



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 10, 2026 – 02:57 AM UTC

PDB ID : 3PV0 / pdb_00003pv0
Title : Crystal Structure of a pre-translocation state MBP-Maltose transporter complex without nucleotide
Authors : Oldham, M.L.; Chen, J.
Deposited on : 2010-12-06
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

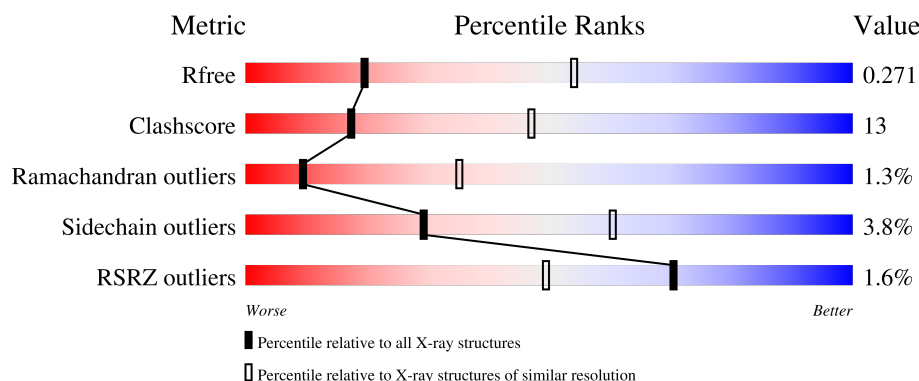
1 Overall quality at a glance

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	E	370	0% 75% 24% .
2	F	514	3% 67% 25% 6%
3	G	296	0% 65% 26% 5%
4	A	381	0% 65% 29% .
4	B	381	2% 71% 24% .

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Mol	Chain	Length	Quality of chain
5	C	2	 50%50%
5	D	2	 50%50%

2 Entry composition

There are 6 unique types of molecules in this entry. The entry contains 14643 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 Maltose transporter subunit; periplasmic-binding component of ABC superfamily.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	E	370	Total	C	N	O	S	0	0	0
			2880	1854	469	549	8			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
E	69	CYS	GLY	engineered mutation	UNP B1XC33
E	337	CYS	SER	engineered mutation	UNP B1XC33

- Molecule 2 is a protein called Maltose transporter subunit; membrane component of ABC superfamily.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	F	483	Total	C	N	O	S	0	0	0
			3742	2458	596	671	17			

- Molecule 3 is a protein called Maltose transporter subunit; membrane component of ABC superfamily.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	G	282	Total	C	N	O	S	0	0	0
			2182	1461	348	364	9			

- Molecule 4 is a protein called Fused maltose transport subunit, ATP-binding component of ABC superfamily; regulatory protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	A	370	Total	C	N	O	S	0	0	0
			2871	1816	514	528	13			
4	B	370	Total	C	N	O	S	0	0	0
			2871	1816	514	528	13			

There are 20 discrepancies between the modelled and reference sequences:

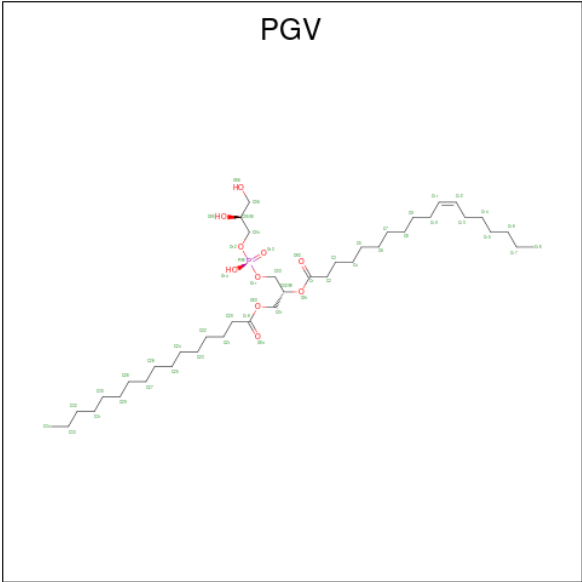
Chain	Residue	Modelled	Actual	Comment	Reference
A	372	ALA	-	expression tag	UNP B1XC34
A	373	SER	-	expression tag	UNP B1XC34
A	374	ALA	-	expression tag	UNP B1XC34
A	375	SER	-	expression tag	UNP B1XC34
A	376	HIS	-	expression tag	UNP B1XC34
A	377	HIS	-	expression tag	UNP B1XC34
A	378	HIS	-	expression tag	UNP B1XC34
A	379	HIS	-	expression tag	UNP B1XC34
A	380	HIS	-	expression tag	UNP B1XC34
A	381	HIS	-	expression tag	UNP B1XC34
B	372	ALA	-	expression tag	UNP B1XC34
B	373	SER	-	expression tag	UNP B1XC34
B	374	ALA	-	expression tag	UNP B1XC34
B	375	SER	-	expression tag	UNP B1XC34
B	376	HIS	-	expression tag	UNP B1XC34
B	377	HIS	-	expression tag	UNP B1XC34
B	378	HIS	-	expression tag	UNP B1XC34
B	379	HIS	-	expression tag	UNP B1XC34
B	380	HIS	-	expression tag	UNP B1XC34
B	381	HIS	-	expression tag	UNP B1XC34

- Molecule 5 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
5	C	2	Total	C	O	0	0	0
			23	12	11			
5	D	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 6 is (1R)-2-{{[(2S)-2,3-DIHYDROXYPROPYL]OXY}(HYDROXY)PHOSPHORYL]OXY}-1-[(PALMITOYLOXY)METHYL]ETHYL (11E)-OCTADEC-11-ENOATE (CCD ID: PGV) (formula: C₄₀H₇₇O₁₀P).

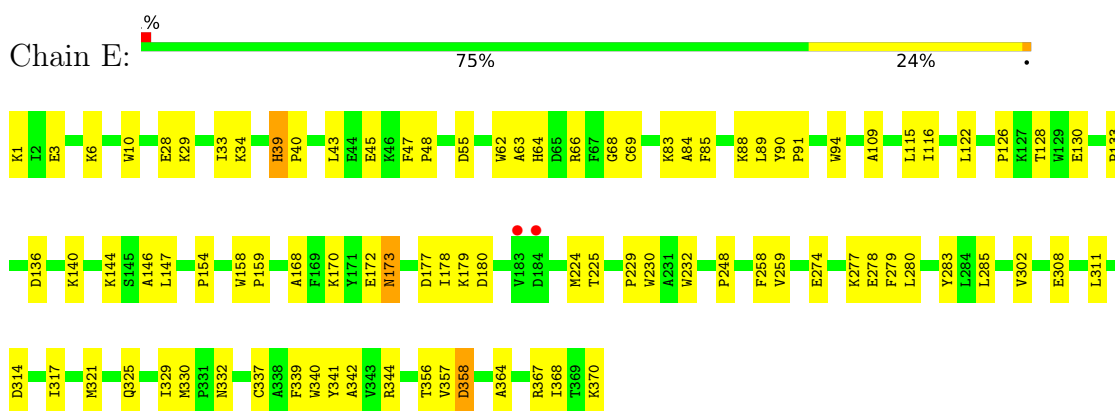


Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	F	1	Total	C	O	P	0	0
			51	40	10	1		

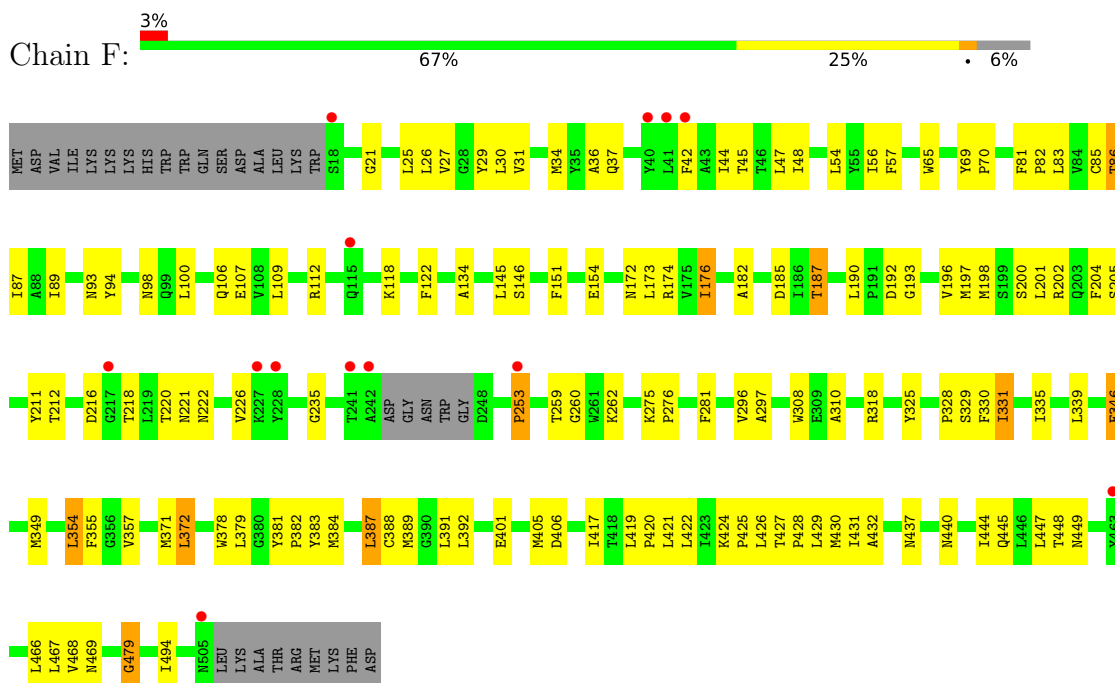
3 Residue-property plots

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.

