



Full wwPDB X-ray Structure Validation Report ⓘ

Aug 7, 2020 – 12:50 PM BST

PDB ID : 5DIS
Title : Crystal structure of a CRM1-RanGTP-SPN1 export complex bound to a 113 amino acid FG-repeat containing fragment of Nup214
Authors : Monecke, T.; Port, S.A.; Dickmanns, A.; Kehlenbach, R.H.; Ficner, R.
Deposited on : 2015-09-01
Resolution : 2.85 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 following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.13.1
buster-report : 1.1.7 (2018)
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.13.1

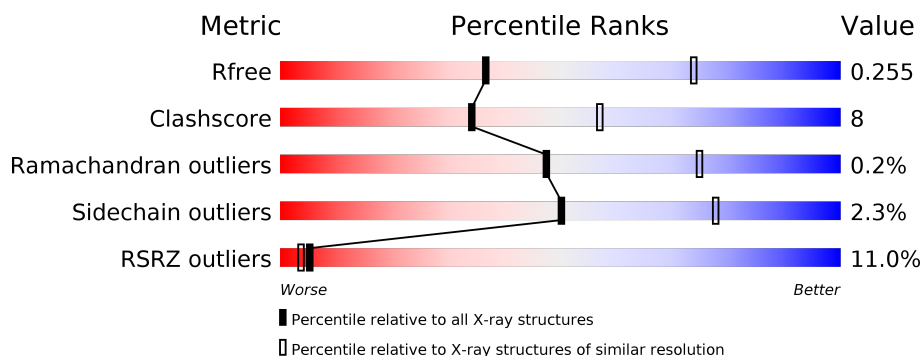
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.85 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}	130704	3168 (2.90-2.82)
Clashscore	141614	3438 (2.90-2.82)
Ramachandran outliers	138981	3348 (2.90-2.82)
Sidechain outliers	138945	3351 (2.90-2.82)
RSRZ outliers	127900	3103 (2.90-2.82)

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 on 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	1044	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> % 79% 20% . </div> </div>
2	B	172	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> % 85% 14% . </div> </div>
3	C	289	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> 3% 67% 23% . 9% </div> </div>
4	D	479	<div> <div style="width: 100%; height: 10px; background-color: red;"></div> <div style="display: flex; justify-content: space-between;"> 39% 63% 17% . 18% </div> </div>
5	E	2	<div> <div style="width: 100%; height: 10px; background-color: yellow;"></div> <div style="display: flex; justify-content: space-between;"> 50% 50% </div> </div>

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
6	PRO	C	301	-	-	-	X

2 Entry composition

There are 9 unique types of molecules in this entry. The entry contains 14991 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 Exportin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	1032	Total	C	N	O	S	0	0	0
			8366	5370	1400	1541	55			

- Molecule 2 is a protein called GTP-binding nuclear protein Ran.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	172	Total	C	N	O	S	0	0	0
			1398	909	245	239	5			

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	69	LEU	GLN	engineered mutation	UNP P62826

- Molecule 3 is a protein called Snurportin-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	C	264	Total	C	N	O	S	0	0	0
			2131	1359	365	393	14			

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	-1	GLY	-	linker	UNP O95149
C	0	SER	-	linker	UNP O95149

- Molecule 4 is a protein called Maltose-binding periplasmic protein,Nuclear pore complex protein Nup214.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
4	D	395	Total	C	N	O	S	0	0	0
			3012	1941	489	579	3			

There are 11 discrepancies between the modelled and reference sequences:

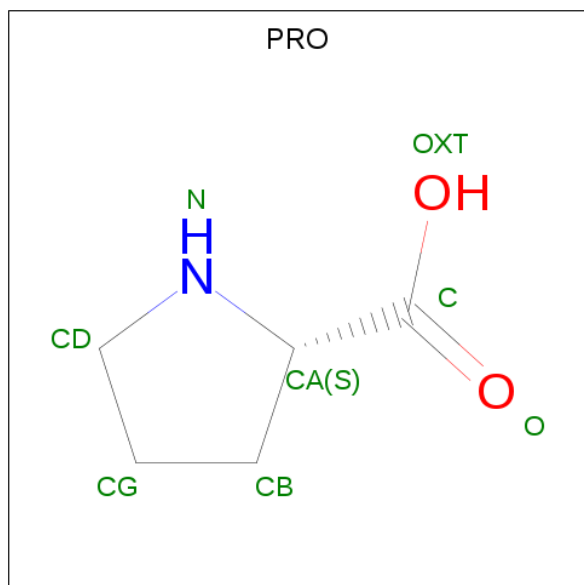
Chain	Residue	Modelled	Actual	Comment	Reference
D	362	ALA	-	linker	UNP P0AEX9
D	363	ALA	-	linker	UNP P0AEX9
D	364	ALA	-	linker	UNP P0AEX9
D	365	GLN	-	linker	UNP P0AEX9
D	366	THR	-	linker	UNP P0AEX9
D	367	ASN	-	linker	UNP P0AEX9
D	368	ALA	-	linker	UNP P0AEX9
D	1912	ALA	-	linker	UNP P0AEX9
D	1913	ALA	-	linker	UNP P0AEX9
D	1914	GLU	-	linker	UNP P0AEX9
D	1915	PHE	-	linker	UNP P0AEX9

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



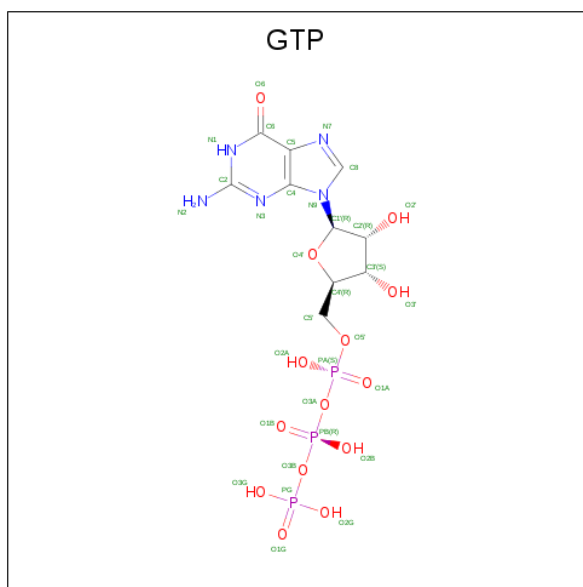
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf	Trace
5	E	2	Total	C	O	0	0	0
			23	12	11			

- Molecule 6 is PROLINE (three-letter code: PRO) (formula: C₅H₉NO₂).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	A	1	Total	C	N	O	0	0
			8	5	1	2		
6	C	1	Total	C	N	O	0	0
			8	5	1	2		

- Molecule 7 is GUANOSINE-5'-TRIPHOSPHATE (three-letter code: GTP) (formula: $C_{10}H_{16}N_5O_{14}P_3$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
7	B	1	Total	C	N	O	P	0	0
			32	10	5	14	3		

- Molecule 8 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
8	B	1	Total	Mg	0	0
			1	1		

