



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 21, 2024 – 03:41 AM EDT

PDB ID : 1OT5
Title : The 2.4 Angstrom Crystal Structure of Kex2 in complex with a peptidyl-boronic acid inhibitor
Authors : Holyoak, T.; Wilson, M.A.; Fenn, T.D.; Kettner, C.A.; Petsko, G.A.; Fuller, R.S.; Ringe, D.
Deposited on : 2003-03-21
Resolution : 2.40 Å(reported)

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

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

A user guide is available at

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

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity	:	4.02b-467
Mogul	:	2022.3.0, CSD as543be (2022)
Xtriage (Phenix)	:	1.20.1
EDS	:	3.0
Percentile statistics	:	20231227.v01 (using entries in the PDB archive December 27th 2023)
CCP4	:	9.0.003 (Gargrove)
Density-Fitness	:	1.0.11
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.39

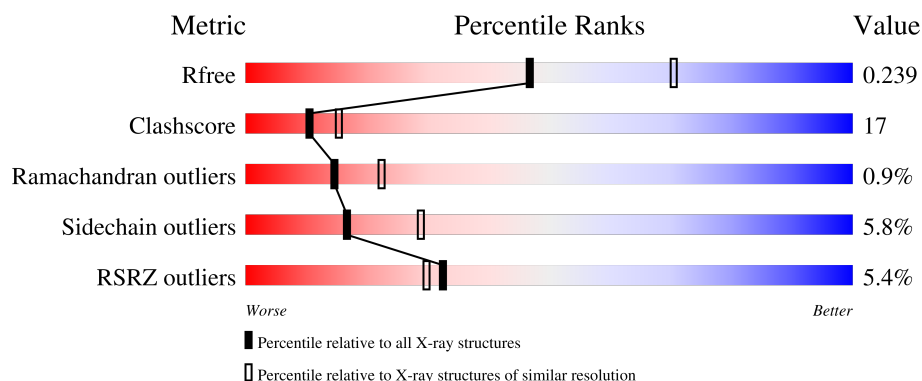
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 Å.

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




Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	164625	4642 (2.40-2.40)
Clashscore	180529	5218 (2.40-2.40)
Ramachandran outliers	177936	5158 (2.40-2.40)
Sidechain outliers	177891	5159 (2.40-2.40)
RSRZ outliers	164620	4642 (2.40-2.40)

The table below summarises the geometric issues observed across the polymeric chains and their fit to the electron density. The red, orange, yellow and green segments of the lower bar indicate the fraction of residues that contain outliers for ≥ 3 , 2, 1 and 0 types of geometric quality criteria respectively. A grey segment represents the fraction of residues that are not modelled. The numeric value for each fraction is indicated below the corresponding segment, with a dot representing fractions $\leq 5\%$. The upper red bar (where present) indicates the fraction of residues that have poor fit to the electron density. The numeric value is given above the bar.

Mol	Chain	Length	Quality of chain
1	A	477	<div> <div>5%</div> <div> <div></div> <div>72%</div> <div>23%</div> <div>.</div> </div> </div>
1	B	477	<div> <div>6%</div> <div> <div></div> <div>72%</div> <div>24%</div> <div>.</div> </div> </div>
2	C	4	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
2	D	4	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>
3	E	2	<div> <div></div> <div> <div>50%</div> <div>50%</div> </div> </div>

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Mol	Chain	Length	Quality of chain
3	F	2	

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 7992 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 Kexin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	477	Total	C	N	O	S	0	0	0
			3676	2298	628	739	11			
1	B	477	Total	C	N	O	S	0	0	0
			3676	2298	628	739	11			

- Molecule 2 is a protein called Ac-Ala-Lys-boroArg N-acetylated boronic acid peptide inhibitor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	C	4	Total	B	C	N	O	0	0	0
			29	1	16	7	5			
2	D	4	Total	B	C	N	O	0	0	0
			29	1	16	7	5			

- Molecule 3 is an oligosaccharide called 2-acetamido-2-deoxy-beta-D-glucopyranose-(1-4)-2-acetamido-2-deoxy-beta-D-glucopyranose.



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
3	E	2	Total	C	N	O	0	0	0
			28	16	2	10			
3	F	2	Total	C	N	O	0	0	0
			28	16	2	10			

- Molecule 4 is 2-acetamido-2-deoxy-beta-D-glucopyranose (three-letter code: NAG) (formula: C₈H₁₅NO₆).



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

- Molecule 5 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	3	Total	Ca	0	0
			3	3		
5	B	3	Total	Ca	0	0
			3	3		

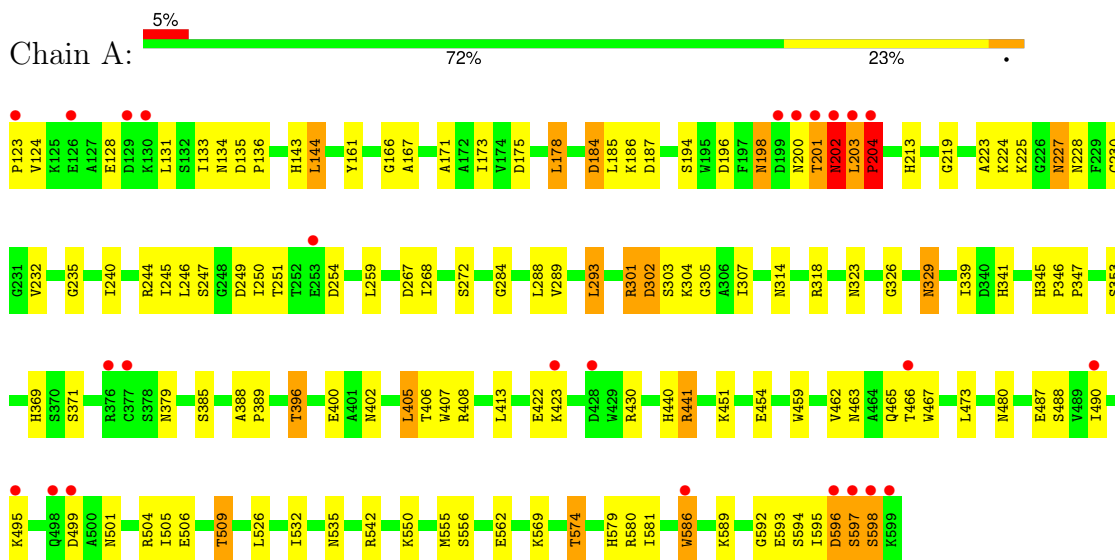
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	241	Total	O	0	0
			241	241		
6	B	243	Total	O	0	0
			243	243		
6	C	5	Total	O	0	0
			5	5		
6	D	3	Total	O	0	0
			3	3		