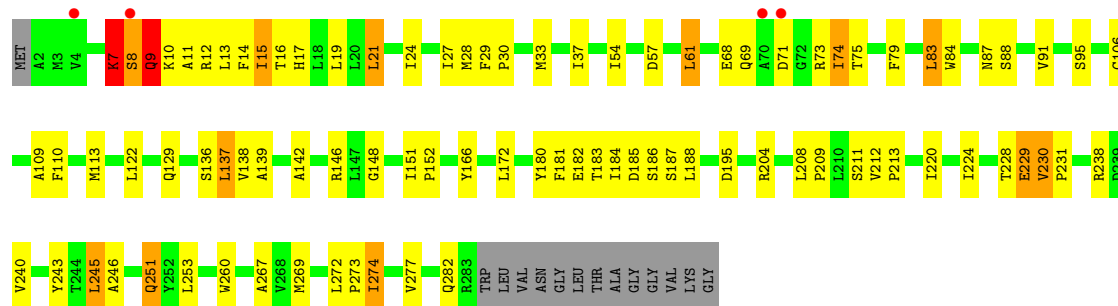
- Molecule 1: Maltose transporter subunit; periplasmic-binding component of ABC superfamily



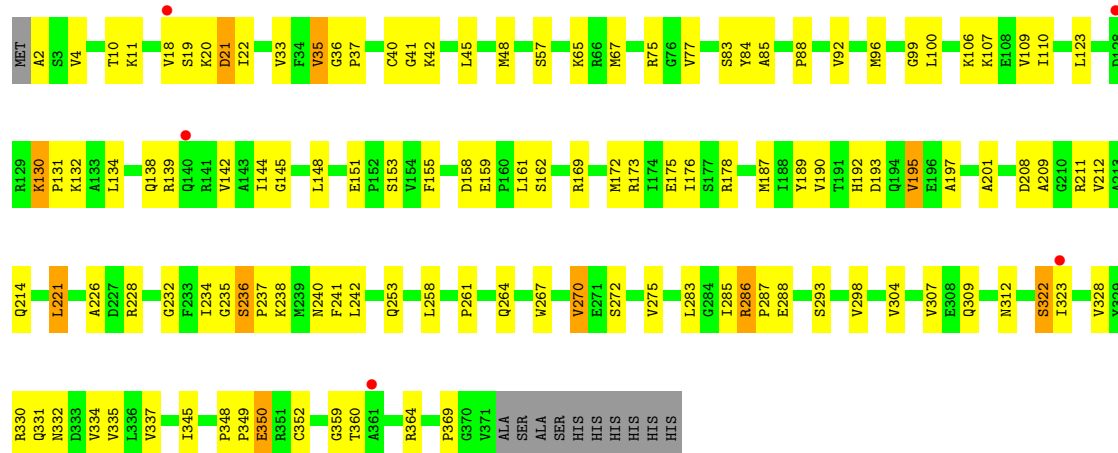
- Molecule 2: Maltose transporter subunit; membrane component of ABC superfamily



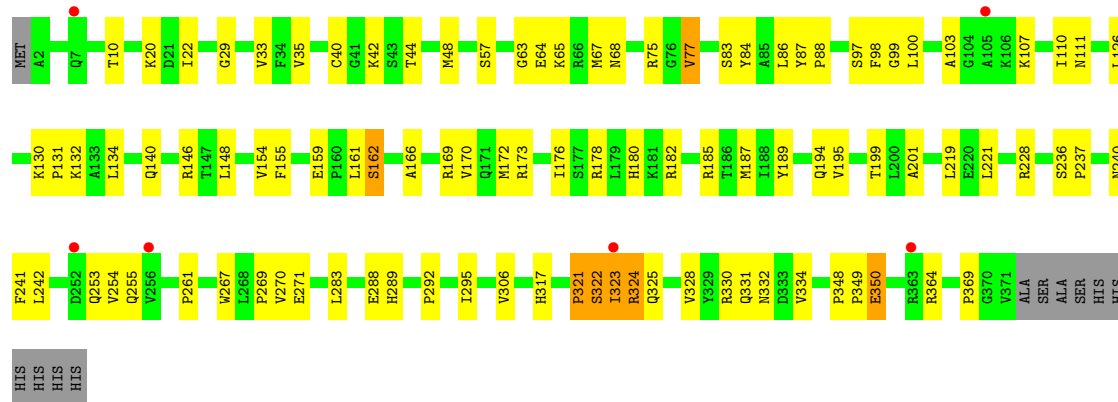
- Molecule 3: Maltose transporter subunit; membrane component of ABC superfamily



- Molecule 4: Fused maltose transport subunit, ATP-binding component of ABC superfamily; regulatory protein



- Molecule 4: Fused maltose transport subunit, ATP-binding component of ABC superfamily; regulatory protein



- Molecule 5: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain C:  50% 50%

GLC1
GLC2

- Molecule 5: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D:  50% 50%

GLC1
GLC2

4 Data and refinement statistics

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	78.54Å 92.63Å 119.13Å 90.48° 102.13° 104.21°	Depositor
Resolution (Å)	19.96 – 3.10 19.96 – 3.10	Depositor EDS
% Data completeness (in resolution range)	75.6 (19.96-3.10) 75.3 (19.96-3.10)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.62 (at 3.09Å)	Xtriage
Refinement program	REFMAC 5.5.0088	Depositor
R, R_{free}	0.231 , 0.274 0.230 , 0.271	Depositor DCC
R_{free} test set	2229 reflections (5.13%)	wwPDB-VP
Wilson B-factor (Å ²)	69.7	Xtriage
Anisotropy	0.031	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.26 , 33.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.91	EDS
Total number of atoms	14643	wwPDB-VP
Average B, all atoms (Å ²)	83.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.51% 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: PGV, GLC

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	E	0.31	0/2949	0.73	0/4001
2	F	0.32	0/3833	0.70	0/5217
3	G	0.34	0/2242	0.75	2/3065 (0.1%)
4	A	0.31	0/2921	0.75	4/3961 (0.1%)
4	B	0.31	0/2921	0.74	2/3961 (0.1%)
All	All	0.32	0/14866	0.73	8/20205 (0.0%)

There are no bond length outliers.

All (8) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	87	TYR	CA-C-N	6.13	126.30	119.32
4	B	87	TYR	C-N-CA	6.13	126.30	119.32
3	G	151	ILE	CA-C-N	5.66	124.86	118.97
3	G	151	ILE	C-N-CA	5.66	124.86	118.97
4	A	286	ARG	CA-C-N	5.25	124.92	119.56
4	A	286	ARG	C-N-CA	5.25	124.92	119.56
4	A	130	LYS	CA-C-N	5.02	126.12	119.84
4	A	130	LYS	C-N-CA	5.02	126.12	119.84

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	E	2880	0	2859	63	0
2	F	3742	0	3763	102	0
3	G	2182	0	2271	76	0
4	A	2871	0	2937	83	0
4	B	2871	0	2937	67	0
5	C	23	0	21	1	0
5	D	23	0	21	2	0
6	F	51	0	76	1	0
All	All	14643	0	14885	370	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 13.