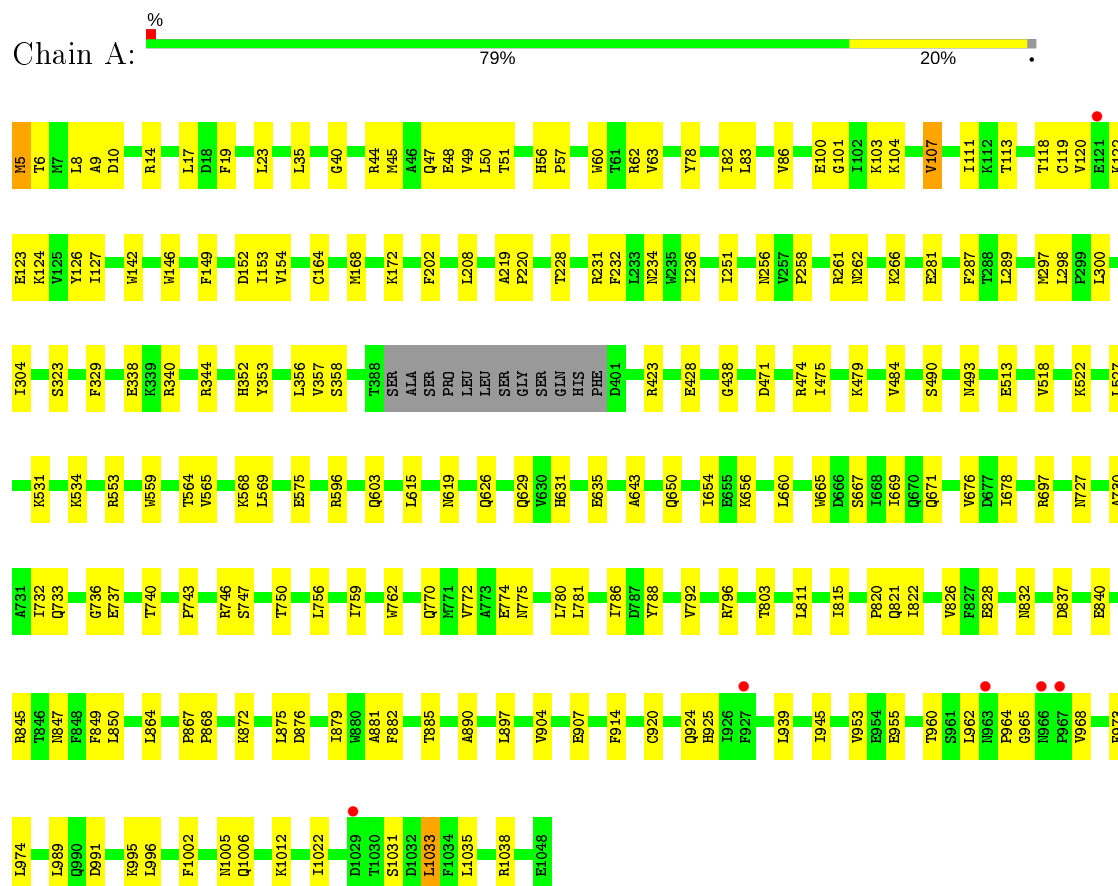
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	3	Total	O	0	0
			3	3		
9	B	9	Total	O	0	0
			9	9		

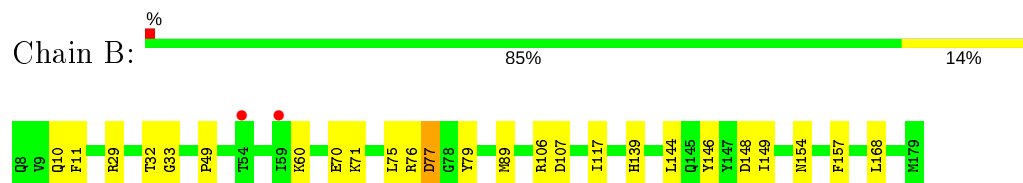
3 Residue-property plots

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: Exportin-1

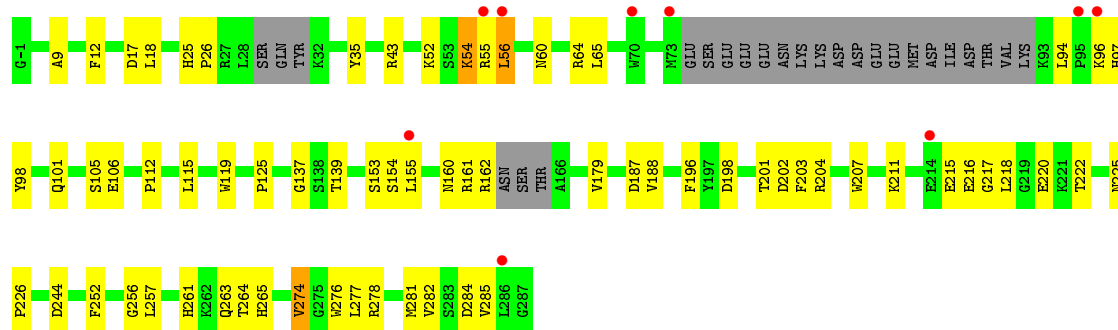


• Molecule 2: GTP-binding nuclear protein Ran

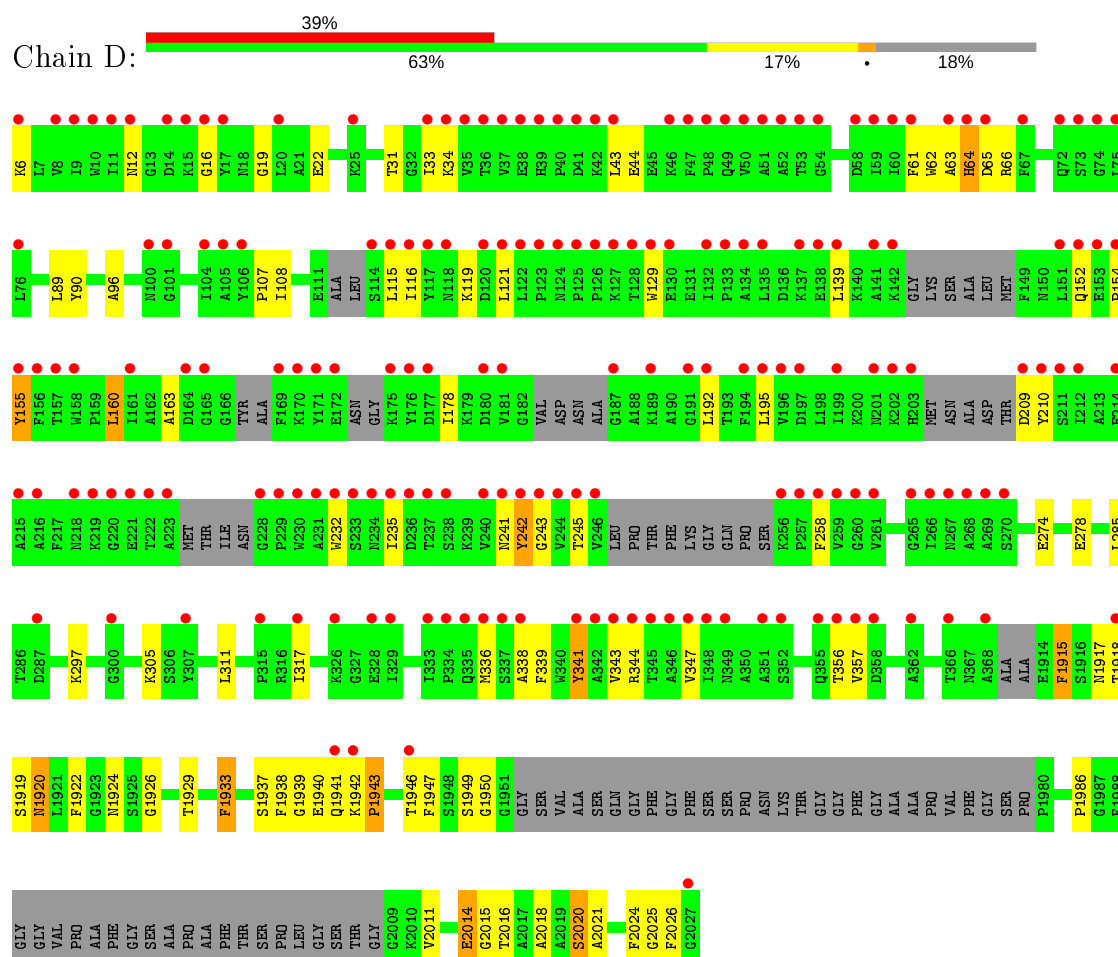


• Molecule 3: Snurportin-1





- Molecule 4: Maltose-binding periplasmic protein, Nuclear pore complex protein Nup214



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



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	112.33Å 248.97Å 210.57Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.48 – 2.85 48.49 – 2.85	Depositor EDS
% Data completeness (in resolution range)	98.2 (48.48-2.85) 98.3 (48.49-2.85)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.12 (at 2.86Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.206 , 0.249 0.212 , 0.255	Depositor DCC
R_{free} test set	3396 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å ²)	80.0	Xtriage
Anisotropy	0.811	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 97.6	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	0.95	EDS
Total number of atoms	14991	wwPDB-VP
Average B, all atoms (Å ²)	125.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.15% of the height of the origin peak. No significant pseudotranslation is detected.*

¹Intensities estimated from amplitudes.

²Theoretical values of $\langle |L| \rangle$, $\langle L^2 \rangle$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.

5 Model quality [i](#)

5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: GTP, MG, 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	A	0.33	0/8537	0.48	0/11566
2	B	0.35	0/1432	0.48	0/1932
3	C	0.30	0/2186	0.48	0/2957
4	D	0.32	0/3080	0.49	0/4158
All	All	0.32	0/15235	0.48	0/20613

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no planarity outliers.