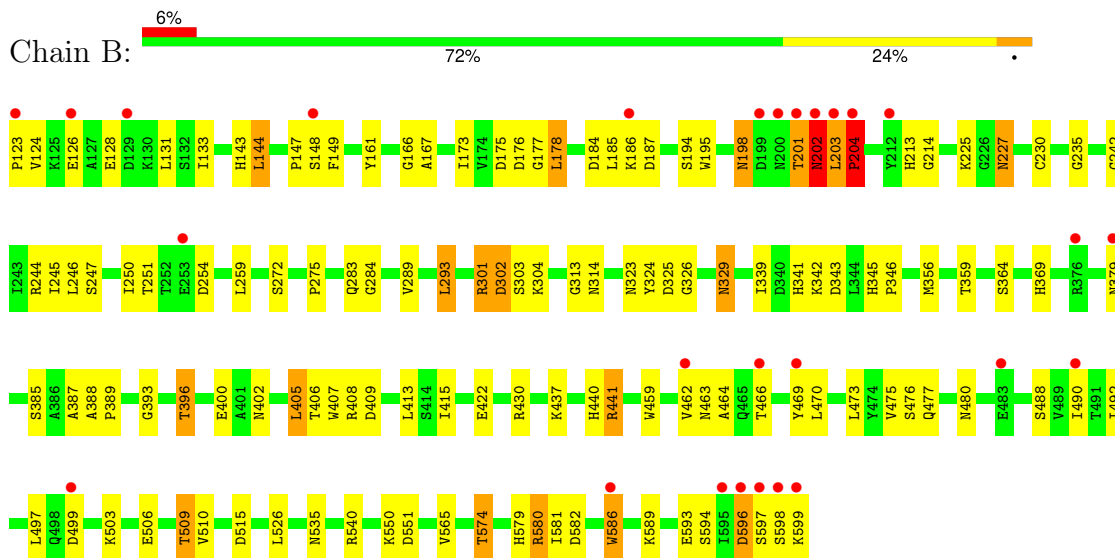
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. Residues are color-coded according to the number of geometric quality criteria for which they contain at least one outlier: green = 0, yellow = 1, orange = 2 and red = 3 or more. A red dot above a residue indicates a poor fit to the electron density ($RSRZ > 2$). Stretches of 2 or more consecutive residues without any outlier are shown as a green connector. Residues present in the sample, but not in the model, are shown in grey.

- Molecule 1: Kexin



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- Molecule 2: Ac-Ala-Lys-boroArg N-acetylated boronic acid peptide inhibitor





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



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



4 Data and refinement statistics

Property	Value	Source
Space group	P 65 2 2	Depositor
Cell constants a, b, c, α , β , γ	113.84Å 113.84Å 370.22Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	49.30 – 2.40 49.30 – 2.40	Depositor EDS
% Data completeness (in resolution range)	92.2 (49.30-2.40) 92.3 (49.30-2.40)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.00 (at 2.39Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.209 , 0.245 0.205 , 0.239	Depositor DCC
R_{free} test set	3033 reflections (5.80%)	wwPDB-VP
Wilson B-factor (Å ²)	28.4	Xtriage
Anisotropy	0.532	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	7992	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.44% 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: BOR, ACE, NAG, CA

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	0.34	0/3759	0.63	1/5105 (0.0%)
1	B	0.34	0/3759	0.64	1/5105 (0.0%)
2	C	0.25	0/14	2.23	1/17 (5.9%)
2	D	0.33	0/14	2.20	1/17 (5.9%)
All	All	0.34	0/7546	0.65	4/10244 (0.0%)

There are no bond length outliers.

All (4) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	C	1	ACE	C-N-CA	8.97	144.12	121.70
2	D	1	ACE	C-N-CA	8.80	143.69	121.70
1	B	204	PRO	N-CA-C	5.77	127.10	112.10
1	A	204	PRO	N-CA-C	5.60	126.67	112.10

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	3676	0	3493	118	0
1	B	3676	0	3492	122	0
2	C	29	0	33	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	D	29	0	33	4	0
3	E	28	0	25	2	0
3	F	28	0	25	1	0
4	A	14	0	13	0	0
4	B	14	0	13	0	0
5	A	3	0	0	0	0
5	B	3	0	0	0	0
6	A	241	0	0	16	0
6	B	243	0	0	14	0
6	C	5	0	0	0	0
6	D	3	0	0	0	0
All	All	7992	0	7127	243	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 17.