All (370) 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:B:236:SER:HB3	4:B:237:PRO:HD3	1.25	1.16
4:A:236:SER:HB3	4:A:237:PRO:HD3	1.32	1.10
3:G:166:TYR:OH	3:G:229:GLU:HG2	1.51	1.09
2:F:259:THR:HB	2:F:262:LYS:HD2	1.41	0.99
3:G:166:TYR:CZ	3:G:229:GLU:HG2	1.99	0.97
1:E:40:PRO:HG2	1:E:43:LEU:HD13	1.54	0.89
3:G:251:GLN:HE21	3:G:251:GLN:HA	1.41	0.86
3:G:166:TYR:OH	3:G:229:GLU:CG	2.24	0.85
3:G:91:VAL:O	3:G:95:SER:HB2	1.77	0.84
3:G:212:VAL:HB	3:G:213:PRO:HD3	1.60	0.84
4:B:236:SER:CB	4:B:237:PRO:HD3	2.07	0.82
4:A:88:PRO:HB3	4:A:132:LYS:HE2	1.62	0.81
3:G:8:SER:O	3:G:10:LYS:N	2.13	0.80
4:B:236:SER:HB3	4:B:237:PRO:CD	2.08	0.80
1:E:115:LEU:HD22	1:E:248:PRO:HD3	1.64	0.79
4:A:236:SER:CB	4:A:237:PRO:HD3	2.12	0.79
3:G:274:ILE:H	3:G:274:ILE:HD12	1.47	0.78
3:G:74:ILE:HD13	3:G:74:ILE:H	1.49	0.78
1:E:90:TYR:OH	1:E:308:GLU:HG2	1.84	0.77
2:F:331:ILE:HD12	3:G:267:ALA:HB1	1.64	0.77
4:A:369:PRO:HG2	4:B:334:VAL:CG2	2.14	0.77
2:F:151:PHE:HD2	2:F:182:ALA:HB3	1.49	0.77
3:G:9:GLN:HE21	3:G:9:GLN:HA	1.50	0.76
1:E:85:PHE:HA	1:E:88:LYS:HE3	1.70	0.74
2:F:354:LEU:HD12	2:F:355:PHE:H	1.51	0.74
3:G:29:PHE:HB3	3:G:30:PRO:HD3	1.71	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:154:PRO:HG3	1:E:344:ARG:HA	1.70	0.72
2:F:387:LEU:HD21	2:F:429:LEU:HD13	1.71	0.71
4:A:155:PHE:HB2	4:A:187:MET:HG2	1.70	0.71
1:E:68:GLY:HA3	1:E:332:ASN:O	1.89	0.71
4:B:33:VAL:HG22	4:B:189:TYR:HB3	1.73	0.71
4:A:175:GLU:OE2	4:A:178:ARG:NH2	2.24	0.70
3:G:17:HIS:O	3:G:21:LEU:HB2	1.91	0.70
2:F:151:PHE:CD2	2:F:182:ALA:HB3	2.28	0.69
4:A:236:SER:HB3	4:A:237:PRO:CD	2.17	0.68
4:A:161:LEU:HB3	4:A:169:ARG:HG3	1.75	0.68
4:A:40:CYS:SG	4:A:42:LYS:HG3	2.34	0.68
4:B:77:VAL:HG23	4:B:154:VAL:HB	1.76	0.68
3:G:7:LYS:O	3:G:9:GLN:N	2.27	0.67
3:G:272:LEU:N	3:G:273:PRO:HD2	2.08	0.67
3:G:79:PHE:HB3	3:G:84:TRP:CH2	2.30	0.67
4:B:331:GLN:HG2	4:B:332:ASN:H	1.60	0.66
4:A:20:LYS:O	4:A:22:ILE:HG23	1.95	0.66
1:E:1:LYS:N	1:E:55:ASP:OD1	2.29	0.66
4:B:67:MET:CE	4:B:75:ARG:HA	2.25	0.65
3:G:251:GLN:HE21	3:G:251:GLN:CA	2.08	0.65
2:F:83:LEU:O	2:F:86:THR:HG22	1.97	0.65
1:E:356:THR:HG22	1:E:357:VAL:H	1.62	0.65
2:F:384:MET:HE2	2:F:384:MET:HA	1.79	0.65
1:E:28:GLU:OE2	1:E:34:LYS:HG2	1.97	0.64
2:F:406:ASP:HB3	4:B:99:GLY:HA2	1.79	0.64
3:G:272:LEU:H	3:G:273:PRO:HD2	1.63	0.64
4:B:86:LEU:HA	4:B:146:ARG:NH2	2.12	0.64
4:B:40:CYS:SG	4:B:42:LYS:HG3	2.37	0.63
4:B:44:THR:HG22	4:B:48:MET:HE2	1.80	0.63
2:F:335:ILE:O	2:F:339:LEU:HG	1.98	0.63
4:A:331:GLN:HG2	4:A:332:ASN:H	1.63	0.63
2:F:145:LEU:HD23	2:F:146:SER:O	1.98	0.62
4:B:321:PRO:O	4:B:322:SER:CB	2.46	0.62
4:A:369:PRO:HG2	4:B:334:VAL:HG21	1.81	0.62
2:F:437:ASN:HD21	5:D:2:GLC:H62	1.64	0.61
2:F:331:ILE:O	2:F:335:ILE:HG23	1.99	0.61
2:F:378:TRP:HE3	2:F:379:LEU:HD12	1.65	0.61
2:F:422:LEU:O	2:F:426:LEU:HB2	1.99	0.61
3:G:251:GLN:HA	3:G:251:GLN:NE2	2.12	0.61
2:F:372:LEU:HD13	2:F:447:LEU:HD23	1.83	0.61
3:G:24:ILE:O	3:G:28:MET:HG2	2.01	0.60

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:64:HIS:NE2	1:E:330:MET:O	2.31	0.60
3:G:181:PHE:C	3:G:183:THR:H	2.09	0.60
1:E:10:TRP:CE3	1:E:43:LEU:HD11	2.37	0.60
3:G:7:LYS:C	3:G:9:GLN:H	2.10	0.59
3:G:88:SER:OG	3:G:245:LEU:HB2	2.01	0.59
4:A:2:ALA:HB2	4:A:153:SER:HB2	1.84	0.59
1:E:66:ARG:HD3	1:E:337:CYS:HB3	1.84	0.59
3:G:282:GLN:HA	3:G:282:GLN:OE1	2.00	0.59
2:F:381:TYR:CD2	2:F:382:PRO:HD3	2.37	0.59
4:B:261:PRO:HD3	4:B:322:SER:OG	2.03	0.59
3:G:10:LYS:HA	3:G:13:LEU:HB3	1.85	0.58
2:F:151:PHE:HD2	2:F:182:ALA:CB	2.16	0.58
2:F:27:VAL:HG21	2:F:54:LEU:HD11	1.83	0.58
4:B:240:ASN:HD21	4:B:328:VAL:H	1.51	0.58
2:F:122:PHE:HA	2:F:134:ALA:O	2.03	0.58
4:B:155:PHE:HB2	4:B:187:MET:HG2	1.85	0.58
4:B:321:PRO:O	4:B:322:SER:HB2	2.03	0.57
4:A:88:PRO:HB3	4:A:132:LYS:CE	2.33	0.57
3:G:195:ASP:HB3	4:A:99:GLY:HA2	1.87	0.57
2:F:388:CYS:O	2:F:392:LEU:HB2	2.05	0.56
4:A:228:ARG:HD2	4:A:359:GLY:HA3	1.87	0.56
2:F:85:CYS:O	2:F:89:ILE:HG12	2.06	0.56
1:E:147:LEU:HB2	1:E:224:MET:HE3	1.87	0.56
1:E:1:LYS:O	3:G:238:ARG:NH2	2.36	0.56
2:F:192:ASP:OD1	2:F:193:GLY:N	2.40	0.55
1:E:278:GLU:HG2	2:F:200:SER:HB2	1.87	0.55
4:A:33:VAL:HG22	4:A:189:TYR:HB3	1.88	0.55
4:A:272:SER:O	4:A:275:VAL:HG22	2.07	0.55
4:A:159:GLU:HB3	4:A:162:SER:HB2	1.88	0.55
3:G:185:ASP:HB3	3:G:188:LEU:HD23	1.88	0.55
2:F:100:LEU:HD12	2:F:100:LEU:H	1.72	0.55
1:E:279:PHE:HD1	1:E:280:LEU:HD23	1.72	0.55
4:A:148:LEU:O	4:A:151:GLU:HG3	2.07	0.55
4:A:240:ASN:HB2	4:A:285:ILE:HG23	1.89	0.55
3:G:211:SER:O	3:G:212:VAL:C	2.51	0.54
4:B:67:MET:HE3	4:B:75:ARG:HG2	1.89	0.54
4:A:253:GLN:HG3	4:A:267:TRP:CE3	2.43	0.54
3:G:109:ALA:HA	3:G:113:MET:HE3	1.89	0.54
2:F:176:ILE:HD11	2:F:201:LEU:HD22	1.90	0.54
2:F:383:TYR:CE2	2:F:384:MET:HE3	2.43	0.53
4:A:193:ASP:OD1	4:A:195:VAL:HG23	2.09	0.53

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:158:TRP:N	1:E:159:PRO:CD	2.71	0.53
4:B:288:GLU:HG3	4:B:330:ARG:HD3	1.90	0.53
1:E:314:ASP:HB3	1:E:317:ILE:HD12	1.90	0.53
4:B:350:GLU:CD	4:B:350:GLU:H	2.16	0.53
2:F:354:LEU:CD1	2:F:355:PHE:H	2.19	0.53
3:G:9:GLN:HE21	3:G:9:GLN:CA	2.22	0.53
4:B:306:VAL:HB	4:B:317:HIS:CD2	2.44	0.53
4:B:86:LEU:HA	4:B:146:ARG:HH22	1.74	0.53
4:B:130:LYS:O	4:B:132:LYS:N	2.42	0.53
2:F:31:VAL:HG11	2:F:47:LEU:HD13	1.91	0.53
1:E:47:PHE:HB3	1:E:48:PRO:HD3	1.91	0.52
3:G:224:ILE:O	3:G:228:THR:HG22	2.09	0.52
4:A:334:VAL:HG21	4:B:369:PRO:HG2	1.91	0.52
1:E:258:PHE:HB3	1:E:330:MET:HE2	1.91	0.52
1:E:29:LYS:O	2:F:174:ARG:NH1	2.43	0.52
2:F:30:LEU:O	2:F:34:MET:HG2	2.10	0.52
2:F:212:THR:HG23	2:F:222:ASN:HD21	1.73	0.52
1:E:62:TRP:CD1	1:E:63:ALA:H	2.27	0.52
4:A:232:GLY:O	4:A:238:LYS:HE3	2.10	0.52
1:E:154:PRO:HG3	1:E:344:ARG:CA	2.39	0.52
2:F:444:ILE:HG13	2:F:466:LEU:HG	1.91	0.52
3:G:91:VAL:O	3:G:95:SER:CB	2.54	0.52
2:F:98:ASN:HD21	2:F:235:GLY:HA3	1.74	0.51
4:A:67:MET:HE2	4:A:75:ARG:HA	1.92	0.51
3:G:208:LEU:N	3:G:209:PRO:HD2	2.25	0.51
4:A:22:ILE:HD11	4:A:45:LEU:HD21	1.92	0.51
4:A:35:VAL:HG11	4:A:197:ALA:HB2	1.92	0.51
2:F:392:LEU:HD13	2:F:422:LEU:HD11	1.92	0.51
2:F:445:GLN:HA	2:F:449:ASN:HA	1.92	0.51
1:E:339:PHE:HA	1:E:368:ILE:HD12	1.92	0.51
2:F:330:PHE:CE1	2:F:331:ILE:HG22	2.46	0.51
4:A:234:ILE:HG22	4:A:235:GLY:N	2.26	0.51
4:B:159:GLU:HB3	4:B:162:SER:HB2	1.92	0.51
1:E:172:GLU:O	1:E:173:ASN:C	2.53	0.51
2:F:86:THR:HA	2:F:89:ILE:HG13	1.93	0.51
4:A:236:SER:HB3	4:A:330:ARG:NH1	2.25	0.51
3:G:212:VAL:HB	3:G:213:PRO:CD	2.37	0.51
4:A:264:GLN:HE22	4:A:298:VAL:HA	1.76	0.51
2:F:187:THR:O	2:F:187:THR:OG1	2.30	0.51
2:F:371:MET:O	2:F:372:LEU:C	2.53	0.51
1:E:89:LEU:HD12	1:E:94:TRP:CZ2	2.45	0.50