5.2 Too-close contacts [i](#)

In the following table, the Non-H and H(model) columns list the number of non-hydrogen atoms and hydrogen atoms in the chain respectively. The H(added) column lists the number of hydrogen atoms added and optimized by MolProbity. The Clashes column lists the number of clashes within the asymmetric unit, whereas Symm-Clashes lists symmetry related clashes.

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
1	A	8366	0	8417	139	0
2	B	1398	0	1425	15	0
3	C	2131	0	2083	44	0
4	D	3012	0	2923	68	0
5	E	23	0	21	1	0
6	A	8	0	7	0	0
6	C	8	0	7	1	0
7	B	32	0	12	0	0
8	B	1	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
9	A	3	0	0	1	0
9	B	9	0	0	0	0
All	All	14991	0	14895	251	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 8.

All (251) 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:338:ALA:HA	4:D:341:TYR:CE2	2.12	0.84
4:D:2018:ALA:O	4:D:2021:ALA:HB3	1.83	0.78
4:D:155:TYR:HE2	4:D:258:PHE:CE1	2.02	0.77
1:A:251:ILE:HG21	1:A:289:LEU:HB3	1.67	0.77
1:A:471:ASP:OD1	1:A:474:ARG:NH2	2.23	0.72
1:A:19:PHE:HA	1:A:62:ARG:NH2	2.05	0.71
1:A:953:VAL:HG21	1:A:974:LEU:HD11	1.73	0.70
4:D:64:HIS:CE1	4:D:96:ALA:HB1	2.27	0.69
3:C:160:ASN:OD1	3:C:161:ARG:N	2.26	0.69
4:D:2016:THR:O	4:D:2020:SER:OG	2.12	0.68
4:D:339:PHE:O	4:D:343:VAL:HG23	1.94	0.68
1:A:23:LEU:HD22	1:A:62:ARG:HD3	1.76	0.67
4:D:1918:THR:OG1	4:D:1919:SER:N	2.25	0.67
3:C:137:GLY:HA2	3:C:160:ASN:O	1.94	0.67
3:C:65:LEU:HD21	3:C:101:GLN:HE21	1.61	0.66
1:A:358:SER:O	1:A:423:ARG:NH1	2.29	0.65
2:B:70:GLU:O	2:B:76:ARG:NH2	2.30	0.65
1:A:123:GLU:HB2	1:A:126:TYR:HB3	1.79	0.65
4:D:356:THR:HG22	4:D:357:VAL:H	1.61	0.65
1:A:338:GLU:O	1:A:344:ARG:NH2	2.30	0.65
1:A:23:LEU:HB2	1:A:62:ARG:NH1	2.11	0.64
1:A:820:PRO:HB3	4:D:1938:PHE:O	1.97	0.63
4:D:152:GLN:O	4:D:344:ARG:HG3	1.98	0.62
4:D:155:TYR:CE2	4:D:258:PHE:CE1	2.86	0.62
1:A:9:ALA:HA	1:A:49:VAL:HG22	1.80	0.62
1:A:56:HIS:CD2	1:A:57:PRO:HD2	2.34	0.62
2:B:49:PRO:HB3	2:B:60:LYS:HE2	1.81	0.61
4:D:343:VAL:O	4:D:347:VAL:HG23	1.99	0.61
1:A:103:LYS:O	1:A:107:VAL:HG13	2.00	0.61
3:C:54:LYS:HD2	3:C:198:ASP:OD1	2.00	0.61
4:D:258:PHE:O	4:D:258:PHE:CD1	2.54	0.61

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:475:ILE:O	1:A:479:LYS:HG2	1.99	0.61
1:A:840:GLU:O	1:A:845:ARG:NH1	2.33	0.60
4:D:2014:GLU:OE1	4:D:2015:GLY:N	2.35	0.60
1:A:5:MET:SD	1:A:6:THR:N	2.72	0.60
1:A:6:THR:HA	1:A:9:ALA:HB3	1.84	0.60
4:D:61:PHE:HE1	4:D:108:ILE:HG13	1.67	0.59
4:D:31:THR:HG22	4:D:33:ILE:HG13	1.84	0.59
1:A:864:LEU:HD11	1:A:907:GLU:HG3	1.85	0.59
1:A:955:GLU:OE1	1:A:955:GLU:N	2.35	0.59
1:A:100:GLU:O	1:A:104:LYS:HG3	2.03	0.59
1:A:733:GLN:HG3	1:A:792:VAL:HG21	1.84	0.59
2:B:10:GLN:HB3	2:B:60:LYS:HB3	1.84	0.58
1:A:939:LEU:HG	1:A:1012:LYS:HG3	1.86	0.58
4:D:154:PRO:HD3	4:D:344:ARG:HB2	1.85	0.58
3:C:155:LEU:HG	3:C:225:ASN:HB2	1.86	0.57
1:A:231:ARG:O	1:A:234:ASN:HB2	2.05	0.57
1:A:756:LEU:HB3	1:A:803:THR:HG21	1.85	0.57
1:A:8:LEU:HD22	1:A:45:MET:SD	2.45	0.57
1:A:828:GLU:O	1:A:832:ASN:ND2	2.38	0.57
4:D:274:GLU:O	4:D:278:GLU:HG2	2.05	0.57
1:A:231:ARG:NH2	9:A:1202:HOH:O	2.37	0.57
3:C:278:ARG:HB2	3:C:281:MET:HG3	1.87	0.56
3:C:277:LEU:HD21	3:C:285:VAL:HG21	1.88	0.56
4:D:1949:SER:OG	4:D:1950:GLY:N	2.40	0.55
1:A:925:HIS:HA	4:D:1986:PRO:HB3	1.86	0.55
2:B:106:ARG:HG3	2:B:107:ASP:N	2.20	0.55
4:D:116:ILE:HD11	4:D:232:TRP:CD1	2.42	0.55
1:A:298:LEU:O	1:A:353:TYR:OH	2.18	0.55
1:A:60:TRP:CG	1:A:86:VAL:HG21	2.43	0.55
4:D:16:GLY:HA2	4:D:297:LYS:HD2	1.89	0.55
1:A:837:ASP:O	1:A:845:ARG:NH2	2.40	0.54
4:D:64:HIS:ND1	4:D:96:ALA:HB1	2.22	0.54
1:A:153:ILE:HG22	4:D:2024:PHE:CG	2.43	0.54
1:A:484:VAL:HA	1:A:527:LEU:HD13	1.90	0.54
3:C:155:LEU:HG	3:C:225:ASN:CB	2.38	0.53
1:A:615:LEU:HB3	1:A:656:LYS:HD2	1.90	0.53
1:A:113:THR:HG23	1:A:122:LYS:HE3	1.91	0.53
1:A:438:GLY:N	1:A:746:ARG:HD3	2.24	0.53
4:D:6:LYS:HD2	4:D:34:LYS:HD2	1.91	0.53
1:A:619:ASN:HB2	1:A:660:LEU:HD21	1.91	0.52
1:A:281:GLU:OE2	1:A:340:ARG:NH2	2.42	0.52

