	12/15	0.88	0.18	95,100,103,108	0
4	YYB	D	1	20/20	0.91	0.11	78,79,85,85	0
4	GU6	D	3	23/24	0.91	0.09	70,77,86,87	0
4	U9M	D	4	14/15	0.92	0.12	81,83,85,86	0
4	U9G	D	5	17/18	0.92	0.12	67,81,85,90	0
4	U9J	D	2	14/15	0.95	0.12	78,80,82,82	0

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

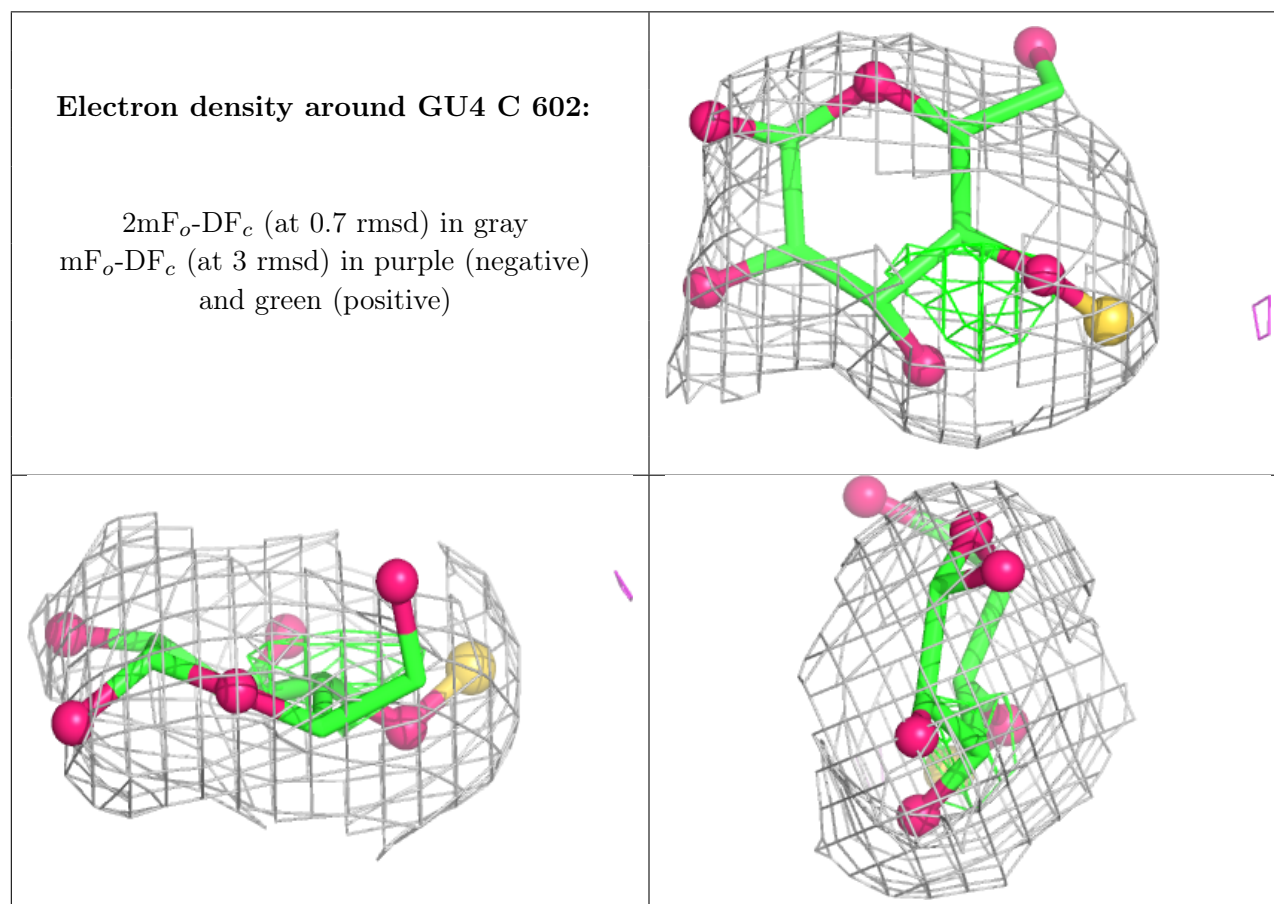


6.4 Ligands [i](#)

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	NAG	A	502	14/15	0.57	0.17	125,127,128,129	0
5	NAG	A	501	14/15	0.67	0.16	103,105,105,105	0
5	NAG	C	503	14/15	0.76	0.14	101,104,105,105	0
6	GU4	C	602	13/28	0.86	0.18	115,118,119,120	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.



6.5 Other polymers [i](#)

There are no such residues in this entry.