All (243) 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)
1:B:574:THR:HG21	1:B:579:HIS:O	1.63	0.97
1:A:488:SER:HG	1:A:586:TRP:HZ3	1.05	0.97
1:A:574:THR:HG21	1:A:579:HIS:O	1.69	0.91
1:A:201:THR:C	1:A:202:ASN:HD22	1.77	0.87
1:A:423:LYS:HB2	6:A:825:HOH:O	1.76	0.85
1:A:272:SER:HB3	1:A:385:SER:HB2	1.62	0.82
1:B:440:HIS:HE1	1:B:535:ASN:H	1.28	0.81
1:B:202:ASN:N	1:B:202:ASN:HD22	1.80	0.79
1:A:495:LYS:HB3	6:A:820:HOH:O	1.82	0.79
1:B:464:ALA:H	1:B:597:SER:HB3	1.48	0.78
1:B:198:ASN:HD22	1:B:244:ARG:HG2	1.48	0.78
1:A:466:THR:HG22	1:A:467:TRP:H	1.48	0.77
1:A:466:THR:OG1	1:A:594:SER:HB3	1.84	0.76
1:A:430:ARG:HH22	1:A:535:ASN:HD21	1.30	0.76
1:A:385:SER:HB3	2:C:4:BOR:HB2	1.67	0.75
1:A:509:THR:HG22	1:A:589:LYS:HB2	1.67	0.75
1:B:201:THR:C	1:B:202:ASN:HD22	1.89	0.74
1:B:540:ARG:NH1	6:B:634:HOH:O	2.20	0.74
1:B:470:LEU:HD21	1:B:492:ILE:HD11	1.70	0.74
1:A:202:ASN:HD22	1:A:202:ASN:N	1.86	0.73
1:A:198:ASN:HD22	1:A:244:ARG:HG2	1.52	0.73
1:B:430:ARG:HH22	1:B:535:ASN:HD21	1.35	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:596:ASP:C	1:A:596:ASP:OD1	2.31	0.68
1:B:385:SER:HB3	2:D:4:BOR:HB2	1.77	0.67
1:A:385:SER:HB3	2:C:4:BOR:CB	2.25	0.66
1:A:272:SER:HB3	1:A:385:SER:CB	2.25	0.66
1:B:406:THR:HG21	6:B:665:HOH:O	1.96	0.66
1:B:143:HIS:CD2	1:B:144:LEU:HD13	2.31	0.65
1:B:488:SER:HG	1:B:586:TRP:HZ3	1.45	0.65
1:B:475:VAL:HG12	1:B:477:GLN:HG3	1.78	0.65
1:A:440:HIS:HE1	1:A:535:ASN:H	1.45	0.64
1:B:201:THR:HG22	6:B:768:HOH:O	1.96	0.64
1:A:203:LEU:HD12	1:A:204:PRO:HD2	1.80	0.64
1:A:202:ASN:N	1:A:202:ASN:ND2	2.45	0.64
1:B:466:THR:HG23	1:B:594:SER:HB3	1.81	0.63
1:B:345:HIS:CE1	1:B:441:ARG:HD2	2.34	0.62
1:B:124:VAL:O	1:B:128:GLU:HG3	1.99	0.62
1:B:509:THR:HG22	1:B:589:LYS:HB2	1.80	0.62
1:B:356:MET:HE1	1:B:415:ILE:HD11	1.82	0.62
1:B:476:SER:HB2	6:B:740:HOH:O	2.00	0.62
1:A:166:GLY:HA3	1:A:396:THR:HG23	1.82	0.61
1:B:440:HIS:CE1	1:B:535:ASN:H	2.14	0.61
1:A:440:HIS:CE1	1:A:535:ASN:H	2.18	0.61
1:B:464:ALA:H	1:B:597:SER:CB	2.12	0.61
1:B:202:ASN:N	1:B:202:ASN:ND2	2.47	0.61
1:A:301:ARG:O	1:A:304:LYS:HE3	2.01	0.60
1:B:128:GLU:HA	1:B:133:ILE:HB	1.82	0.60
1:A:143:HIS:CD2	1:A:144:LEU:HD13	2.36	0.59
1:B:329:ASN:C	1:B:329:ASN:HD22	2.04	0.59
1:A:329:ASN:C	1:A:329:ASN:HD22	2.06	0.59
1:B:178:LEU:HD13	1:B:185:LEU:HD13	1.84	0.59
1:A:462:VAL:HG23	1:A:593:GLU:OE2	2.02	0.59
1:A:454:GLU:HG2	6:A:748:HOH:O	2.03	0.59
1:B:393:GLY:O	1:B:396:THR:HB	2.03	0.59
1:A:430:ARG:NH2	1:A:535:ASN:HD21	1.99	0.58
1:A:175:ASP:OD2	1:A:213:HIS:HB3	2.01	0.58
1:A:430:ARG:HH12	1:A:535:ASN:ND2	2.02	0.58
1:B:272:SER:HB3	1:B:385:SER:CB	2.33	0.58
1:A:198:ASN:ND2	1:A:247:SER:H	2.02	0.58
1:A:441:ARG:HD3	6:A:785:HOH:O	2.04	0.58
1:A:227:ASN:HD22	1:A:227:ASN:H	1.52	0.58
1:A:487:GLU:OE2	1:A:569:LYS:HE3	2.04	0.58
1:A:369:HIS:HD2	1:A:379:ASN:OD1	1.86	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:473:LEU:HD11	1:B:490:ILE:HG21	1.86	0.57
1:B:574:THR:HG22	6:B:619:HOH:O	2.05	0.57
1:B:462:VAL:HG13	1:B:593:GLU:CD	2.25	0.57
1:B:198:ASN:ND2	1:B:247:SER:H	2.03	0.57
1:B:126:GLU:HB3	6:B:738:HOH:O	2.04	0.57
1:B:480:ASN:HB3	1:B:580:ARG:NH1	2.19	0.57
1:B:173:ILE:N	1:B:173:ILE:HD12	2.20	0.56
1:B:198:ASN:HD22	1:B:244:ARG:CG	2.17	0.56
1:B:369:HIS:HD2	1:B:379:ASN:OD1	1.88	0.56
1:B:509:THR:HG21	6:B:791:HOH:O	2.06	0.55
1:B:301:ARG:O	1:B:304:LYS:HE3	2.05	0.55
1:B:178:LEU:C	1:B:178:LEU:HD12	2.25	0.55
1:B:356:MET:CE	1:B:415:ILE:HD11	2.36	0.55
1:A:250:ILE:HG23	1:A:254:ASP:HB2	1.88	0.55
1:B:187:ASP:HB2	6:B:790:HOH:O	2.06	0.55
1:B:324:TYR:CG	1:B:540:ARG:NH1	2.74	0.55
1:B:385:SER:HB3	2:D:4:BOR:CB	2.36	0.55
1:B:227:ASN:H	1:B:227:ASN:HD22	1.55	0.55
1:A:235:GLY:HA3	1:A:396:THR:HG21	1.89	0.55
1:B:147:PRO:HG2	1:B:148:SER:H	1.71	0.55
1:B:462:VAL:HG13	1:B:593:GLU:OE2	2.06	0.55
1:B:167:ALA:O	1:B:400:GLU:HG3	2.07	0.54
1:A:259:LEU:HD12	1:A:289:VAL:HG13	1.90	0.54
1:A:123:PRO:HG2	1:A:124:VAL:H	1.72	0.54
1:B:284:GLY:HA3	1:B:326:GLY:HA3	1.89	0.54
1:A:406:THR:HG21	6:A:698:HOH:O	2.06	0.54
1:A:413:LEU:HD11	1:A:459:TRP:CD2	2.43	0.54
1:B:388:ALA:HB3	1:B:389:PRO:HD3	1.89	0.53
1:A:134:ASN:ND2	1:A:228:ASN:HB2	2.23	0.53
1:B:250:ILE:HG23	1:B:254:ASP:HB2	1.89	0.53
1:A:198:ASN:HD21	1:A:245:ILE:C	2.12	0.53
1:A:597:SER:O	1:A:598:SER:HB2	2.07	0.53
1:B:166:GLY:HA3	1:B:396:THR:HG23	1.90	0.53
1:A:184:ASP:OD2	1:A:223:ALA:HB1	2.09	0.52
1:A:509:THR:CG2	6:A:606:HOH:O	2.58	0.52
1:A:227:ASN:HD22	1:A:227:ASN:N	2.07	0.52
1:B:194:SER:HB3	1:B:204:PRO:CG	2.40	0.52
1:B:406:THR:HG22	1:B:408:ARG:H	1.75	0.52
1:A:128:GLU:HA	1:A:133:ILE:HB	1.91	0.52
1:A:224:LYS:HD2	6:A:640:HOH:O	2.09	0.52
1:A:249:ASP:HA	6:A:757:HOH:O	2.09	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:284:GLY:CA	1:A:326:GLY:HA3	2.40	0.52
1:A:504:ARG:O	1:A:592:GLY:HA3	2.11	0.51
1:A:402:ASN:HB3	1:A:405:LEU:HD22	1.92	0.51
1:A:501:ASN:OD1	1:A:595:ILE:HB	2.10	0.51
1:A:388:ALA:HB3	1:A:389:PRO:HD3	1.93	0.50
1:A:167:ALA:O	1:A:400:GLU:HG3	2.11	0.50
1:A:314:ASN:ND2	2:C:4:BOR:O2	2.40	0.50
1:B:329:ASN:C	1:B:329:ASN:ND2	2.65	0.50
1:A:473:LEU:HD23	1:A:586:TRP:CZ3	2.46	0.50
1:A:462:VAL:HG23	1:A:593:GLU:CD	2.32	0.49
1:A:194:SER:HB3	1:A:204:PRO:CG	2.42	0.49
1:A:131:LEU:O	1:A:225:LYS:HE2	2.12	0.49
1:B:324:TYR:CD1	1:B:540:ARG:NH1	2.80	0.49
1:A:341:HIS:HD2	6:A:629:HOH:O	1.95	0.49
1:B:599:LYS:HD2	6:B:699:HOH:O	2.12	0.49
1:A:505:ILE:HG22	1:A:506:GLU:N	2.26	0.49
1:A:596:ASP:OD1	1:A:597:SER:O	2.30	0.49
1:B:123:PRO:N	1:B:126:GLU:HG3	2.28	0.49
1:A:318:ARG:HD2	1:A:542:ARG:NH1	2.28	0.49
1:B:475:VAL:CG1	1:B:477:GLN:HG3	2.42	0.49