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
3:C:261:HIS:CD2	3:C:263:GLN:H	2.26	0.52
1:A:152:ASP:HB3	4:D:2025:GLY:H	1.75	0.52
1:A:60:TRP:HB3	1:A:86:VAL:HG21	1.92	0.52
1:A:1033:LEU:HD12	1:A:1033:LEU:H	1.75	0.52
2:B:77:ASP:N	2:B:77:ASP:OD1	2.42	0.52
1:A:19:PHE:HA	1:A:62:ARG:HH21	1.71	0.51
4:D:89:LEU:HD13	4:D:107:PRO:HG2	1.91	0.51
4:D:192:LEU:HD23	4:D:357:VAL:HG13	1.91	0.51
3:C:276:TRP:CE3	6:C:301:PRO:HG3	2.46	0.51
4:D:235:ILE:HG22	4:D:235:ILE:O	2.09	0.51
4:D:108:ILE:HD13	4:D:285:LEU:HD21	1.93	0.51
3:C:60:ASN:O	3:C:64:ARG:HG3	2.11	0.50
1:A:40:GLY:O	1:A:44:ARG:HB2	2.11	0.50
4:D:336:MET:O	4:D:339:PHE:HB3	2.11	0.50
1:A:17:LEU:HD13	1:A:56:HIS:ND1	2.27	0.50
2:B:139:HIS:HB2	2:B:144:LEU:HB2	1.92	0.50
1:A:953:VAL:HG11	1:A:974:LEU:HD12	1.93	0.50
1:A:287:PHE:HB2	1:A:329:PHE:CZ	2.46	0.50
1:A:882:PHE:HA	1:A:890:ALA:HA	1.93	0.50
4:D:235:ILE:HG21	4:D:242:TYR:HD2	1.75	0.50
4:D:339:PHE:CE2	4:D:343:VAL:HG21	2.47	0.50
4:D:119:LYS:HE3	4:D:243:GLY:HA3	1.93	0.49
4:D:119:LYS:HB2	4:D:241:ASN:HB3	1.94	0.49
1:A:732:ILE:O	1:A:736:GLY:N	2.45	0.49
1:A:811:LEU:HD12	1:A:815:ILE:HD12	1.93	0.49
3:C:257:LEU:HD12	3:C:282:VAL:HG21	1.94	0.49
1:A:879:ILE:HA	1:A:882:PHE:CE2	2.47	0.49
1:A:991:ASP:O	1:A:995:LYS:HG2	2.12	0.49
3:C:202:ASP:OD1	3:C:203:PHE:N	2.46	0.49
1:A:568:LYS:HE2	3:C:12:PHE:HB3	1.95	0.49
1:A:60:TRP:HA	1:A:63:VAL:HG23	1.95	0.48
4:D:338:ALA:HA	4:D:341:TYR:CD2	2.47	0.48
1:A:78:TYR:CE2	1:A:82:ILE:HD11	2.48	0.48
1:A:676:VAL:HG12	4:D:1922:PHE:HB2	1.95	0.48
1:A:438:GLY:H	1:A:746:ARG:HD3	1.78	0.48
1:A:202:PHE:CZ	1:A:236:ILE:HG21	2.49	0.48
1:A:172:LYS:HB2	1:A:228:THR:HG23	1.95	0.48
1:A:490:SER:HB3	1:A:493:ASN:OD1	2.14	0.48
4:D:160:LEU:HD23	4:D:163:ALA:HB3	1.96	0.48
2:B:89:MET:CE	2:B:149:ILE:HD11	2.43	0.48
3:C:264:THR:HG22	3:C:265:HIS:O	2.14	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
4:D:1915:PHE:N	4:D:1915:PHE:CD1	2.76	0.48
3:C:115:LEU:HD12	3:C:119:TRP:HB2	1.95	0.47
1:A:1002:PHE:O	1:A:1005:ASN:ND2	2.47	0.47
4:D:1920:ASN:OD1	4:D:1920:ASN:N	2.46	0.47
1:A:119:CYS:HA	1:A:122:LYS:HB3	1.95	0.47
1:A:1005:ASN:OD1	1:A:1006:GLN:HG3	2.14	0.47
2:B:32:THR:OG1	2:B:33:GLY:N	2.48	0.47
3:C:201:THR:HG23	3:C:264:THR:O	2.14	0.47
1:A:847:ASN:HA	1:A:850:LEU:HD12	1.95	0.47
3:C:56:LEU:HD12	3:C:56:LEU:N	2.30	0.47
3:C:160:ASN:CG	3:C:162:ARG:HG2	2.35	0.47
3:C:96:LYS:O	3:C:97:HIS:HB2	2.14	0.47
4:D:311:LEU:HB3	4:D:317:ILE:HD12	1.96	0.47
3:C:153:SER:O	3:C:226:PRO:HD2	2.15	0.47
4:D:116:ILE:HD11	4:D:232:TRP:HD1	1.80	0.47
1:A:631:HIS:HB3	1:A:697:ARG:HG3	1.97	0.46
4:D:1939:GLY:C	4:D:1940:GLU:HG3	2.36	0.46
1:A:849:PHE:CE1	1:A:881:ALA:HB2	2.50	0.46
2:B:75:LEU:HD12	2:B:79:TYR:CE1	2.51	0.46
1:A:770:GLN:O	1:A:774:GLU:HG2	2.15	0.46
4:D:155:TYR:HE2	4:D:258:PHE:CD1	2.34	0.46
3:C:105:SER:HB3	3:C:274:VAL:HG22	1.98	0.46
1:A:996:LEU:HD21	1:A:1038:ARG:HG2	1.98	0.46
1:A:56:HIS:HD2	1:A:57:PRO:HD2	1.80	0.46
3:C:207:TRP:CH2	3:C:211:LYS:HD3	2.51	0.46
1:A:8:LEU:HD12	1:A:8:LEU:H	1.81	0.46
1:A:104:LYS:HB3	4:D:2021:ALA:CB	2.46	0.46
1:A:743:PRO:O	1:A:746:ARG:HB3	2.16	0.45
1:A:868:PRO:HG2	4:D:1946:THR:OG1	2.17	0.45
3:C:215:GLU:C	3:C:216:GLU:HG2	2.36	0.45
4:D:129:TRP:CZ3	4:D:195:LEU:HD11	2.52	0.45
1:A:60:TRP:CB	1:A:86:VAL:HG21	2.47	0.45
3:C:217:GLY:HA2	3:C:220:GLU:OE1	2.16	0.45
3:C:125:PRO:HB3	3:C:252:PHE:CG	2.51	0.45
3:C:55:ARG:N	3:C:56:LEU:HD12	2.31	0.45
1:A:228:THR:HG22	1:A:232:PHE:CE2	2.51	0.45
2:B:11:PHE:CG	2:B:168:LEU:HD13	2.52	0.45
2:B:117:ILE:HB	2:B:144:LEU:HD22	1.99	0.45
2:B:146:TYR:OH	2:B:148:ASP:OD1	2.24	0.45
1:A:1035:LEU:H	1:A:1035:LEU:HD12	1.81	0.45
1:A:104:LYS:O	4:D:2021:ALA:HB2	2.16	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:6:THR:O	1:A:10:ASP:HB2	2.16	0.45
1:A:596:ARG:HB2	1:A:643:ALA:HB2	1.99	0.45
1:A:759:ILE:HD13	1:A:780:LEU:HD21	1.99	0.45
1:A:872:LYS:NZ	1:A:876:ASP:OD2	2.38	0.45
1:A:727:ASN:HA	4:D:1918:THR:HB	1.99	0.45
3:C:125:PRO:HB3	3:C:252:PHE:CD1	2.52	0.45
3:C:139:THR:OG1	3:C:154:SER:HB3	2.17	0.45
3:C:18:LEU:HD23	3:C:35:TYR:HA	1.99	0.45
4:D:1942:LYS:HA	4:D:1943:PRO:HD3	1.85	0.45
4:D:235:ILE:CG2	4:D:242:TYR:HD2	2.30	0.45
1:A:107:VAL:O	1:A:111:ILE:HG12	2.17	0.44
1:A:960:THR:HG21	1:A:965:GLY:HA2	1.99	0.44
3:C:196:PHE:O	3:C:204:ARG:HD3	2.17	0.44
3:C:198:ASP:O	3:C:265:HIS:NE2	2.49	0.44
1:A:1031:SER:HA	1:A:1033:LEU:CD1	2.47	0.44
1:A:258:PRO:O	1:A:261:ARG:HG2	2.17	0.44
1:A:788:TYR:CZ	1:A:796:ARG:HD3	2.52	0.44
3:C:216:GLU:O	3:C:218:LEU:N	2.49	0.44
1:A:564:THR:HG23	3:C:9:ALA:HB2	1.99	0.44
1:A:304:ILE:HG13	1:A:356:LEU:HB3	2.00	0.44
1:A:490:SER:OG	5:E:1:GLC:H61	2.18	0.44
1:A:35:LEU:HD22	1:A:50:LEU:HD12	1.98	0.44
2:B:89:MET:HE2	2:B:149:ILE:HD11	1.98	0.44
3:C:112:PRO:HG3	3:C:119:TRP:CE2	2.52	0.44
3:C:97:HIS:O	3:C:98:TYR:HB2	2.16	0.44
1:A:63:VAL:HG11	1:A:83:LEU:HD22	2.00	0.44
1:A:897:LEU:HD23	1:A:945:ILE:HD13	1.99	0.44
4:D:62:TRP:CG	4:D:63:ALA:N	2.85	0.44
1:A:635:GLU:OE1	1:A:697:ARG:HD2	2.17	0.44
4:D:65:ASP:OD2	4:D:66:ARG:HG2	2.18	0.44
1:A:534:LYS:NZ	1:A:575:GLU:OE2	2.50	0.44
1:A:146:TRP:CD1	1:A:149:PHE:HB2	2.53	0.43
1:A:565:VAL:O	1:A:569:LEU:HD13	2.18	0.43
1:A:730:ALA:HB3	4:D:1918:THR:HG22	1.99	0.43
1:A:120:VAL:HG13	1:A:124:LYS:HE3	1.98	0.43
1:A:667:SER:O	1:A:671:GLN:HG3	2.18	0.43
1:A:747:SER:O	1:A:750:THR:HB	2.19	0.43
3:C:54:LYS:H	3:C:54:LYS:HG2	1.57	0.43
4:D:90:TYR:CE1	4:D:305:LYS:HG2	2.53	0.43
1:A:172:LYS:HB3	1:A:172:LYS:HE2	1.88	0.43
1:A:518:VAL:O	1:A:522:LYS:HB2	2.18	0.43