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:F:275:LYS:HB3	2:F:276:PRO:HD3	1.93	0.50
4:A:211:ARG:HG2	4:A:212:VAL:N	2.27	0.50
4:B:178:ARG:O	4:B:182:ARG:HB2	2.12	0.50
1:E:122:LEU:HD21	1:E:126:PRO:HD3	1.93	0.50
2:F:221:ASN:OD1	2:F:222:ASN:N	2.44	0.50
6:F:4001:PGV:H21	3:G:16:THR:OG1	2.12	0.50
4:B:130:LYS:C	4:B:132:LYS:H	2.20	0.50
1:E:177:ASP:C	1:E:179:LYS:H	2.20	0.50
2:F:387:LEU:HD21	2:F:429:LEU:CD1	2.41	0.49
4:B:194:GLN:NE2	4:B:195:VAL:HG22	2.25	0.49
4:A:130:LYS:HG2	4:A:131:PRO:HD2	1.94	0.49
4:A:20:LYS:O	4:A:21:ASP:C	2.55	0.49
4:A:37:PRO:O	4:A:42:LYS:NZ	2.45	0.49
4:B:170:VAL:HA	4:B:173:ARG:HE	1.78	0.49
2:F:34:MET:HE2	2:F:42:PHE:O	2.13	0.49
4:B:161:LEU:HB3	4:B:169:ARG:HG3	1.94	0.49
2:F:82:PRO:O	2:F:86:THR:HB	2.13	0.49
2:F:346:GLU:HG3	3:G:33:MET:HE2	1.95	0.49
4:B:253:GLN:HG3	4:B:267:TRP:CE3	2.48	0.49
1:E:136:ASP:O	1:E:140:LYS:HB2	2.13	0.48
1:E:259:VAL:HB	1:E:329:ILE:HA	1.95	0.48
1:E:158:TRP:N	1:E:159:PRO:HD2	2.28	0.48
2:F:36:ALA:O	2:F:37:GLN:HB2	2.14	0.48
4:A:11:LYS:HB2	4:A:48:MET:SD	2.53	0.48
1:E:66:ARG:CD	1:E:337:CYS:HB3	2.43	0.48
2:F:69:TYR:N	2:F:70:PRO:HD2	2.29	0.48
4:A:214:GLN:HE21	4:A:221:LEU:HD22	1.78	0.48
4:A:335:VAL:HG12	4:A:337:VAL:HG23	1.95	0.48
1:E:116:ILE:HB	1:E:225:THR:HG23	1.96	0.48
2:F:346:GLU:HA	2:F:349:MET:HG3	1.95	0.48
3:G:27:ILE:C	3:G:27:ILE:HD12	2.38	0.47
3:G:37:ILE:HD13	3:G:260:TRP:NE1	2.28	0.47
4:B:20:LYS:O	4:B:22:ILE:HG23	2.14	0.47
4:B:323:ILE:C	4:B:325:GLN:H	2.22	0.47
1:E:229:PRO:HA	1:E:232:TRP:CE2	2.49	0.47
2:F:431:ILE:HG13	2:F:432:ALA:N	2.27	0.47
4:B:254:VAL:HG12	4:B:255:GLN:N	2.28	0.47
2:F:187:THR:HA	2:F:197:MET:HG2	1.95	0.47
2:F:401:GLU:O	2:F:405:MET:HG2	2.14	0.47
3:G:148:GLY:O	3:G:152:PRO:HA	2.14	0.47
2:F:381:TYR:N	2:F:382:PRO:HD2	2.29	0.47