1:B:194:SER:HB3	1:B:204:PRO:HG2	1.94	0.48
1:B:574:THR:HG23	1:B:581:ILE:HG23	1.94	0.48
1:A:227:ASN:H	1:A:227:ASN:ND2	2.12	0.48
1:A:178:LEU:HD12	1:A:178:LEU:C	2.33	0.48
1:B:599:LYS:CD	6:B:699:HOH:O	2.61	0.48
1:A:488:SER:OG	1:A:586:TRP:HZ3	1.83	0.48
1:A:406:THR:HG22	1:A:407:TRP:N	2.29	0.48
1:A:490:ILE:HG23	1:A:490:ILE:O	2.13	0.48
1:B:463:ASN:HB2	1:B:593:GLU:HG3	1.96	0.48
1:B:314:ASN:ND2	2:D:4:BOR:O1	2.47	0.47
1:B:413:LEU:HD11	1:B:459:TRP:CD2	2.49	0.47
1:A:329:ASN:C	1:A:329:ASN:ND2	2.67	0.47
1:B:186:LYS:HG3	1:B:187:ASP:N	2.30	0.47
1:A:302:ASP:O	1:A:303:SER:HB2	2.15	0.47
1:B:342:LYS:O	1:B:343:ASP:HB2	2.14	0.47
1:B:198:ASN:HD21	1:B:245:ILE:C	2.18	0.47
1:A:408:ARG:NH2	1:A:463:ASN:O	2.38	0.46
1:B:198:ASN:HD21	1:B:246:LEU:N	2.13	0.46
1:A:198:ASN:HA	1:A:250:ILE:HD11	1.96	0.46
1:A:219:GLY:HA3	1:A:371:SER:OG	2.16	0.46
1:B:313:GLY:HA2	2:D:4:BOR:HD1	1.97	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:339:ILE:HA	1:A:346:PRO:HD3	1.96	0.46
1:B:204:PRO:HG3	1:B:242:GLY:O	2.16	0.46
1:B:509:THR:CG2	6:B:616:HOH:O	2.63	0.46
1:B:406:THR:HB	1:B:409:ASP:OD1	2.15	0.46
1:B:259:LEU:HD12	1:B:289:VAL:HG13	1.97	0.46
1:B:466:THR:CG2	1:B:594:SER:HB3	2.45	0.46
1:A:466:THR:HG22	1:A:467:TRP:N	2.24	0.46
1:A:135:ASP:HA	1:A:136:PRO:HD3	1.85	0.46
1:A:385:SER:HB3	2:C:4:BOR:CA	2.46	0.46
1:A:480:ASN:HB3	1:A:580:ARG:NH1	2.30	0.46
1:A:178:LEU:HD13	1:A:185:LEU:HD13	1.97	0.46
1:A:284:GLY:HA2	1:A:326:GLY:HA3	1.97	0.46
1:B:175:ASP:OD2	1:B:213:HIS:HB3	2.16	0.45
1:B:250:ILE:HG22	1:B:251:THR:O	2.16	0.45
1:A:203:LEU:HD23	6:A:657:HOH:O	2.14	0.45
1:A:288:LEU:HD13	6:A:682:HOH:O	2.16	0.45
1:B:422:GLU:HB2	6:B:684:HOH:O	2.14	0.45
1:A:250:ILE:HG22	1:A:251:THR:O	2.16	0.45
1:A:259:LEU:HD13	1:A:293:LEU:HD11	1.98	0.45
1:A:267:ASP:OD1	1:A:301:ARG:HD2	2.17	0.45
1:A:173:ILE:HD12	1:A:173:ILE:N	2.32	0.45
1:A:178:LEU:CD1	1:A:185:LEU:HD13	2.46	0.45
1:A:284:GLY:HA3	1:A:326:GLY:HA3	1.99	0.45
1:A:301:ARG:HG3	1:A:305:GLY:O	2.17	0.45
1:B:301:ARG:O	1:B:304:LYS:HB2	2.16	0.45
1:B:341:HIS:HE1	1:B:364:SER:O	1.99	0.45
1:B:402:ASN:HB3	1:B:405:LEU:HD22	1.99	0.45
1:B:497:LEU:HD12	1:B:565:VAL:HG22	1.99	0.45
1:B:488:SER:OG	1:B:586:TRP:HZ3	1.98	0.45
1:A:318:ARG:NH1	6:A:787:HOH:O	2.50	0.44
1:A:532:ILE:HD12	1:A:562:GLU:CD	2.37	0.44
1:A:574:THR:HG23	1:A:581:ILE:HG23	1.99	0.44
6:A:759:HOH:O	3:E:1:NAG:H82	2.18	0.44
1:B:195:TRP:HZ2	1:B:201:THR:HB	1.82	0.44
1:B:430:ARG:HH12	1:B:535:ASN:ND2	2.14	0.44
1:B:470:LEU:HD21	1:B:492:ILE:CD1	2.45	0.44
3:F:1:NAG:O3	3:F:2:NAG:C7	2.65	0.44
1:A:131:LEU:HD21	1:A:161:TYR:CE1	2.53	0.44
1:A:166:GLY:CA	1:A:396:THR:HG23	2.46	0.44
1:A:451:LYS:HE3	1:A:451:LYS:HB2	1.73	0.44
1:A:555:MET:SD	1:A:556:SER:N	2.90	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:441:ARG:HD3	6:B:775:HOH:O	2.17	0.44
1:A:198:ASN:HD21	1:A:246:LEU:N	2.15	0.44
1:A:259:LEU:HD13	1:A:293:LEU:CD1	2.47	0.44
1:A:353:SER:HB3	1:A:440:HIS:CE1	2.53	0.44
1:B:166:GLY:HA3	1:B:396:THR:CG2	2.47	0.43
1:B:441:ARG:CD	6:B:775:HOH:O	2.65	0.43
1:A:124:VAL:O	1:A:128:GLU:HG3	2.17	0.43
1:A:597:SER:O	1:A:598:SER:CB	2.66	0.43
1:B:227:ASN:HD22	1:B:227:ASN:N	2.13	0.43
1:B:422:GLU:OE1	1:B:437:LYS:HG3	2.17	0.43
1:B:469:TYR:CE2	1:B:589:LYS:HD3	2.53	0.43
1:B:406:THR:HG22	1:B:407:TRP:N	2.33	0.43
1:B:408:ARG:NH1	1:B:506:GLU:OE1	2.51	0.43
1:A:347:PRO:HB2	6:A:706:HOH:O	2.18	0.43
1:B:339:ILE:HA	1:B:346:PRO:HD3	1.99	0.43
1:B:473:LEU:CD1	1:B:490:ILE:HG21	2.49	0.43
1:A:301:ARG:O	1:A:304:LYS:HB2	2.19	0.43
1:A:406:THR:HG21	6:A:808:HOH:O	2.19	0.43
1:B:131:LEU:O	1:B:225:LYS:HE2	2.18	0.43
1:B:408:ARG:HD2	1:B:506:GLU:OE2	2.19	0.43
1:A:550:LYS:HA	1:A:550:LYS:HD3	1.80	0.43
1:B:203:LEU:HA	1:B:204:PRO:HD3	1.72	0.43
1:A:413:LEU:HD11	1:A:459:TRP:CG	2.53	0.42
1:A:131:LEU:N	1:A:131:LEU:HD22	2.34	0.42
1:B:302:ASP:O	1:B:303:SER:HB2	2.18	0.42
1:B:596:ASP:OD1	1:B:598:SER:HB2	2.20	0.42
1:A:345:HIS:CE1	1:A:441:ARG:HD2	2.55	0.42
1:B:359:THR:HG21	1:B:387:ALA:O	2.20	0.42
1:B:413:LEU:HD11	1:B:459:TRP:CG	2.53	0.42
1:B:227:ASN:H	1:B:227:ASN:ND2	2.16	0.42
1:B:275:PRO:HB3	1:B:283:GLN:CG	2.50	0.42
1:A:194:SER:HB3	1:A:204:PRO:HG2	2.02	0.42
1:B:177:GLY:O	1:B:214:GLY:HA3	2.19	0.42
1:B:550:LYS:HA	1:B:550:LYS:HD3	1.80	0.42
1:A:268:ILE:HG12	1:A:307:ILE:HB	2.02	0.42
1:B:201:THR:O	1:B:202:ASN:HB3	2.19	0.41
1:B:430:ARG:NH2	1:B:535:ASN:HD21	2.09	0.41
1:A:186:LYS:HG3	1:A:187:ASP:N	2.34	0.41
1:B:235:GLY:HA3	1:B:396:THR:HG21	2.01	0.41
1:B:259:LEU:HD13	1:B:293:LEU:HD11	2.02	0.41
1:A:408:ARG:NE	1:A:465:GLN:HB2	2.35	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:149:PHE:CZ	1:B:342:LYS:HE2	2.56	0.41
1:B:325:ASP:C	1:B:325:ASP:OD2	2.59	0.41
1:B:503:LYS:HB3	1:B:593:GLU:O	2.21	0.41
1:A:171:ALA:O	1:A:240:ILE:HA	2.21	0.41
1:A:196:ASP:OD1	1:A:196:ASP:C	2.58	0.41
1:B:131:LEU:HD21	1:B:161:TYR:CE1	2.55	0.41
1:A:422:GLU:HG2	6:A:720:HOH:O	2.21	0.41
1:B:131:LEU:HD22	1:B:131:LEU:N	2.36	0.41
1:B:510:VAL:HG13	1:B:586:TRP:HD1	1.85	0.41
1:B:515:ASP:HB2	1:B:582:ASP:HB2	2.03	0.41
1:A:430:ARG:HH12	1:A:535:ASN:HD21	1.67	0.41
3:E:1:NAG:O3	3:E:2:NAG:H2	2.21	0.40
1:B:175:ASP:OD2	1:B:176:ASP:N	2.54	0.40
1:B:550:LYS:O	1:B:551:ASP:HB2	2.20	0.40
1:A:505:ILE:CG2	1:A:506:GLU:N	2.84	0.40
1:B:304:LYS:HE3	1:B:304:LYS:HB2	1.93	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	A	475/477 (100%)	444 (94%)	26 (6%)	5 (1%)	12	18
1	B	475/477 (100%)	444 (94%)	27 (6%)	4 (1%)	16	26
2	C	2/4 (50%)	2 (100%)	0	0	100	100
2	D	2/4 (50%)	2 (100%)	0	0	100	100
All	All	954/962 (99%)	892 (94%)	53 (6%)	9 (1%)	14	22