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:920:CYS:O	1:A:924:GLN:HG2	2.19	0.43
1:A:123:GLU:O	1:A:127:ILE:HG13	2.19	0.43
1:A:154:VAL:HG22	1:A:208:LEU:HD12	2.01	0.43
3:C:256:GLY:O	3:C:257:LEU:HD23	2.19	0.43
4:D:115:LEU:HD13	4:D:245:THR:HG23	2.00	0.43
4:D:43:LEU:HD12	4:D:44:GLU:N	2.32	0.43
1:A:968:VAL:CG1	1:A:973:PHE:HB2	2.49	0.43
2:B:71:LYS:HE3	2:B:71:LYS:HB2	1.84	0.43
1:A:774:GLU:HG3	1:A:775:ASN:OD1	2.19	0.42
1:A:781:LEU:O	1:A:786:ILE:HG13	2.19	0.42
3:C:43:ARG:NH2	3:C:106:GLU:OE2	2.51	0.42
1:A:300:LEU:HB3	1:A:352:HIS:CE1	2.55	0.42
1:A:559:TRP:CD2	1:A:603:GLN:HG3	2.55	0.42
4:D:1917:ASN:OD1	4:D:1918:THR:N	2.52	0.42
1:A:19:PHE:CA	1:A:62:ARG:HH21	2.32	0.42
1:A:904:VAL:HG11	1:A:914:PHE:CD2	2.53	0.42
4:D:1933:PHE:C	4:D:1933:PHE:CD1	2.92	0.42
4:D:19:GLY:HA2	4:D:22:GLU:CD	2.40	0.42
1:A:168:MET:HB3	1:A:168:MET:HE3	1.86	0.42
3:C:55:ARG:H	3:C:56:LEU:HD12	1.85	0.42
4:D:1926:GLY:HA2	4:D:1929:THR:HG22	2.00	0.42
1:A:626:GLN:HG2	1:A:629:GLN:HG3	2.02	0.42
1:A:118:THR:O	1:A:122:LYS:HB2	2.20	0.42
1:A:256:ASN:HA	1:A:297:MET:SD	2.60	0.42
3:C:25:HIS:HA	3:C:26:PRO:HD3	1.87	0.42
4:D:155:TYR:CE2	4:D:258:PHE:CD1	3.08	0.42
1:A:1033:LEU:N	1:A:1033:LEU:HD12	2.33	0.42
1:A:344:ARG:HA	1:A:344:ARG:HD3	1.75	0.42
3:C:215:GLU:HG3	3:C:215:GLU:O	2.20	0.42
1:A:737:GLU:O	1:A:740:THR:HG22	2.20	0.41
1:A:821:GLN:HG2	1:A:821:GLN:H	1.68	0.41
1:A:104:LYS:HA	4:D:2021:ALA:HB1	2.02	0.41
1:A:531:LYS:HA	1:A:531:LYS:HD3	1.89	0.41
3:C:187:ASP:OD1	3:C:188:VAL:N	2.53	0.41
4:D:1937:SER:O	4:D:1938:PHE:HB2	2.20	0.41
1:A:513:GLU:CD	1:A:553:ARG:HH21	2.23	0.41
1:A:164:CYS:O	1:A:168:MET:HG2	2.20	0.41
1:A:262:ASN:O	1:A:266:LYS:HG3	2.20	0.41
1:A:650:GLN:O	1:A:654:ILE:HG13	2.20	0.41
3:C:277:LEU:HG	3:C:281:MET:HB2	2.01	0.41
1:A:219:ALA:HB3	1:A:220:PRO:HD3	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:107:VAL:HG11	1:A:146:TRP:HH2	1.86	0.41
1:A:665:TRP:O	1:A:669:ILE:HG12	2.21	0.41
1:A:867:PRO:HA	1:A:868:PRO:HD3	1.84	0.41
1:A:101:GLY:HA3	4:D:2011:VAL:HG13	2.03	0.41
1:A:142:TRP:HD1	1:A:146:TRP:O	2.04	0.41
1:A:323:SER:HB3	1:A:357:VAL:HG11	2.03	0.41
1:A:762:TRP:CH2	1:A:772:VAL:HG22	2.55	0.41
1:A:822:ILE:O	1:A:826:VAL:HG22	2.21	0.41
1:A:962:LEU:HB3	1:A:964:PRO:HD2	2.02	0.41
4:D:209:ASP:OD1	4:D:210:TYR:N	2.50	0.41
1:A:953:VAL:HG21	1:A:974:LEU:CD1	2.48	0.41
4:D:121:LEU:HB3	4:D:139:LEU:HD11	2.02	0.41
1:A:104:LYS:CA	4:D:2021:ALA:HB1	2.51	0.41
1:A:44:ARG:O	1:A:48:GLU:HG3	2.21	0.40
2:B:29:ARG:HG2	2:B:157:PHE:CZ	2.57	0.40

There are no symmetry-related clashes.

5.3 Torsion angles

5.3.1 Protein backbone

In the following table, the Percentiles column shows the percent Ramachandran outliers of the chain as a percentile score with respect to all X-ray entries followed by that with respect to entries of similar resolution.

The Analysed column shows the number of residues for which the backbone conformation was analysed, and the total number of residues.

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	A	1028/1044 (98%)	983 (96%)	45 (4%)	0	100	100
2	B	170/172 (99%)	162 (95%)	8 (5%)	0	100	100
3	C	256/289 (89%)	241 (94%)	15 (6%)	0	100	100
4	D	371/479 (78%)	334 (90%)	34 (9%)	3 (1%)	19	46
All	All	1825/1984 (92%)	1720 (94%)	102 (6%)	3 (0%)	47	75

All (3) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
4	D	1941	GLN
4	D	1933	PHE
4	D	1943	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	941/951 (99%)	929 (99%)	12 (1%)	69	88
2	B	151/151 (100%)	149 (99%)	2 (1%)	69	88
3	C	237/262 (90%)	227 (96%)	10 (4%)	30	60
4	D	304/360 (84%)	290 (95%)	14 (5%)	27	56
All	All	1633/1724 (95%)	1595 (98%)	38 (2%)	50	78

All (38) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	5	MET
1	A	14	ARG
1	A	47	GLN
1	A	51	THR
1	A	107	VAL
1	A	428	GLU
1	A	678	ILE
1	A	875	LEU
1	A	885	THR
1	A	989	LEU
1	A	1022	ILE
1	A	1033	LEU
2	B	77	ASP
2	B	154	ASN
3	C	17	ASP
3	C	52	LYS
3	C	54	LYS
3	C	56	LEU
3	C	94	LEU

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Mol	Chain	Res	Type
3	C	179	VAL
3	C	222	THR
3	C	244	ASP
3	C	274	VAL
3	C	284	ASP
4	D	12	ASN
4	D	64	HIS
4	D	155	TYR
4	D	160	LEU
4	D	178	ILE
4	D	242	TYR
4	D	341	TYR
4	D	1915	PHE
4	D	1920	ASN
4	D	1924	ASN
4	D	1947	PHE
4	D	2014	GLU
4	D	2020	SER
4	D	2026	PHE

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (2) such sidechains are listed below:

Mol	Chain	Res	Type
3	C	101	GLN
3	C	261	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 ⓘ

2 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	E	1	5	12,12,12	0.52	0	17,17,17	1.25	1 (5%)
5	GLC	E	2	5	11,11,12	0.28	0	15,15,17	2.38	4 (26%)

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	E	1	5	-	2/2/22/22	0/1/1/1
5	GLC	E	2	5	-	1/2/19/22	0/1/1/1

There are no bond length outliers.