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:136:ASP:HA	1:E:146:ALA:HB2	1.96	0.47
2:F:417:ILE:O	2:F:421:LEU:HB2	2.13	0.47
3:G:73:ARG:HB3	3:G:74:ILE:HD13	1.95	0.47
3:G:204:ARG:HA	3:G:208:LEU:HD12	1.97	0.47
4:A:236:SER:CB	4:A:237:PRO:CD	2.84	0.47
4:B:33:VAL:CG2	4:B:201:ALA:HB2	2.45	0.47
4:B:140:GLN:NE2	4:B:161:LEU:HD23	2.30	0.47
3:G:69:GLN:C	3:G:71:ASP:H	2.21	0.47
4:B:63:GLY:O	4:B:64:GLU:HB2	2.14	0.47
4:B:172:MET:O	4:B:176:ILE:HG12	2.14	0.47
2:F:176:ILE:HD11	2:F:201:LEU:CD2	2.44	0.47
1:E:364:ALA:O	1:E:368:ILE:HG12	2.14	0.47
2:F:26:LEU:HA	2:F:29:TYR:HB3	1.97	0.46
3:G:181:PHE:C	3:G:183:THR:N	2.72	0.46
4:B:97:SER:O	4:B:98:PHE:C	2.58	0.46
1:E:109:ALA:HA	1:E:302:VAL:HA	1.98	0.46
4:A:10:THR:N	4:A:57:SER:O	2.48	0.46
4:A:138:GLN:O	4:A:142:VAL:HG23	2.15	0.46
4:A:312:ASN:HB2	4:B:288:GLU:HG2	1.97	0.46
3:G:136:SER:O	3:G:137:LEU:C	2.58	0.46
4:B:172:MET:HE2	4:B:172:MET:HA	1.98	0.46
2:F:383:TYR:CD2	2:F:384:MET:HE3	2.51	0.46
2:F:154:GLU:HA	2:F:185:ASP:HB3	1.97	0.46
2:F:426:LEU:O	2:F:430:MET:HG2	2.15	0.46
3:G:240:VAL:HA	3:G:243:TYR:CD1	2.51	0.46
3:G:129:GLN:NE2	3:G:172:LEU:HG	2.31	0.46
1:E:154:PRO:HD3	1:E:344:ARG:HG3	1.98	0.45
2:F:190:LEU:H	2:F:190:LEU:HD22	1.81	0.45
4:A:287:PRO:HB3	4:A:328:VAL:O	2.16	0.45
3:G:7:LYS:C	3:G:9:GLN:N	2.70	0.45
3:G:106:CYS:HG	3:G:110:PHE:HE1	1.59	0.45
3:G:220:ILE:HG12	3:G:277:VAL:CG1	2.46	0.45
4:B:86:LEU:O	4:B:88:PRO:HD3	2.17	0.45
2:F:281:PHE:HA	2:F:467:LEU:HD21	1.98	0.45
2:F:427:THR:HB	2:F:428:PRO:CD	2.47	0.45
4:A:241:PHE:C	4:A:242:LEU:HD12	2.41	0.45
3:G:10:LYS:O	3:G:11:ALA:C	2.58	0.45
4:A:286:ARG:HA	4:A:287:PRO:HD3	1.86	0.45
4:B:40:CYS:SG	4:B:42:LYS:CG	3.03	0.45
3:G:230:VAL:HB	3:G:231:PRO:HD3	1.99	0.45
4:B:67:MET:O	4:B:68:ASN:C	2.60	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:G:272:LEU:N	3:G:273:PRO:CD	2.78	0.45
4:A:348:PRO:HA	4:A:349:PRO:HD2	1.82	0.45
1:E:274:GLU:HG2	2:F:198:MET:HE3	1.98	0.45
3:G:106:CYS:SG	3:G:110:PHE:HE1	2.40	0.45
1:E:130:GLU:O	1:E:133:PRO:HD2	2.17	0.44
1:E:358:ASP:OD1	1:E:358:ASP:N	2.50	0.44
2:F:387:LEU:HD11	2:F:429:LEU:HD13	1.99	0.44
4:B:126:LEU:HD13	4:B:134:LEU:HD22	1.99	0.44
1:E:170:LYS:HB3	1:E:180:ASP:HB3	1.98	0.44
2:F:81:PHE:N	2:F:82:PRO:HD2	2.32	0.44
1:E:277:LYS:HE3	2:F:200:SER:HB3	1.98	0.44
2:F:391:LEU:HD23	2:F:426:LEU:HD13	2.00	0.44
4:A:258:LEU:H	4:A:258:LEU:HD22	1.82	0.44
4:A:345:ILE:HD12	4:A:345:ILE:O	2.17	0.44
2:F:173:LEU:HD11	2:F:202:ARG:NH2	2.32	0.44
2:F:106:GLN:HG3	2:F:107:GLU:N	2.33	0.44
4:A:309:GLN:HB3	4:B:219:LEU:HD13	1.99	0.44
4:A:134:LEU:HB2	4:A:139:ARG:HG3	1.99	0.44
4:A:18:VAL:HG13	4:A:19:SER:H	1.83	0.44
4:A:36:GLY:N	4:A:42:LYS:HD3	2.32	0.44
3:G:180:TYR:O	3:G:183:THR:HB	2.17	0.44
2:F:406:ASP:CB	4:B:99:GLY:HA2	2.46	0.44
3:G:136:SER:O	3:G:139:ALA:N	2.51	0.44
4:A:106:LYS:HD3	4:A:109:VAL:HG21	1.99	0.44
4:A:350:GLU:H	4:A:350:GLU:CD	2.25	0.44
1:E:28:GLU:CD	1:E:34:LYS:HG2	2.42	0.43
4:A:144:ILE:O	4:A:145:GLY:C	2.61	0.43
1:E:10:TRP:HE3	1:E:43:LEU:HD11	1.80	0.43
4:A:41:GLY:O	4:A:42:LYS:C	2.61	0.43
4:B:110:ILE:O	4:B:111:ASN:C	2.60	0.43
1:E:356:THR:HG22	1:E:357:VAL:N	2.31	0.43
2:F:25:LEU:O	2:F:29:TYR:HB2	2.18	0.43
3:G:269:MET:O	3:G:272:LEU:HB2	2.18	0.43
4:A:40:CYS:SG	4:A:42:LYS:CG	3.06	0.43
4:B:331:GLN:HG2	4:B:332:ASN:N	2.29	0.43
1:E:90:TYR:HA	1:E:91:PRO:HD3	1.86	0.43
3:G:166:TYR:CE1	3:G:229:GLU:HG2	2.49	0.43
4:B:292:PRO:HD2	4:B:295:ILE:HD12	2.01	0.43
2:F:93:ASN:O	2:F:94:TYR:C	2.62	0.43
4:A:67:MET:CE	4:A:75:ARG:HA	2.49	0.43
4:A:158:ASP:HA	4:A:190:VAL:HB	2.00	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:B:270:VAL:HG22	4:B:271:GLU:H	1.83	0.43
2:F:44:ILE:O	2:F:48:ILE:HG12	2.19	0.43
3:G:136:SER:O	3:G:138:VAL:N	2.52	0.43
4:A:109:VAL:O	4:A:110:ILE:C	2.61	0.43
4:B:242:LEU:HB2	4:B:283:LEU:HB3	2.01	0.43
2:F:83:LEU:O	2:F:87:ILE:HG13	2.19	0.43
2:F:318:ARG:HD2	2:F:389:MET:HE1	2.00	0.43
3:G:273:PRO:HG2	3:G:274:ILE:HD12	2.01	0.43
4:A:261:PRO:HD2	4:A:322:SER:OG	2.19	0.43
2:F:45:THR:HG21	2:F:81:PHE:HE1	1.84	0.42
3:G:204:ARG:O	3:G:209:PRO:HD3	2.18	0.42
4:A:258:LEU:HD23	4:A:264:GLN:HB3	2.00	0.42
2:F:216:ASP:C	2:F:218:THR:H	2.27	0.42
2:F:466:LEU:H	2:F:469:ASN:HB2	1.82	0.42
3:G:10:LYS:HD2	3:G:14:PHE:HB2	2.01	0.42
4:A:208:ASP:O	4:A:209:ALA:C	2.60	0.42
4:A:228:ARG:HD3	4:A:228:ARG:N	2.34	0.42
1:E:321:MET:O	1:E:325:GLN:HG2	2.19	0.42
1:E:83:LYS:HG3	1:E:84:ALA:H	1.84	0.42
2:F:118:LYS:HA	2:F:118:LYS:HD3	1.85	0.42
3:G:11:ALA:O	3:G:15:ILE:HB	2.19	0.42
2:F:196:VAL:HG23	2:F:205:SER:C	2.45	0.42
3:G:83:LEU:HD22	3:G:87:ASN:HD21	1.84	0.42
4:B:289:HIS:O	4:B:348:PRO:HG3	2.19	0.42
1:E:39:HIS:CD2	1:E:39:HIS:N	2.87	0.42
3:G:142:ALA:O	3:G:146:ARG:HD2	2.20	0.42
4:B:29:GLY:HA2	4:B:185:ARG:C	2.44	0.42
4:B:148:LEU:HD23	4:B:148:LEU:HA	1.87	0.42
2:F:221:ASN:HB3	2:F:226:VAL:H	1.83	0.42
2:F:330:PHE:CE1	3:G:246:ALA:HA	2.55	0.42
3:G:7:LYS:HD3	3:G:12:ARG:HH22	1.84	0.42
4:B:348:PRO:HA	4:B:349:PRO:HD2	1.93	0.42
1:E:62:TRP:CD1	1:E:63:ALA:N	2.88	0.42
1:E:279:PHE:O	1:E:283:TYR:HB2	2.19	0.42
2:F:406:ASP:CG	4:B:99:GLY:HA2	2.45	0.42
2:F:467:LEU:HD12	2:F:494:ILE:HD11	2.02	0.42
3:G:129:GLN:HE22	3:G:172:LEU:HG	1.85	0.42
4:A:270:VAL:HG23	4:A:364:ARG:HA	2.02	0.42
4:A:283:LEU:HD11	4:A:352:CYS:HB3	2.02	0.42
4:A:304:VAL:HG11	4:A:307:VAL:HG23	2.01	0.42
1:E:85:PHE:HZ	1:E:285:LEU:HD13	1.83	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:E:367:ARG:O	1:E:370:LYS:HG3	2.20	0.42
2:F:196:VAL:HG22	2:F:204:PHE:HB3	2.02	0.42
4:B:324:ARG:HD3	4:B:324:ARG:HA	1.86	0.42
2:F:21:GLY:O	2:F:25:LEU:HG	2.20	0.41
4:A:33:VAL:CG2	4:A:201:ALA:HB2	2.50	0.41
2:F:81:PHE:HB3	2:F:82:PRO:CD	2.50	0.41
2:F:172:ASN:O	2:F:176:ILE:HG23	2.19	0.41
2:F:308:TRP:CE2	2:F:310:ALA:HB3	2.55	0.41
2:F:329:SER:HB2	3:G:228:THR:OG1	2.20	0.41
2:F:56:ILE:HD13	2:F:65:TRP:HB3	2.01	0.41
2:F:379:LEU:HB3	5:D:2:GLC:H4	2.02	0.41
2:F:424:LYS:N	2:F:425:PRO:HD2	2.35	0.41
3:G:30:PRO:O	3:G:33:MET:HB2	2.19	0.41
3:G:74:ILE:H	3:G:74:ILE:CD1	2.27	0.41
4:A:345:ILE:HD12	4:A:345:ILE:C	2.45	0.41
2:F:109:LEU:HD21	2:F:253:PRO:HG2	2.02	0.41
2:F:346:GLU:CD	2:F:346:GLU:H	2.27	0.41
4:A:45:LEU:HA	4:A:48:MET:CE	2.51	0.41
4:A:96:MET:HE3	4:A:145:GLY:HA3	2.02	0.41
4:A:173:ARG:HH12	4:A:195:VAL:HG12	1.86	0.41
4:A:192:HIS:CE1	4:B:166:ALA:H	2.39	0.41
4:B:10:THR:HB	4:B:57:SER:HB3	2.01	0.41
4:A:106:LYS:CB	4:A:109:VAL:HB	2.50	0.41
1:E:342:ALA:HB3	1:E:368:ILE:HD11	2.03	0.41
2:F:419:LEU:N	2:F:420:PRO:HD2	2.35	0.41
4:B:270:VAL:HG23	4:B:364:ARG:HA	2.03	0.41
4:A:242:LEU:HB2	4:A:283:LEU:HB3	2.02	0.41
4:B:180:HIS:HB2	4:B:187:MET:HE2	2.02	0.41
1:E:6:LYS:HA	1:E:33:ILE:HG23	2.03	0.41
2:F:447:LEU:HG	2:F:448:THR:HG23	2.02	0.41
3:G:184:ILE:HG22	3:G:185:ASP:N	2.35	0.41
3:G:209:PRO:O	3:G:212:VAL:HG23	2.20	0.41
4:A:234:ILE:CG2	4:A:235:GLY:N	2.83	0.41
4:B:173:ARG:HH12	4:B:199:THR:HG21	1.85	0.41
1:E:83:LYS:HG3	1:E:84:ALA:N	2.36	0.41
1:E:140:LYS:HA	1:E:144:LYS:O	2.21	0.41
4:A:214:GLN:OE1	4:A:226:ALA:N	2.49	0.41
4:B:130:LYS:C	4:B:132:LYS:N	2.79	0.41
1:E:3:GLU:OE1	1:E:6:LYS:HE2	2.20	0.40
1:E:62:TRP:CG	1:E:63:ALA:H	2.39	0.40
3:G:68:GLU:HB2	3:G:74:ILE:HG22	2.03	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:A:106:LYS:O	4:A:107:LYS:C	2.64	0.40
4:A:175:GLU:CD	4:A:178:ARG:HH21	2.28	0.40
1:E:341:TYR:CD2	2:F:479:GLY:HA3	2.55	0.40
4:A:172:MET:O	4:A:176:ILE:HG12	2.21	0.40
2:F:112:ARG:HD3	2:F:211:TYR:HE1	1.84	0.40
2:F:296:VAL:O	2:F:297:ALA:C	2.64	0.40
2:F:328:PRO:HB2	2:F:331:ILE:HG23	2.04	0.40
2:F:467:LEU:HD13	2:F:467:LEU:HA	1.95	0.40
3:G:187:SER:HB3	4:A:85:ALA:HB2	2.03	0.40
4:A:92:VAL:HG22	4:A:134:LEU:HD11	2.03	0.40
4:B:83:SER:O	4:B:84:TYR:HB2	2.21	0.40
1:E:47:PHE:O	1:E:48:PRO:C	2.64	0.40
1:E:340:TRP:CD1	5:C:2:GLC:H4	2.57	0.40
3:G:57:ASP:O	3:G:61:LEU:HD23	2.20	0.40
4:A:83:SER:O	4:A:84:TYR:HB2	2.21	0.40
4:B:228:ARG:HH11	4:B:241:PHE:HB3	1.87	0.40

There are no symmetry-related clashes.