All (9) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	204	PRO
1	B	202	ASN
1	B	204	PRO
1	A	202	ASN
1	B	198	ASN
1	A	198	ASN
1	A	230	CYS
1	A	200	ASN
1	B	230	CYS

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	398/398 (100%)	374 (94%)	24 (6%)	16	27
1	B	398/398 (100%)	376 (94%)	22 (6%)	18	31
2	C	1/1 (100%)	1 (100%)	0	100	100
2	D	1/1 (100%)	1 (100%)	0	100	100
All	All	798/798 (100%)	752 (94%)	46 (6%)	17	29

All (46) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	144	LEU
1	A	178	LEU
1	A	184	ASP
1	A	201	THR
1	A	202	ASN
1	A	203	LEU
1	A	227	ASN
1	A	232	VAL
1	A	293	LEU
1	A	301	ARG
1	A	302	ASP
1	A	323	ASN
1	A	329	ASN

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Mol	Chain	Res	Type
1	A	396	THR
1	A	405	LEU
1	A	441	ARG
1	A	499	ASP
1	A	509	THR
1	A	526	LEU
1	A	574	THR
1	A	586	TRP
1	A	596	ASP
1	A	597	SER
1	A	598	SER
1	B	144	LEU
1	B	178	LEU
1	B	184	ASP
1	B	201	THR
1	B	202	ASN
1	B	203	LEU
1	B	227	ASN
1	B	293	LEU
1	B	301	ARG
1	B	302	ASP
1	B	323	ASN
1	B	329	ASN
1	B	396	THR
1	B	405	LEU
1	B	441	ARG
1	B	499	ASP
1	B	509	THR
1	B	526	LEU
1	B	574	THR
1	B	580	ARG
1	B	586	TRP
1	B	596	ASP

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (26) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	198	ASN
1	A	200	ASN
1	A	202	ASN
1	A	227	ASN
1	A	237	ASN

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Mol	Chain	Res	Type
1	A	329	ASN
1	A	341	HIS
1	A	369	HIS
1	A	379	ASN
1	A	440	HIS
1	A	477	GLN
1	A	498	GLN
1	A	507	HIS
1	A	535	ASN
1	B	162	ASN
1	B	198	ASN
1	B	202	ASN
1	B	227	ASN
1	B	329	ASN
1	B	341	HIS
1	B	369	HIS
1	B	379	ASN
1	B	440	HIS
1	B	477	GLN
1	B	507	HIS
1	B	535	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

2 non-standard protein/DNA/RNA residues 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	$\# Z > 2$
2	BOR	C	4	2,1	6,11,11	0.39	0	5,13,13	0.72	0
2	BOR	D	4	2,1	6,11,11	0.47	0	5,13,13	0.91	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
2	BOR	C	4	2,1	-	0/7/11/11	-
2	BOR	D	4	2,1	-	0/7/11/11	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 8 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	C	4	BOR	4	0
2	D	4	BOR	4	0

5.5 Carbohydrates

4 monosaccharides are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
3	NAG	E	1	3,1	14,14,15	1.01	0	17,19,21	0.84	0
3	NAG	E	2	3	14,14,15	0.70	0	17,19,21	0.94	1 (5%)
3	NAG	F	1	3,1	14,14,15	0.66	0	17,19,21	1.33	2 (11%)
3	NAG	F	2	3	14,14,15	0.64	0	17,19,21	0.68	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
3	NAG	E	1	3,1	-	2/6/23/26	0/1/1/1
3	NAG	E	2	3	-	2/6/23/26	0/1/1/1
3	NAG	F	1	3,1	-	0/6/23/26	0/1/1/1
3	NAG	F	2	3	-	3/6/23/26	0/1/1/1

There are no bond length outliers.