All (5) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
5	E	2	GLC	C1-O5-C5	7.50	122.35	112.19
5	E	1	GLC	O4-C4-C3	3.98	119.54	110.35
5	E	2	GLC	C3-C4-C5	3.15	115.86	110.24
5	E	2	GLC	O5-C5-C4	3.03	118.20	110.83
5	E	2	GLC	C6-C5-C4	-2.06	108.18	113.00

There are no chirality outliers.

All (3) torsion outliers are listed below:

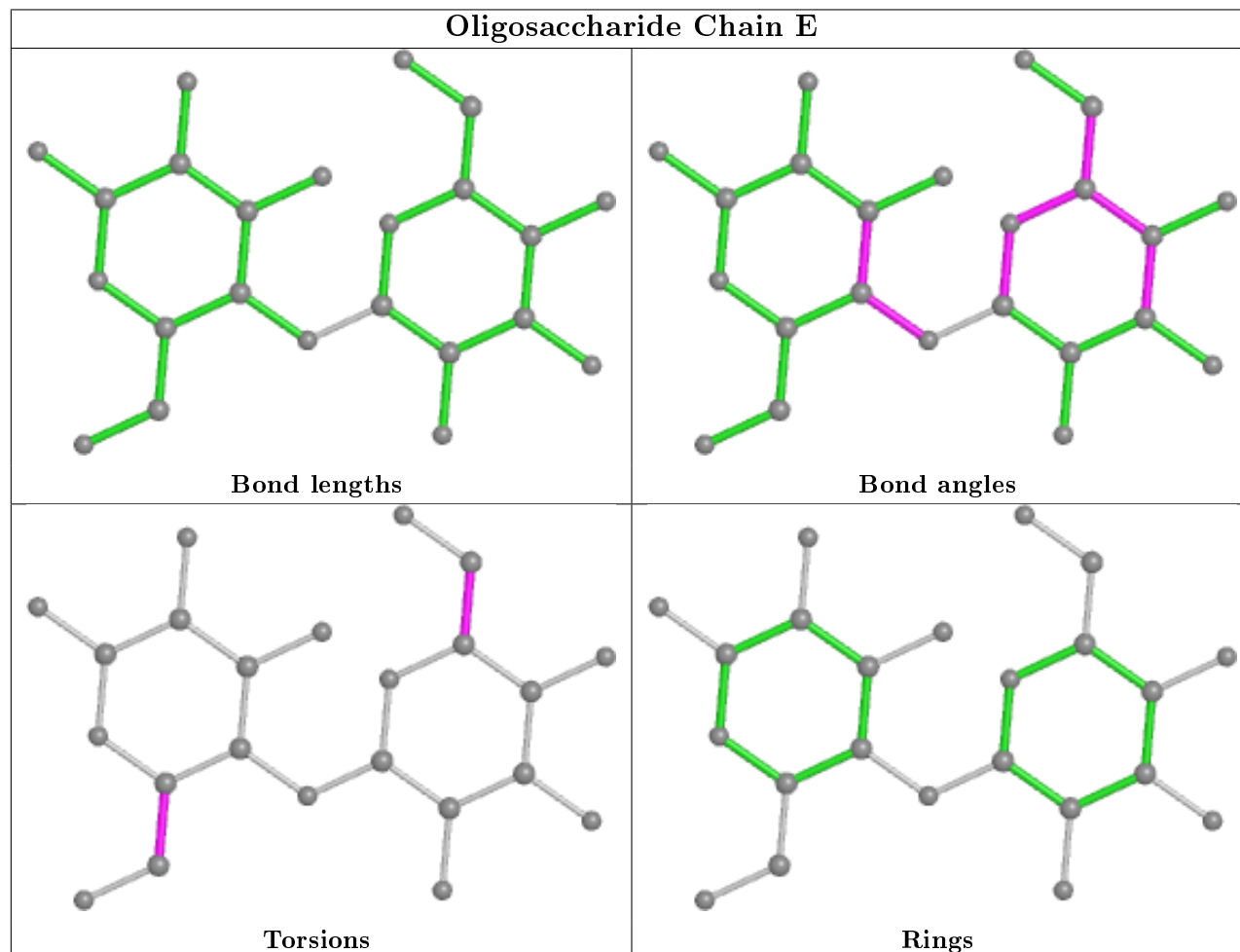
Mol	Chain	Res	Type	Atoms
5	E	1	GLC	O5-C5-C6-O6
5	E	2	GLC	O5-C5-C6-O6
5	E	1	GLC	C4-C5-C6-O6

There are no ring outliers.

1 monomer is involved in 1 short contact:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	E	1	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](#)

Of 4 ligands modelled in this entry, 1 is monoatomic - leaving 3 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
7	GTP	B	201	8	26,34,34	1.14	1 (3%)	33,54,54	2.02	9 (27%)

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
7	GTP	B	201	8	-	1/18/38/38	0/3/3/3

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
7	B	201	GTP	C6-C5	3.87	1.48	1.41

All (9) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
7	B	201	GTP	C2-N3-C4	5.49	121.63	115.36
7	B	201	GTP	C5-C6-N1	-4.24	117.64	123.43
7	B	201	GTP	C6-N1-C2	4.13	122.49	115.93
7	B	201	GTP	C6-C5-C4	-3.75	117.21	120.80
7	B	201	GTP	N3-C2-N1	-3.56	122.47	127.22
7	B	201	GTP	C4-C5-N7	-2.71	106.58	109.40
7	B	201	GTP	PB-O3B-PG	-2.49	124.28	132.83
7	B	201	GTP	PA-O3A-PB	-2.48	124.30	132.83
7	B	201	GTP	C3'-C2'-C1'	2.10	104.14	100.98

There are no chirality outliers.

All (1) torsion outliers are listed below:

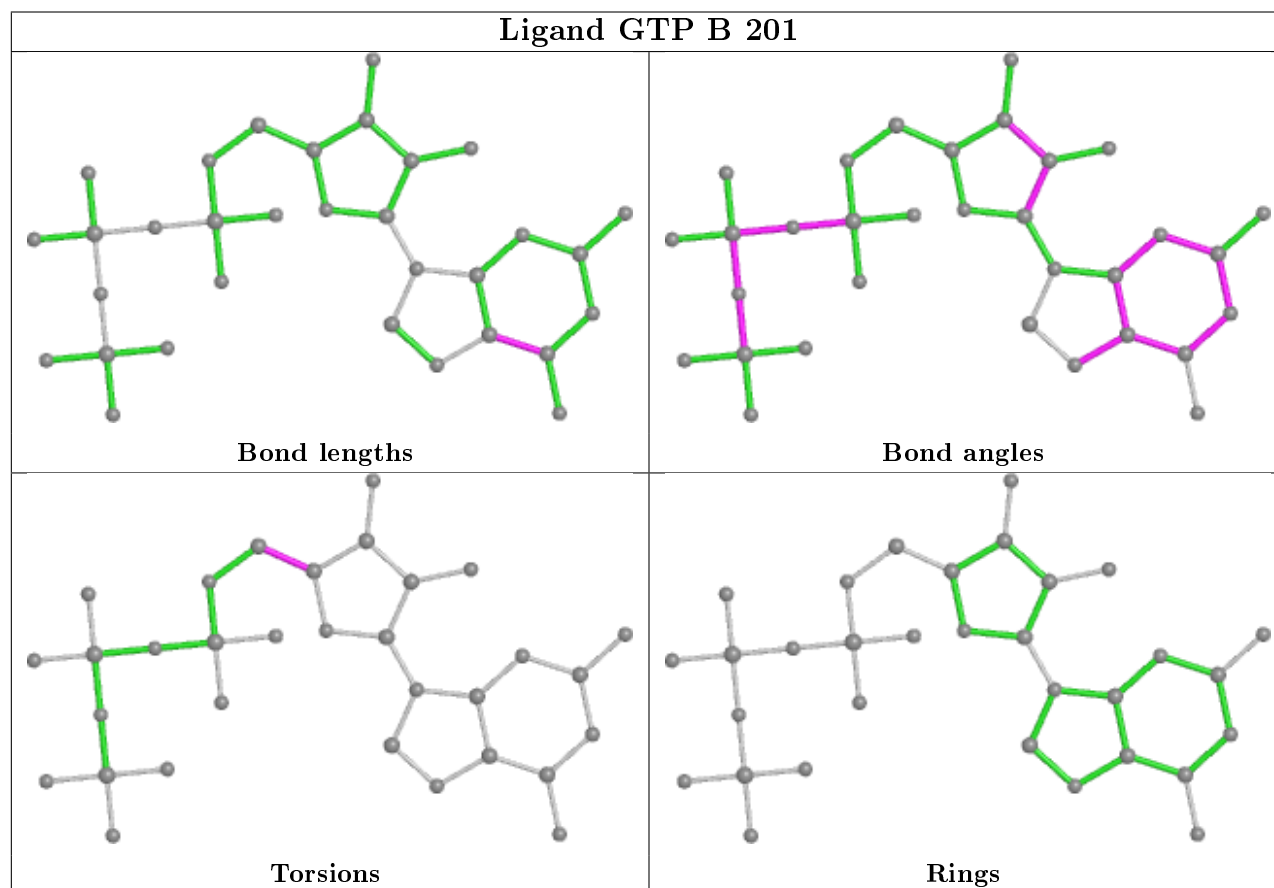
Mol	Chain	Res	Type	Atoms
7	B	201	GTP	O4'-C4'-C5'-O5'

There are no ring outliers.