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	E	368/370 (100%)	343 (93%)	21 (6%)	4 (1%)	11	39
2	F	479/514 (93%)	433 (90%)	43 (9%)	3 (1%)	21	52
3	G	280/296 (95%)	252 (90%)	22 (8%)	6 (2%)	5	25
4	A	368/381 (97%)	329 (89%)	35 (10%)	4 (1%)	11	39
4	B	368/381 (97%)	341 (93%)	20 (5%)	7 (2%)	6	27
All	All	1863/1942 (96%)	1698 (91%)	141 (8%)	24 (1%)	9	35

All (24) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	173	ASN
3	G	8	SER
3	G	9	GLN
4	A	322	SER
4	B	322	SER
2	F	260	GLY
4	B	103	ALA
3	G	137	LEU
3	G	182	GLU
1	E	230	TRP
3	G	7	LYS
4	A	21	ASP
4	B	131	PRO
1	E	168	ALA
3	G	230	VAL
4	A	293	SER
4	B	324	ARG
1	E	178	ILE
2	F	479	GLY
2	F	253	PRO
4	A	236	SER
4	B	269	PRO
4	B	321	PRO
4	B	323	ILE

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	E	298/298 (100%)	292 (98%)	6 (2%)	48	72
2	F	391/424 (92%)	377 (96%)	14 (4%)	31	62
3	G	228/237 (96%)	211 (92%)	17 (8%)	12	39
4	A	314/323 (97%)	301 (96%)	13 (4%)	27	59
4	B	314/323 (97%)	306 (98%)	8 (2%)	42	69
All	All	1545/1605 (96%)	1487 (96%)	58 (4%)	29	60

All (58) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	39	HIS
1	E	45	GLU
1	E	69	CYS
1	E	128	THR
1	E	311	LEU
1	E	358	ASP
2	F	57	PHE
2	F	86	THR
2	F	176	ILE
2	F	187	THR
2	F	220	THR
2	F	325	TYR
2	F	331	ILE
2	F	346	GLU
2	F	354	LEU
2	F	357	VAL
2	F	372	LEU
2	F	387	LEU
2	F	440	ASN
2	F	468	VAL
3	G	7	LYS
3	G	9	GLN
3	G	15	ILE
3	G	19	LEU
3	G	21	LEU
3	G	54	ILE
3	G	61	LEU
3	G	74	ILE
3	G	75	THR
3	G	83	LEU
3	G	122	LEU
3	G	186	SER
3	G	229	GLU
3	G	245	LEU
3	G	251	GLN
3	G	253	LEU
3	G	274	ILE
4	A	4	VAL
4	A	35	VAL
4	A	65	LYS
4	A	77	VAL
4	A	100	LEU

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Mol	Chain	Res	Type
4	A	123	LEU
4	A	195	VAL
4	A	221	LEU
4	A	270	VAL
4	A	288	GLU
4	A	323	ILE
4	A	350	GLU
4	A	360	THR
4	B	35	VAL
4	B	65	LYS
4	B	77	VAL
4	B	100	LEU
4	B	107	LYS
4	B	162	SER
4	B	221	LEU
4	B	350	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (28) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	39	HIS
1	E	152	GLN
2	F	98	ASN
2	F	121	ASN
2	F	143	ASN
2	F	208	GLN
2	F	222	ASN
2	F	307	GLN
2	F	412	GLN
2	F	437	ASN
2	F	439	ASN
3	G	5	GLN
3	G	9	GLN
3	G	17	HIS
3	G	69	GLN
3	G	251	GLN
4	A	116	GLN
4	A	223	HIS
4	A	289	HIS
4	A	315	GLN
4	A	353	HIS
4	B	116	GLN

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Mol	Chain	Res	Type
4	B	223	HIS
4	B	240	ASN
4	B	255	GLN
4	B	262	ASN
4	B	264	GLN
4	B	317	HIS

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

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

5.5 Carbohydrates ⓘ

4 monosaccharides are modelled in this entry.

In the following table, the Counts columns list the number of bonds (or angles) for which Mogul statistics could be retrieved, the number of bonds (or angles) that are observed in the model and the number of bonds (or angles) that are defined in the Chemical Component Dictionary. The Link column lists molecule types, if any, to which the group is linked. The Z score for a bond length (or angle) is the number of standard deviations the observed value is removed from the expected value. A bond length (or angle) with $|Z| > 2$ is considered an outlier worth inspection. RMSZ is the root-mean-square of all Z scores of the bond lengths (or angles).

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
5	GLC	C	1	5	12,12,12	0.48	0	17,17,17	0.60	0
5	GLC	C	2	5	11,11,12	0.31	0	15,15,17	0.53	0
5	GLC	D	1	5	12,12,12	0.46	0	17,17,17	0.59	0
5	GLC	D	2	5	11,11,12	0.30	0	15,15,17	0.82	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	GLC	C	1	5	-	0/2/22/22	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	GLC	C	2	5	-	0/2/19/22	0/1/1/1
5	GLC	D	1	5	-	1/2/22/22	0/1/1/1
5	GLC	D	2	5	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (2) torsion outliers are listed below:

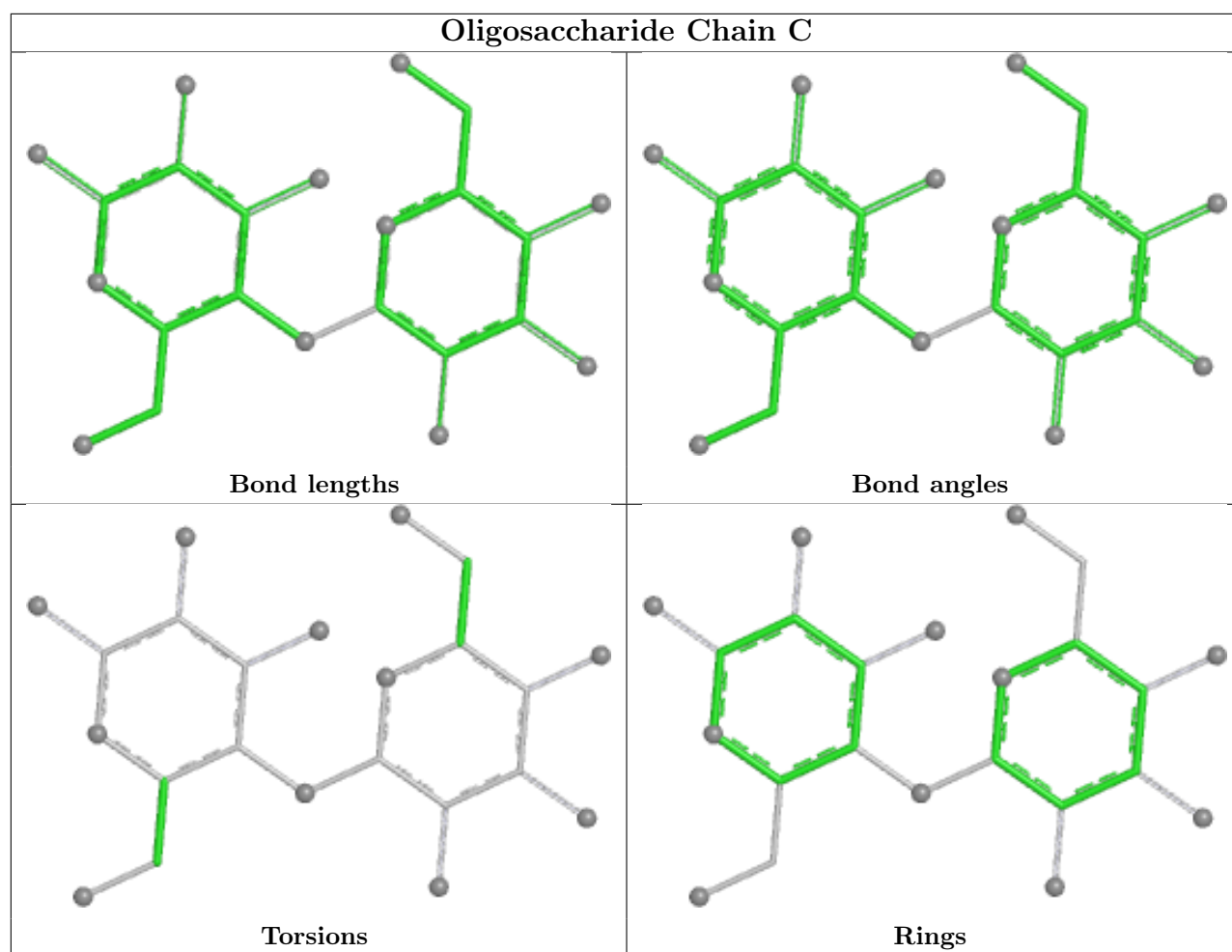
Mol	Chain	Res	Type	Atoms
5	D	2	GLC	O5-C5-C6-O6
5	D	1	GLC	O5-C5-C6-O6