All (3) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	F	1	NAG	C4-C3-C2	4.13	117.07	111.02
3	E	2	NAG	C2-N2-C7	-2.29	119.83	122.90
3	F	1	NAG	C2-N2-C7	-2.03	120.19	122.90

There are no chirality outliers.

All (7) torsion outliers are listed below:

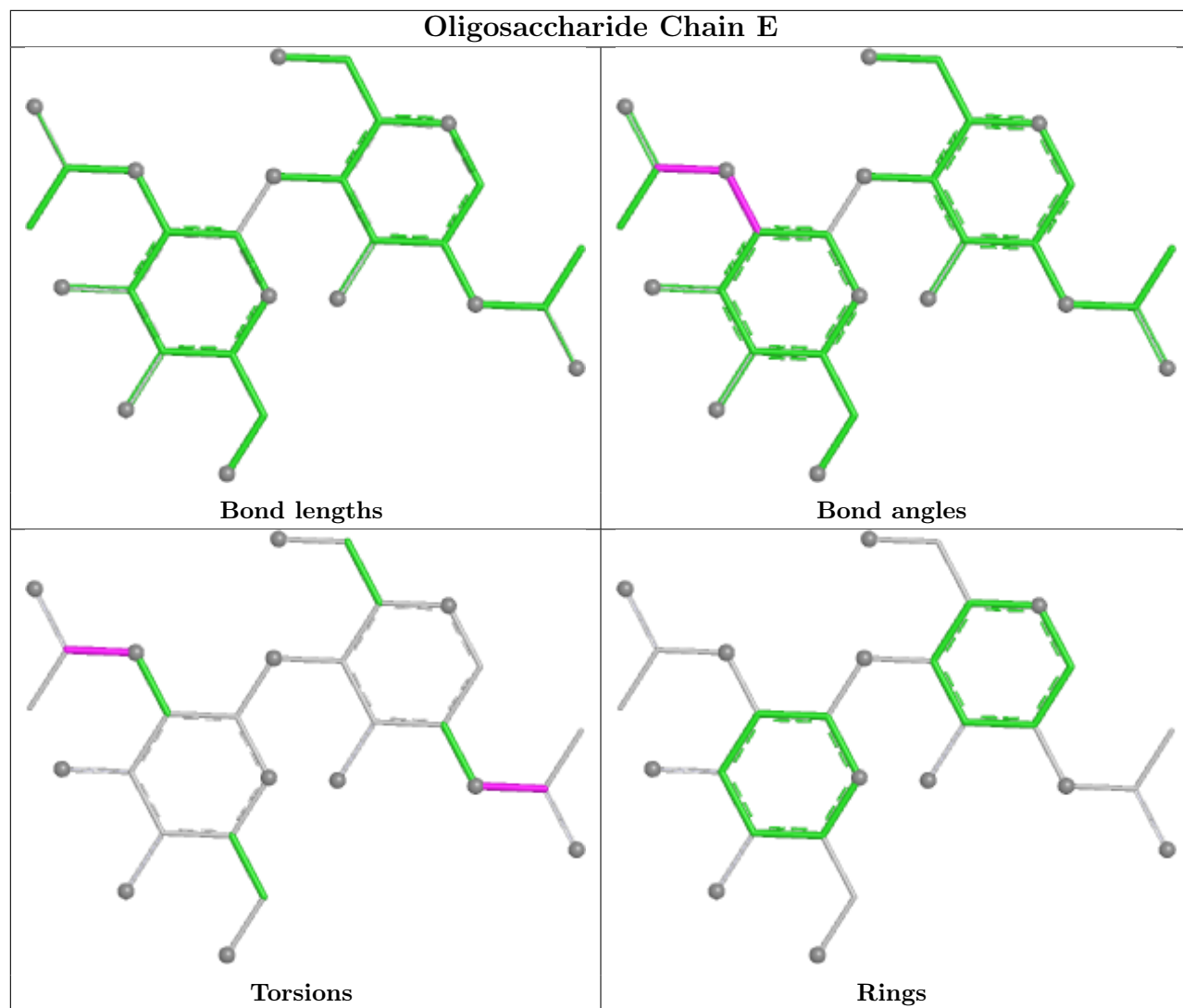
Mol	Chain	Res	Type	Atoms
3	F	2	NAG	C8-C7-N2-C2
3	F	2	NAG	O7-C7-N2-C2
3	E	1	NAG	C8-C7-N2-C2
3	E	2	NAG	C8-C7-N2-C2
3	E	1	NAG	O7-C7-N2-C2
3	E	2	NAG	O7-C7-N2-C2
3	F	2	NAG	C4-C5-C6-O6