No monomer is involved in short contacts.

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for 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	1032/1044 (98%)	-0.00	6 (0%) 89 89	59, 92, 145, 259	0
2	B	172/172 (100%)	0.06	2 (1%) 79 78	57, 83, 128, 204	0
3	C	264/289 (91%)	0.09	9 (3%) 45 39	72, 125, 190, 230	0
4	D	395/479 (82%)	2.35	187 (47%) 0 0	109, 213, 281, 329	0
All	All	1863/1984 (93%)	0.52	204 (10%) 5 4	57, 105, 246, 329	0

All (204) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	346	ALA	19.3
4	D	234	ASN	11.1
4	D	348	ILE	11.1
4	D	201	ASN	10.3
4	D	115	LEU	10.3
4	D	345	THR	10.2
4	D	116	ILE	9.4
4	D	176	TYR	9.2
4	D	152	GLN	8.6
4	D	74	GLY	8.3
4	D	43	LEU	8.2
4	D	210	TYR	8.1
4	D	121	LEU	8.1
4	D	221	GLU	8.1
4	D	151	LEU	8.0
4	D	220	GLY	7.6
4	D	134	ALA	7.2
4	D	9	ILE	7.0
4	D	40	PRO	7.0
4	D	237	THR	6.9
4	D	334	PRO	6.9

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Mol	Chain	Res	Type	RSRZ
4	D	16	GLY	6.8
4	D	211	SER	6.8
4	D	114	SER	6.5
4	D	135	LEU	6.5
4	D	35	VAL	6.4
4	D	15	LYS	6.4
4	D	222	THR	6.3
4	D	141	ALA	6.2
4	D	260	GLY	6.2
4	D	124	ASN	6.2
4	D	47	PHE	6.1
4	D	266	ILE	6.1
4	D	333	ILE	6.0
1	A	967	PRO	5.9
4	D	233	SER	5.9
4	D	244	VAL	5.9
4	D	11	ILE	5.8
4	D	357	VAL	5.4
4	D	242	TYR	5.4
4	D	259	VAL	5.3
4	D	337	SER	5.3
4	D	122	LEU	5.3
4	D	238	SER	5.3
4	D	72	GLN	5.2
4	D	153	GLU	5.2
3	C	55	ARG	5.1
4	D	356	THR	5.1
4	D	197	ASP	5.1
4	D	123	PRO	5.0
4	D	362	ALA	5.0
4	D	241	ASN	4.9
4	D	17	TYR	4.9
3	C	96	LYS	4.9
4	D	214	GLU	4.9
4	D	328	GLU	4.8
3	C	73	MET	4.8
4	D	347	VAL	4.8
4	D	368	ALA	4.8
4	D	61	PHE	4.8
4	D	229	PRO	4.7
4	D	53	THR	4.6
4	D	41	ASP	4.6

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Mol	Chain	Res	Type	RSRZ
4	D	181	VAL	4.6
4	D	209	ASP	4.6
4	D	358	ASP	4.5
4	D	158	TRP	4.5
4	D	75	LEU	4.4
4	D	120	ASP	4.4
4	D	170	LYS	4.4
3	C	286	LEU	4.4
4	D	228	GLY	4.3
4	D	261	VAL	4.3
4	D	8	VAL	4.3
4	D	1918	THR	4.3
4	D	12	ASN	4.2
4	D	349	ASN	4.2
4	D	125	PRO	4.2
4	D	54	GLY	4.2
4	D	2027	GLY	4.2
4	D	10	TRP	4.2
4	D	132	ILE	4.1
4	D	246	VAL	4.1
4	D	117	TYR	4.1
4	D	64	HIS	4.1
4	D	317	ILE	4.0
4	D	39	HIS	4.0
4	D	73	SER	4.0
4	D	129	TRP	4.0
4	D	137	LYS	4.0
3	C	56	LEU	4.0
4	D	118	ASN	3.9
4	D	101	GLY	3.9
4	D	127	LYS	3.9
4	D	133	PRO	3.9
4	D	59	ILE	3.8
4	D	223	ALA	3.8
4	D	216	ALA	3.8
4	D	355	GLN	3.7
4	D	67	PHE	3.7
4	D	218	ASN	3.7
4	D	165	GLY	3.6
4	D	195	LEU	3.6
1	A	1029	ASP	3.6
4	D	352	SER	3.6

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Mol	Chain	Res	Type	RSRZ
4	D	267	ASN	3.6
4	D	130	GLU	3.5
4	D	245	THR	3.5
4	D	139	LEU	3.5
4	D	50	VAL	3.5
4	D	157	THR	3.4
2	B	59	ILE	3.4
4	D	138	GLU	3.4
1	A	121	GLU	3.4
4	D	231	ALA	3.4
4	D	42	LYS	3.3
4	D	104	ILE	3.3
4	D	154	PRO	3.3
4	D	187	GLY	3.3
4	D	172	GLU	3.3
4	D	52	ALA	3.2
4	D	36	THR	3.2
4	D	38	GLU	3.2
4	D	342	ALA	3.2
4	D	235	ILE	3.2
4	D	100	ASN	3.1
4	D	194	PHE	3.1
4	D	58	ASP	3.1
4	D	236	ASP	3.1
4	D	142	LYS	3.1
1	A	963	ASN	3.1
4	D	1946	THR	3.1
4	D	202	LYS	3.0
1	A	966	ASN	3.0
3	C	95	PRO	3.0
4	D	315	PRO	3.0
4	D	155	TYR	3.0
4	D	63	ALA	3.0
4	D	269	ALA	3.0
4	D	164	ASP	3.0
4	D	300	GLY	3.0
4	D	105	ALA	2.9
4	D	344	ARG	2.9
4	D	1942	LYS	2.9
4	D	48	PRO	2.9
4	D	329	ILE	2.9
4	D	243	GLY	2.9

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Mol	Chain	Res	Type	RSRZ
4	D	20	LEU	2.8
4	D	287	ASP	2.8
4	D	258	PHE	2.8
4	D	34	LYS	2.8
4	D	175	LYS	2.7
4	D	76	LEU	2.7
4	D	351	ALA	2.7
4	D	65	ASP	2.7
4	D	199	ILE	2.6
4	D	33	ILE	2.6
4	D	51	ALA	2.6
4	D	37	VAL	2.6
4	D	25	LYS	2.6
4	D	192	LEU	2.6
4	D	60	ILE	2.5
4	D	366	THR	2.5
4	D	1941	GLN	2.5
4	D	203	HIS	2.5
4	D	161	ILE	2.5
3	C	70	TRP	2.5
4	D	335	GLN	2.4
4	D	171	TYR	2.4
4	D	219	LYS	2.4
4	D	265	GLY	2.4
4	D	268	ALA	2.4
4	D	191	GLY	2.4
2	B	54	THR	2.4
4	D	232	TRP	2.4
1	A	927	PHE	2.4
4	D	106	TYR	2.4
4	D	126	PRO	2.3
4	D	256	LYS	2.3
4	D	189	LYS	2.3
4	D	212	ILE	2.3
4	D	343	VAL	2.3
3	C	155	LEU	2.3
4	D	156	PHE	2.3
4	D	240	VAL	2.2
4	D	270	SER	2.2
4	D	341	TYR	2.2
3	C	214	GLU	2.2
4	D	14	ASP	2.2