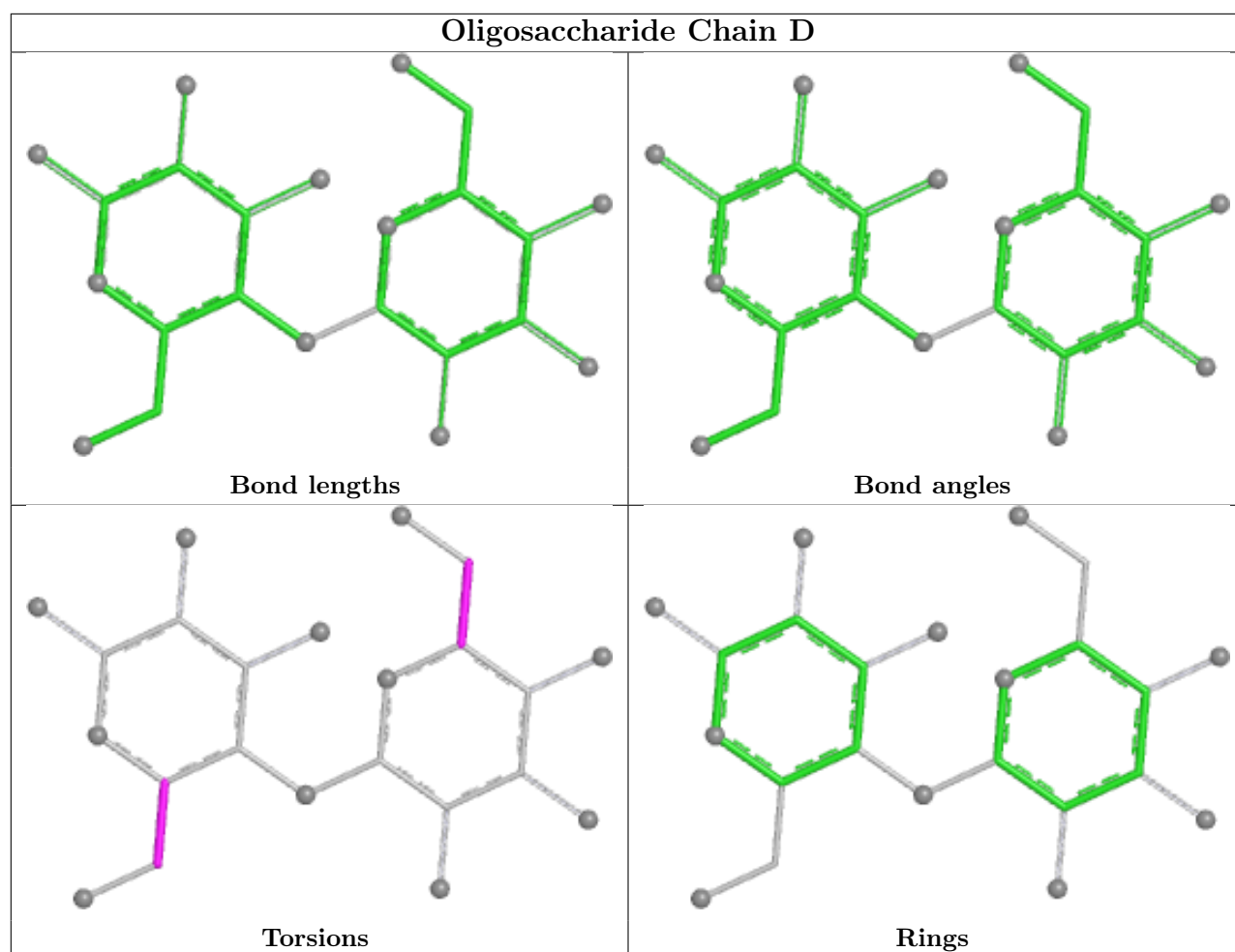
There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	D	2	GLC	2	0
5	C	2	GLC	1	0

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





5.6 Ligand geometry [i](#)

1 ligand is 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	$\# Z > 2$
6	PGV	F	4001	-	50,50,50	1.08	3 (6%)	53,56,56	1.04	2 (3%)

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
6	PGV	F	4001	-	-	31/55/55/55	-

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
6	F	4001	PGV	O03-C19	4.30	1.45	1.33
6	F	4001	PGV	O01-C1	4.20	1.46	1.34
6	F	4001	PGV	C12-C11	3.72	1.52	1.31

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
6	F	4001	PGV	O01-C1-C2	3.95	120.03	111.48
6	F	4001	PGV	O03-C19-C20	2.82	120.44	111.83

There are no chirality outliers.

All (31) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
6	F	4001	PGV	C04-O12-P-O11
6	F	4001	PGV	C04-O12-P-O13
6	F	4001	PGV	O12-C04-C05-C06
6	F	4001	PGV	C04-C05-C06-O06
6	F	4001	PGV	O02-C1-O01-C02
6	F	4001	PGV	C2-C1-O01-C02
6	F	4001	PGV	O12-C04-C05-O05
6	F	4001	PGV	C10-C11-C12-C13
6	F	4001	PGV	C20-C19-O03-C01
6	F	4001	PGV	O05-C05-C06-O06
6	F	4001	PGV	O04-C19-O03-C01
6	F	4001	PGV	C24-C25-C26-C27
6	F	4001	PGV	C2-C3-C4-C5
6	F	4001	PGV	C27-C28-C29-C30
6	F	4001	PGV	C19-C20-C21-C22
6	F	4001	PGV	C29-C30-C31-C32
6	F	4001	PGV	C26-C27-C28-C29
6	F	4001	PGV	C30-C31-C32-C33
6	F	4001	PGV	C20-C21-C22-C23
6	F	4001	PGV	C15-C16-C17-C18
6	F	4001	PGV	C6-C7-C8-C9

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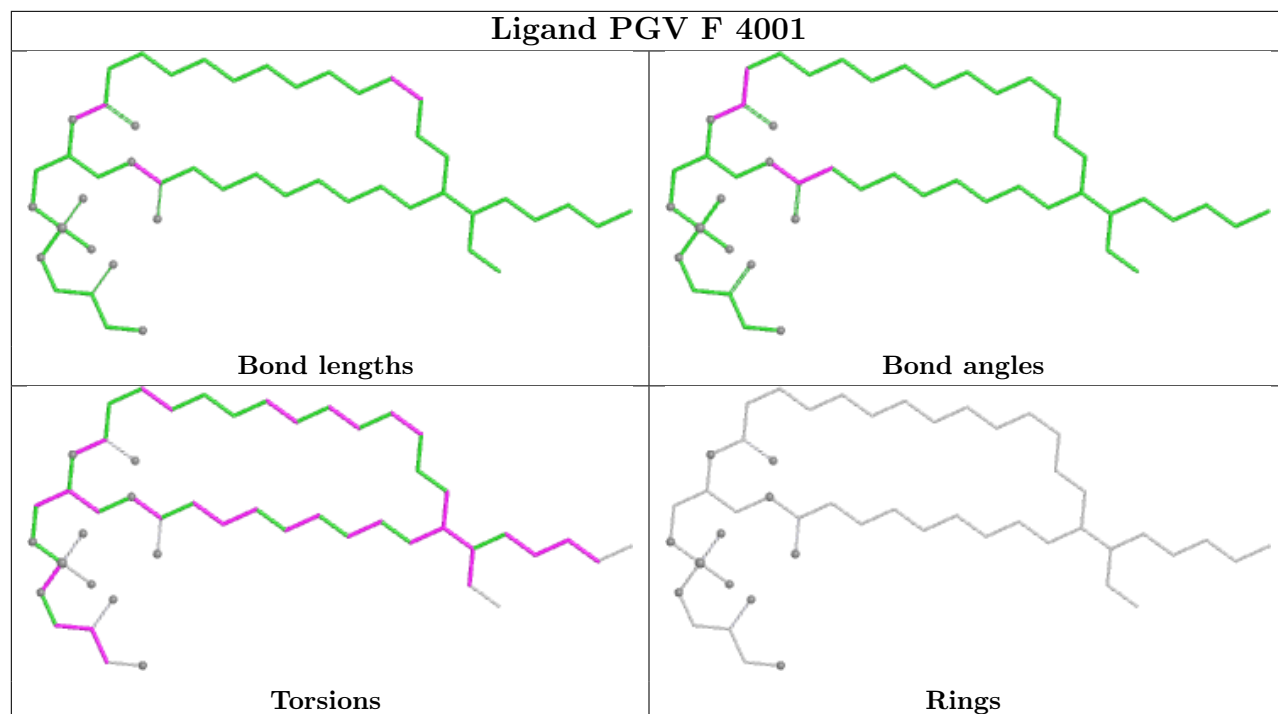
Mol	Chain	Res	Type	Atoms
6	F	4001	PGV	O01-C02-C03-O11
6	F	4001	PGV	C13-C14-C15-C16
6	F	4001	PGV	C01-C02-C03-O11
6	F	4001	PGV	C11-C10-C9-C8
6	F	4001	PGV	O03-C01-C02-C03
6	F	4001	PGV	O03-C01-C02-O01
6	F	4001	PGV	C04-O12-P-O14
6	F	4001	PGV	C14-C15-C16-C17
6	F	4001	PGV	C22-C23-C24-C25
6	F	4001	PGV	C31-C32-C33-C34

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
6	F	4001	PGV	1	0

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



5.7 Other polymers [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	E	370/370 (100%)	-0.16	2 (0%) 87 73	38, 74, 118, 146	0
2	F	483/514 (93%)	0.11	13 (2%) 56 35	43, 86, 144, 177	0
3	G	282/296 (95%)	-0.07	4 (1%) 73 53	35, 64, 111, 141	0
4	A	370/381 (97%)	0.00	5 (1%) 73 53	53, 77, 103, 128	0
4	B	370/381 (97%)	0.14	6 (1%) 70 49	51, 89, 172, 215	0
All	All	1875/1942 (96%)	0.01	30 (1%) 70 49	35, 79, 140, 215	0