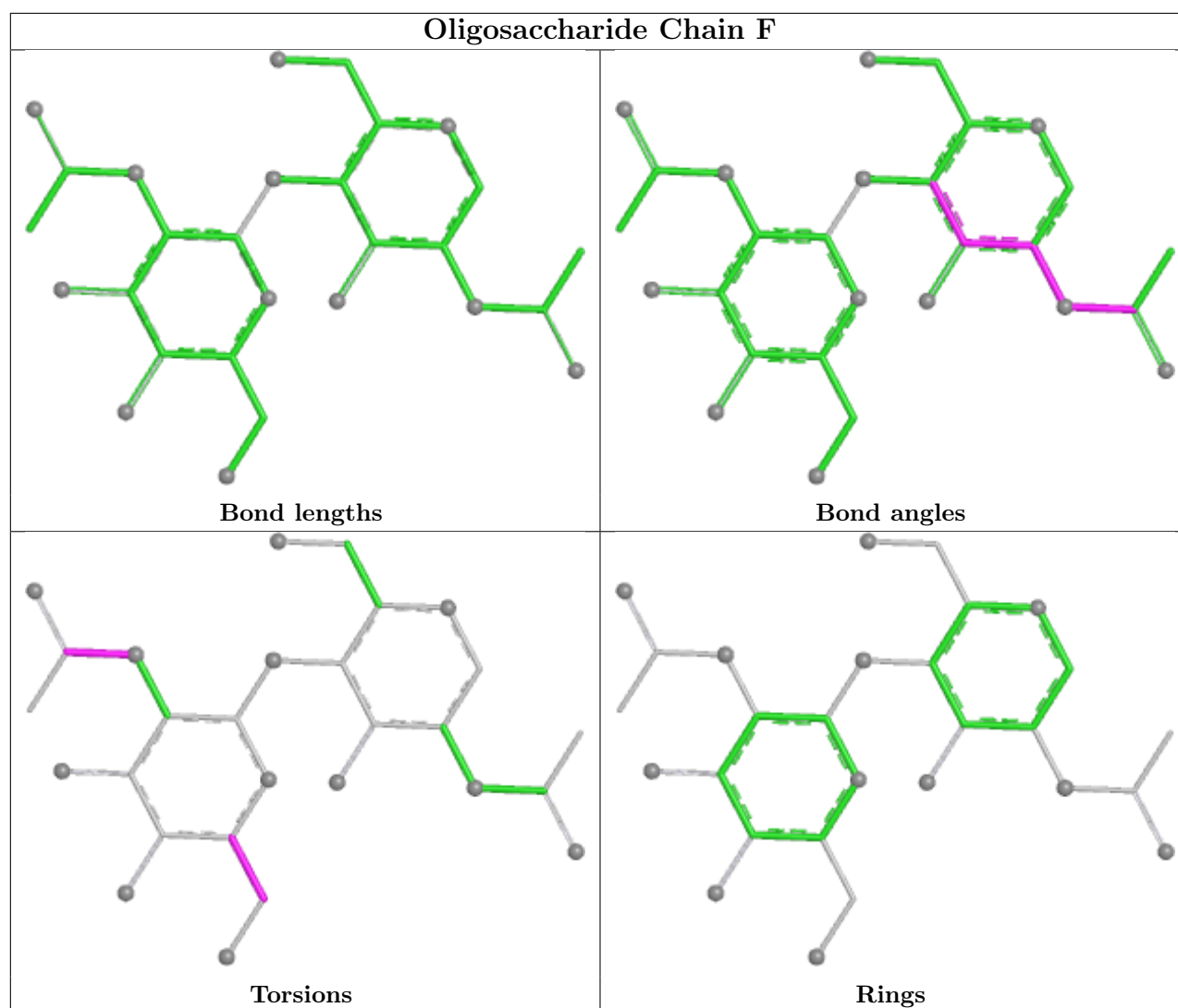
There are no ring outliers.

4 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	F	1	NAG	1	0
3	E	2	NAG	1	0
3	F	2	NAG	1	0
3	E	1	NAG	2	0

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





5.6 Ligand geometry [i](#)

Of 8 ligands modelled in this entry, 6 are monoatomic - leaving 2 for Mogul analysis.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
4	NAG	A	603	1	14,14,15	0.58	0	17,19,21	0.73	1 (5%)
4	NAG	B	603	1	14,14,15	0.47	0	17,19,21	0.76	1 (5%)

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	NAG	A	603	1	-	4/6/23/26	0/1/1/1
4	NAG	B	603	1	-	4/6/23/26	0/1/1/1

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	603	NAG	C2-N2-C7	-2.09	120.10	122.90
4	A	603	NAG	C2-N2-C7	-2.04	120.17	122.90

There are no chirality outliers.

All (8) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	603	NAG	O5-C5-C6-O6
4	B	603	NAG	C8-C7-N2-C2
4	A	603	NAG	O5-C5-C6-O6
4	A	603	NAG	C8-C7-N2-C2
4	B	603	NAG	O7-C7-N2-C2
4	B	603	NAG	C4-C5-C6-O6
4	A	603	NAG	O7-C7-N2-C2
4	A	603	NAG	C4-C5-C6-O6

There are no ring outliers.

No monomer is involved in short contacts.

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	477/477 (100%)	-0.03	25 (5%) 34 31	15, 30, 60, 91	0
1	B	477/477 (100%)	0.08	27 (5%) 30 28	15, 30, 60, 91	0
2	C	2/4 (50%)	-0.83	0 100 100	21, 21, 21, 22	0
2	D	2/4 (50%)	-0.26	0 100 100	31, 31, 31, 31	0
All	All	958/962 (99%)	0.02	52 (5%) 32 30	15, 30, 60, 91	0

All (52) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	201	THR	6.2
1	B	202	ASN	5.7
1	A	123	PRO	4.9
1	B	597	SER	4.8
1	A	199	ASP	4.8
1	B	201	THR	4.5
1	B	123	PRO	4.5
1	B	599	LYS	4.3
1	A	200	ASN	4.0
1	B	126	GLU	4.0
1	B	199	ASP	3.9
1	B	200	ASN	3.9
1	A	202	ASN	3.9
1	A	598	SER	3.9
1	A	599	LYS	3.8
1	A	203	LEU	3.8
1	B	490	ILE	3.7
1	B	212	TYR	3.6
1	A	376	ARG	3.6
1	A	495	LYS	3.5
1	B	586	TRP	3.4

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Mol	Chain	Res	Type	RSRZ
1	A	466	THR	3.0
1	B	204	PRO	3.0
1	B	596	ASP	2.8
1	B	483	GLU	2.8
1	B	376	ARG	2.7
1	A	586	TRP	2.7
1	A	204	PRO	2.7
1	A	126	GLU	2.7
1	B	203	LEU	2.7
1	A	377	CYS	2.7
1	B	253	GLU	2.6
1	B	148	SER	2.6
1	A	129	ASP	2.6
1	A	253	GLU	2.5
1	A	597	SER	2.5
1	A	423	LYS	2.5
1	B	129	ASP	2.4
1	B	186	LYS	2.4
1	B	462	VAL	2.3
1	A	498	GLN	2.3
1	B	469	TYR	2.3
1	B	595	ILE	2.3
1	B	499	ASP	2.3
1	A	499	ASP	2.2
1	A	596	ASP	2.2
1	B	466	THR	2.2
1	B	598	SER	2.2
1	B	379	ASN	2.1
1	A	130	LYS	2.0
1	A	428	ASP	2.0
1	A	490	ILE	2.0