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Mol	Chain	Res	Type	RSRZ
4	D	307	TYR	2.2
4	D	230	TRP	2.2
4	D	180	ASP	2.2
4	D	215	ALA	2.2
4	D	46	LYS	2.2
4	D	196	VAL	2.1
4	D	177	ASP	2.1
4	D	169	PHE	2.1
4	D	6	LYS	2.1
4	D	326	LYS	2.1
4	D	336	MET	2.1
4	D	128	THR	2.1
4	D	257	PRO	2.1
4	D	49	GLN	2.0
4	D	338	ALA	2.0

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

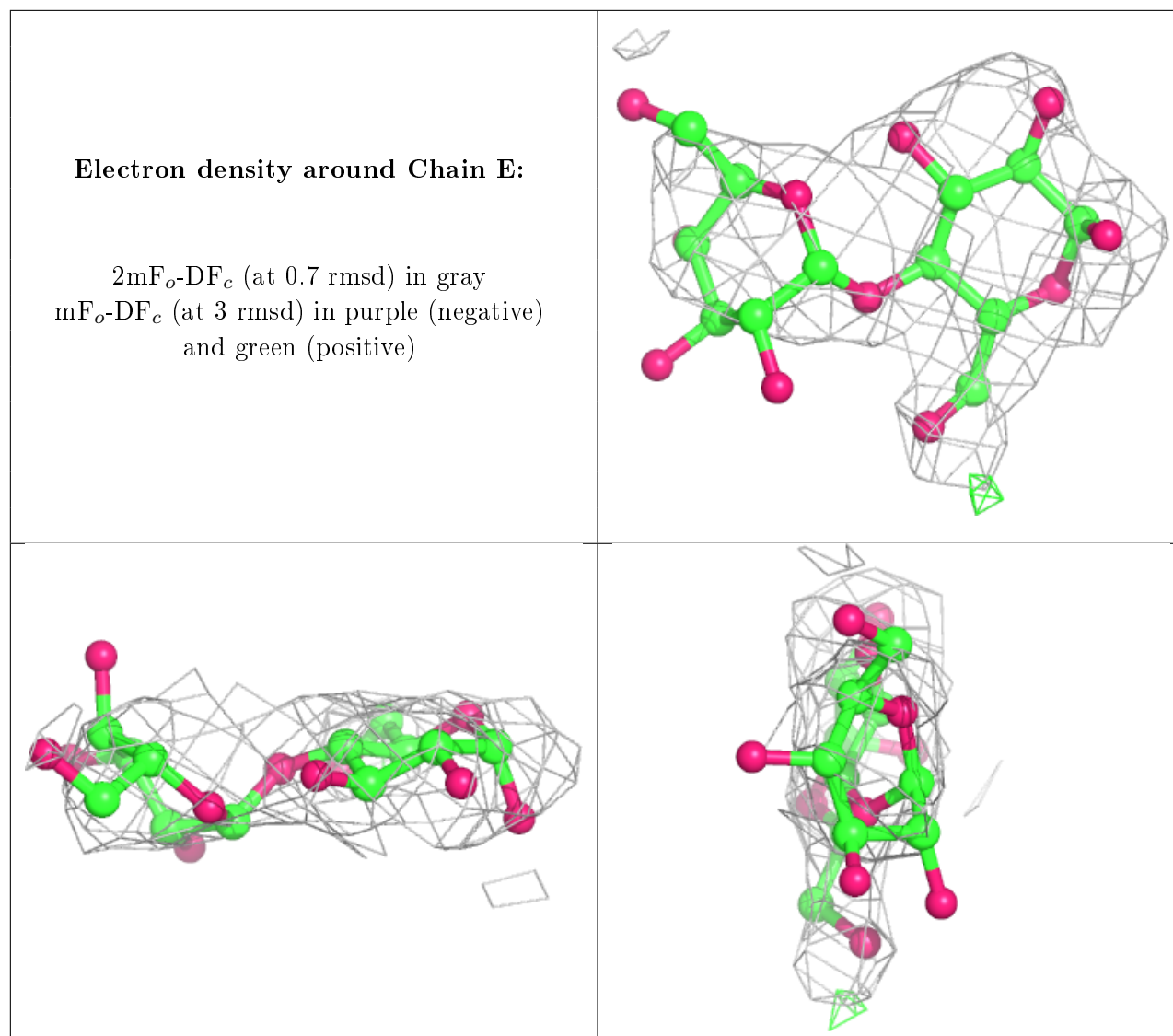
There are no non-standard protein/DNA/RNA residues in this entry.

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(\AA^2)	Q<0.9
5	GLC	E	2	11/12	0.71	0.40	224,231,235,236	0
5	GLC	E	1	12/12	0.74	0.26	153,175,193,210	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.



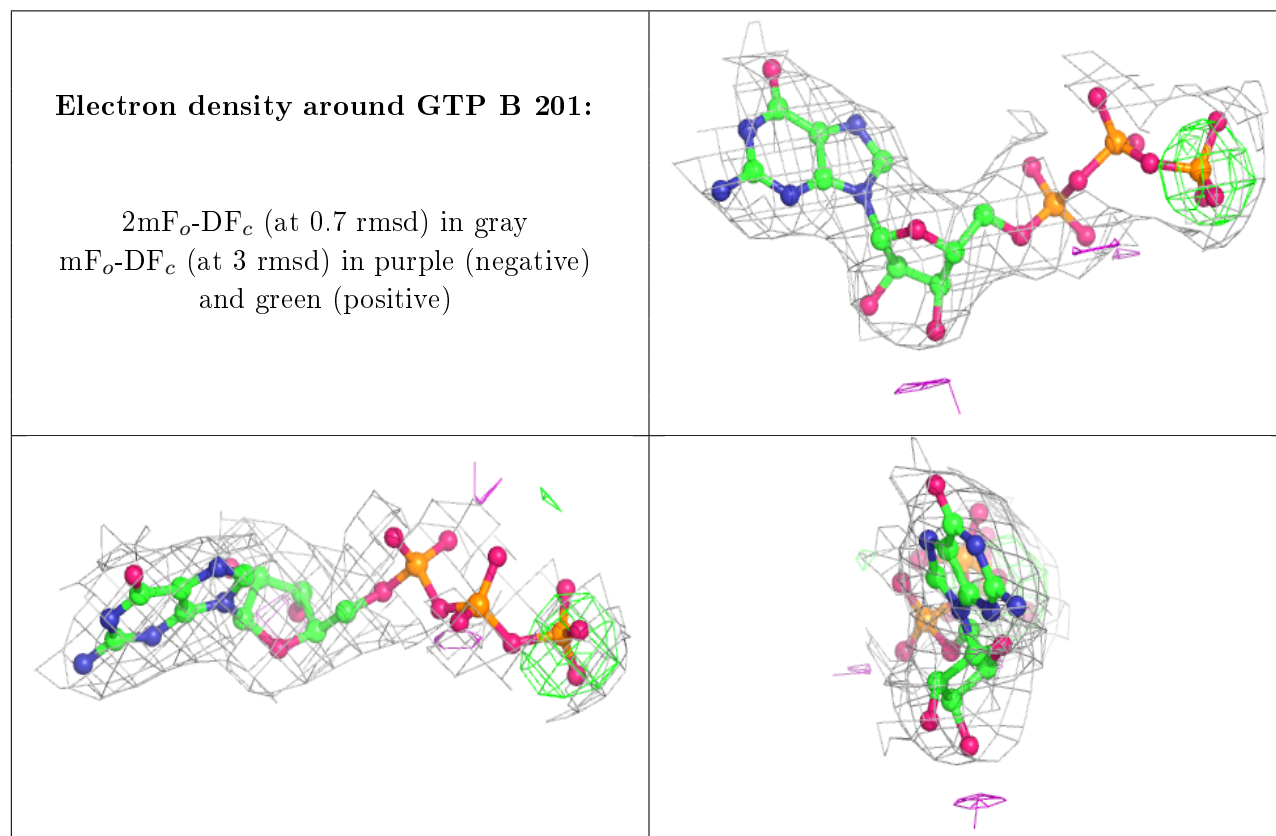
6.4 Ligands ⓘ

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
6	PRO	C	301	8/8	0.76	0.72	166,188,275,329	0
6	PRO	A	1101	8/8	0.80	0.30	122,126,137,140	0
8	MG	B	202	1/1	0.87	0.14	94,94,94,94	0
7	GTP	B	201	32/32	0.95	0.16	56,75,106,135	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 ⓘ

There are no such residues in this entry.