All (30) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
2	F	242	ALA	5.3
1	E	183	VAL	4.7
2	F	227	LYS	4.2
3	G	8	SER	4.1
2	F	253	PRO	4.0
4	B	105	ALA	3.7
2	F	41	LEU	3.6
4	B	252	ASP	3.4
2	F	505	ASN	2.6
2	F	42	PHE	2.5
3	G	4	VAL	2.5
2	F	228	TYR	2.5
2	F	241	THR	2.4
3	G	71	ASP	2.4
1	E	184	ASP	2.4
4	A	128	ASP	2.3
2	F	463	TYR	2.3
4	B	256	VAL	2.3
4	A	323	ILE	2.3
4	B	363	ARG	2.3

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Mol	Chain	Res	Type	RSRZ
2	F	18	SER	2.2
4	B	323	ILE	2.2
2	F	217	GLY	2.2
4	B	7	GLN	2.2
4	A	18	VAL	2.2
2	F	115	GLN	2.2
3	G	70	ALA	2.2
4	A	140	GLN	2.1
2	F	40	TYR	2.1
4	A	361	ALA	2.1

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](#)

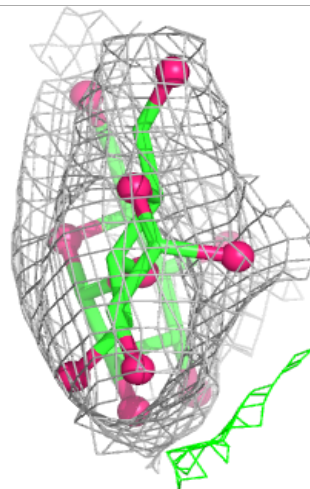
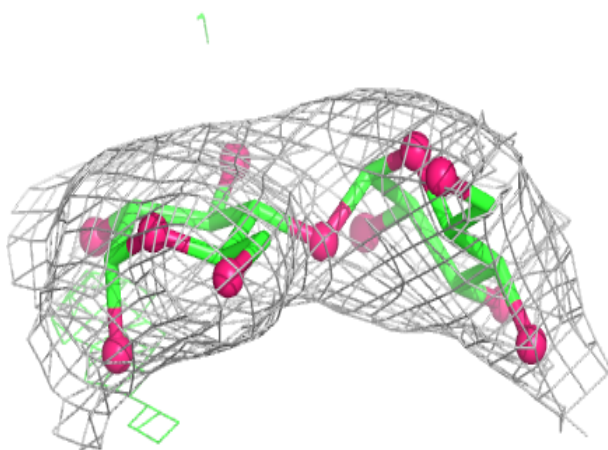
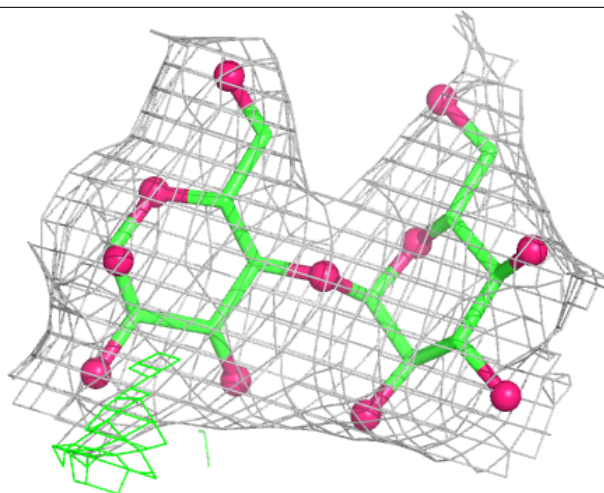
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

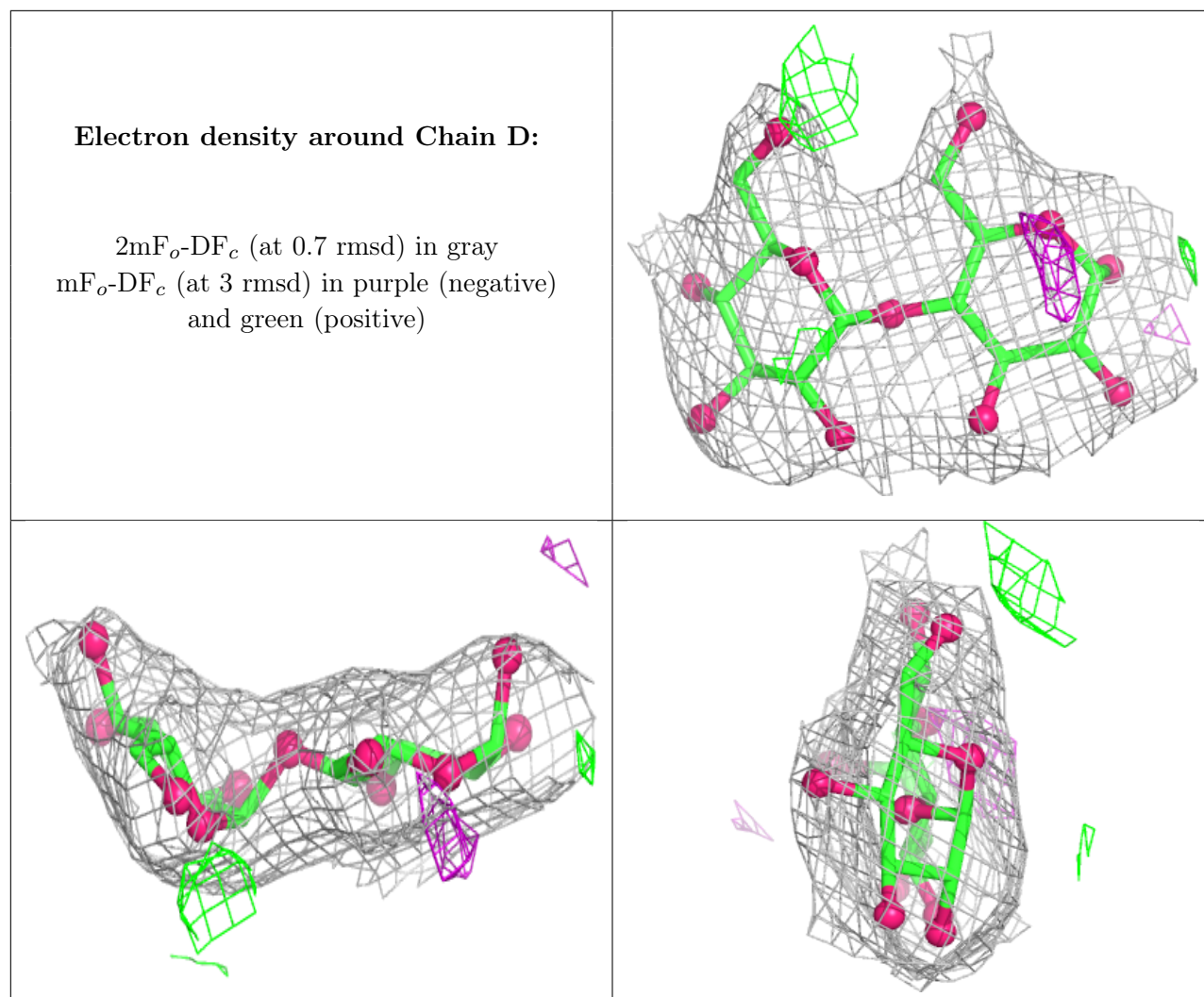
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
5	GLC	C	1	12/12	-	-	37,39,41,41	0
5	GLC	C	2	11/12	-	-	42,44,45,45	0
5	GLC	D	1	12/12	-	-	41,42,43,43	0
5	GLC	D	2	11/12	-	-	40,41,42,42	0

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

Electron density around Chain C:

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





6.4 Ligands ⓘ

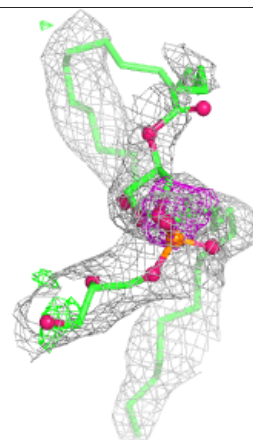
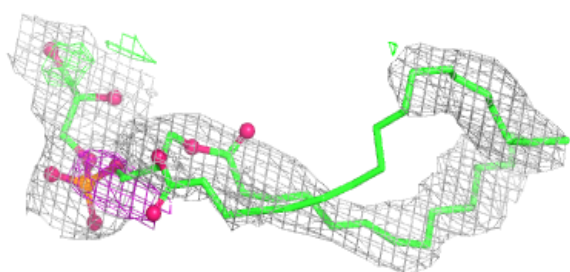
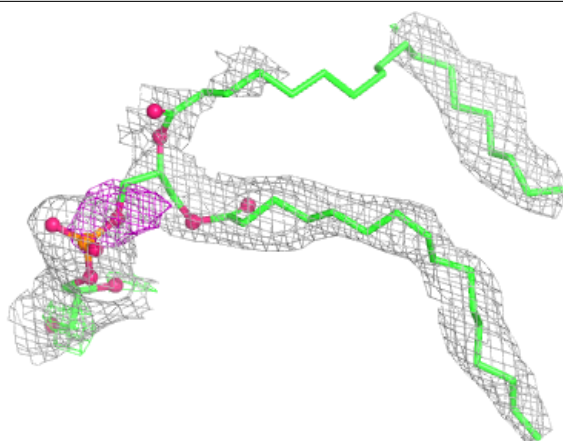
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
6	PGV	F	4001	51/51	0.84	0.19	83,88,89,89	0

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

Electron density around PGV F 4001:

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



6.5 Other polymers [i](#)

There are no such residues in this entry.