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

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

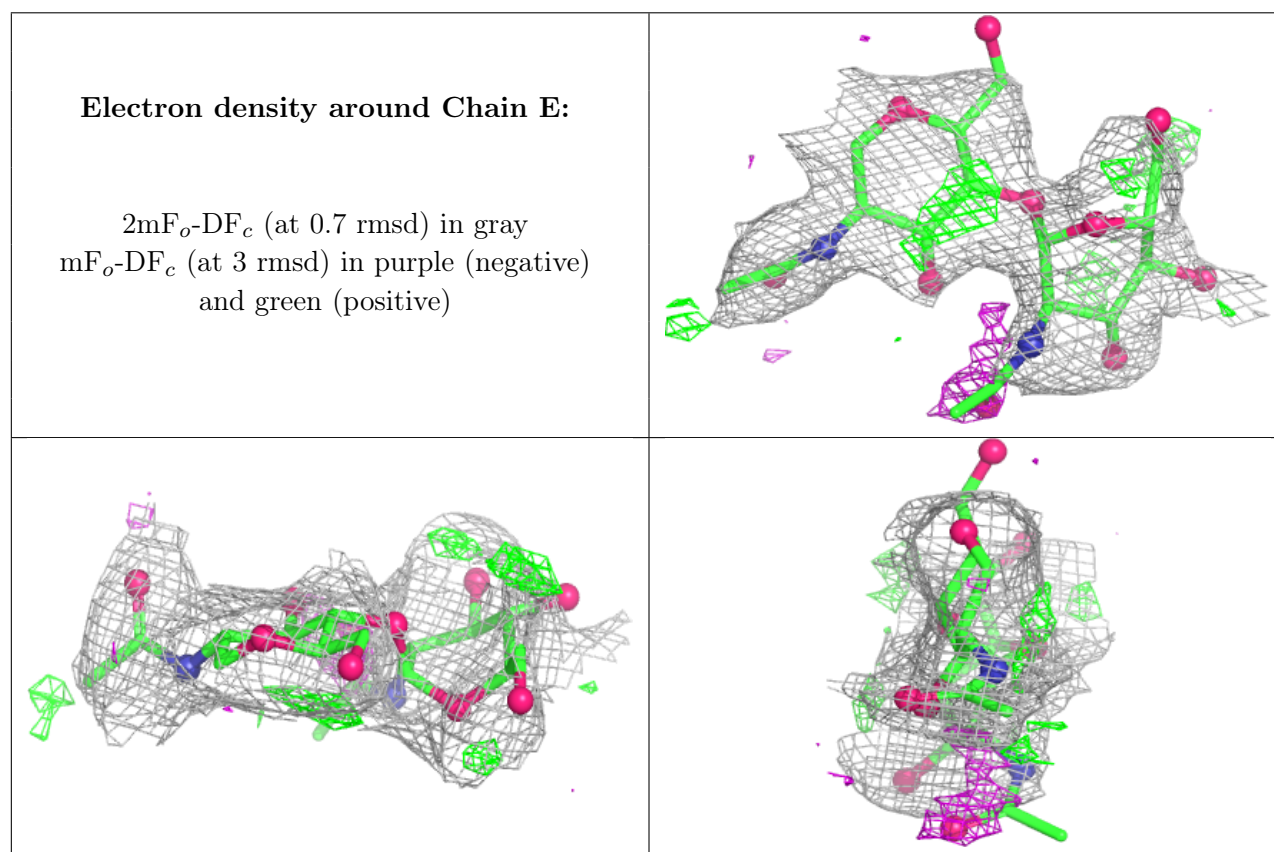
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
2	BOR	D	4	12/12	0.89	0.11	19,22,32,32	0
2	BOR	C	4	12/12	0.90	0.11	21,23,31,33	0

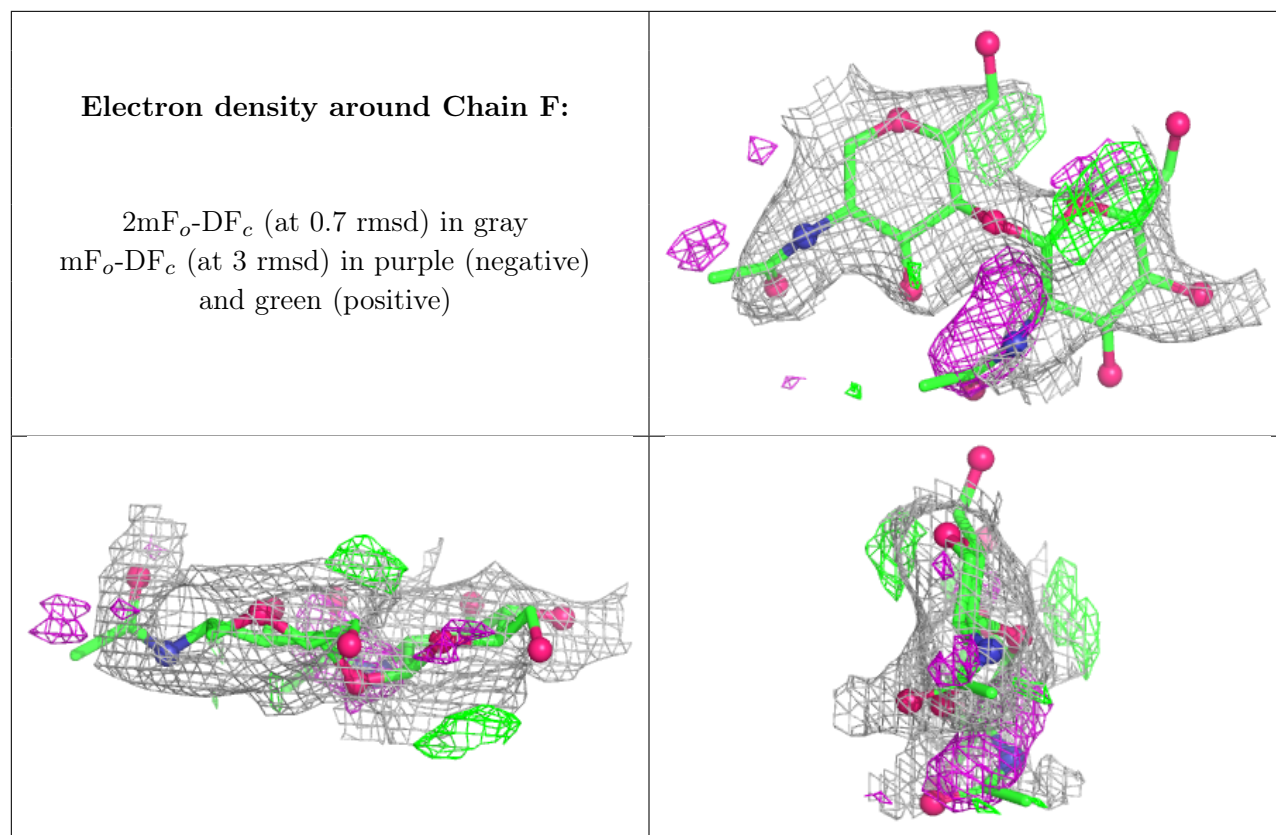
6.3 Carbohydrates ⓘ

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
3	NAG	F	2	14/15	0.41	0.21	65,74,78,80	0
3	NAG	E	2	14/15	0.48	0.21	65,74,78,80	0
3	NAG	F	1	14/15	0.70	0.19	71,78,81,82	0
3	NAG	E	1	14/15	0.70	0.20	65,74,78,80	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
4	NAG	A	603	14/15	0.56	0.25	89,101,104,104	0
4	NAG	B	603	14/15	0.63	0.26	87,99,102,103	0
5	CA	B	602	1/1	0.97	0.16	39,39,39,39	0
5	CA	A	602	1/1	0.98	0.14	45,45,45,45	0
5	CA	A	601	1/1	0.98	0.04	28,28,28,28	0
5	CA	B	600	1/1	0.99	0.02	19,19,19,19	0
5	CA	B	601	1/1	0.99	0.04	29,29,29,29	0
5	CA	A	600	1/1	0.99	0.03	19,19,19,19	0

6.5 Other polymers [i](#)

There are no such residues in this entry.