



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 8, 2026 – 01:34 AM UTC

PDB ID : 8JYX / pdb_00008jyx
Title : Crystal structure of the gasdermin-like protein RCD-1-1 from *Neurospora crassa*
Authors : Li, Y.; Hou, Y.J.; Ding, J.
Deposited on : 2023-07-04
Resolution : 2.35 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
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

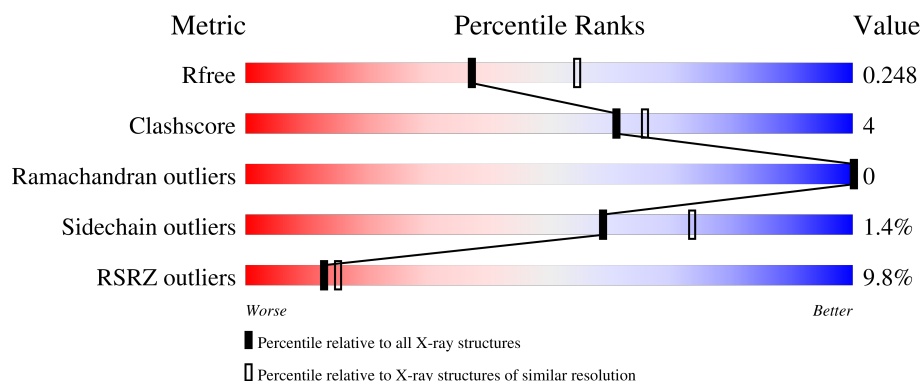
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.35 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	1596 (2.36-2.36)
Clashscore	190562	1663 (2.36-2.36)
Ramachandran outliers	187476	1646 (2.36-2.36)
Sidechain outliers	187428	1646 (2.36-2.36)
RSRZ outliers	180081	1598 (2.36-2.36)

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	635	6% 80% 8% 11%
1	B	635	11% 75% 12% 12%
2	C	2	100%
2	D	2	100%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 8949 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 Maltodextrin-binding protein, Gasdermin-like protein rcd-1-1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	565	Total	C	N	O	S	0	0	0
			4396	2829	736	812	19			
1	B	558	Total	C	N	O	S	0	0	0
			4345	2796	727	803	19			

There are 44 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	-377	SER	-	expression tag	UNP A0A376KDN7
A	-376	GLY	-	expression tag	UNP A0A376KDN7
A	-375	ARG	-	expression tag	UNP A0A376KDN7
A	-374	PRO	-	expression tag	UNP A0A376KDN7
A	-373	MET	-	expression tag	UNP A0A376KDN7
A	-291	ALA	ASP	engineered mutation	UNP A0A376KDN7
A	-290	ALA	LYS	engineered mutation	UNP A0A376KDN7
A	-201	ALA	GLU	engineered mutation	UNP A0A376KDN7
A	-200	ALA	ASN	engineered mutation	UNP A0A376KDN7
A	-134	ALA	LYS	engineered mutation	UNP A0A376KDN7
A	-11	ALA	LYS	engineered mutation	UNP A0A376KDN7
A	-10	ALA	ASP	engineered mutation	UNP A0A376KDN7
A	-6	ASN	-	linker	UNP A0A376KDN7
A	-5	ALA	-	linker	UNP A0A376KDN7
A	-4	ALA	-	linker	UNP A0A376KDN7
A	-3	ARG	-	linker	UNP A0A376KDN7
A	-2	ALA	-	linker	UNP A0A376KDN7
A	-1	ALA	-	linker	UNP A0A376KDN7
A	0	ALA	-	linker	UNP A0A376KDN7
A	174	ALA	LYS	engineered mutation	UNP Q7SBA0
A	175	ALA	LYS	engineered mutation	UNP Q7SBA0
A	176	ALA	LYS	engineered mutation	UNP Q7SBA0
B	-377	SER	-	expression tag	UNP A0A376KDN7
B	-376	GLY	-	expression tag	UNP A0A376KDN7
B	-375	ARG	-	expression tag	UNP A0A376KDN7

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Chain	Residue	Modelled	Actual	Comment	Reference
B	-374	PRO	-	expression tag	UNP A0A376KDN7
B	-373	MET	-	expression tag	UNP A0A376KDN7
B	-291	ALA	ASP	engineered mutation	UNP A0A376KDN7
B	-290	ALA	LYS	engineered mutation	UNP A0A376KDN7
B	-201	ALA	GLU	engineered mutation	UNP A0A376KDN7
B	-200	ALA	ASN	engineered mutation	UNP A0A376KDN7
B	-134	ALA	LYS	engineered mutation	UNP A0A376KDN7
B	-11	ALA	LYS	engineered mutation	UNP A0A376KDN7
B	-10	ALA	ASP	engineered mutation	UNP A0A376KDN7
B	-6	ASN	-	linker	UNP A0A376KDN7
B	-5	ALA	-	linker	UNP A0A376KDN7
B	-4	ALA	-	linker	UNP A0A376KDN7
B	-3	ARG	-	linker	UNP A0A376KDN7
B	-2	ALA	-	linker	UNP A0A376KDN7
B	-1	ALA	-	linker	UNP A0A376KDN7
B	0	ALA	-	linker	UNP A0A376KDN7
B	174	ALA	LYS	engineered mutation	UNP Q7SBA0
B	175	ALA	LYS	engineered mutation	UNP Q7SBA0
B	176	ALA	LYS	engineered mutation	UNP Q7SBA0

- Molecule 2 is an oligosaccharide called alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose.



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

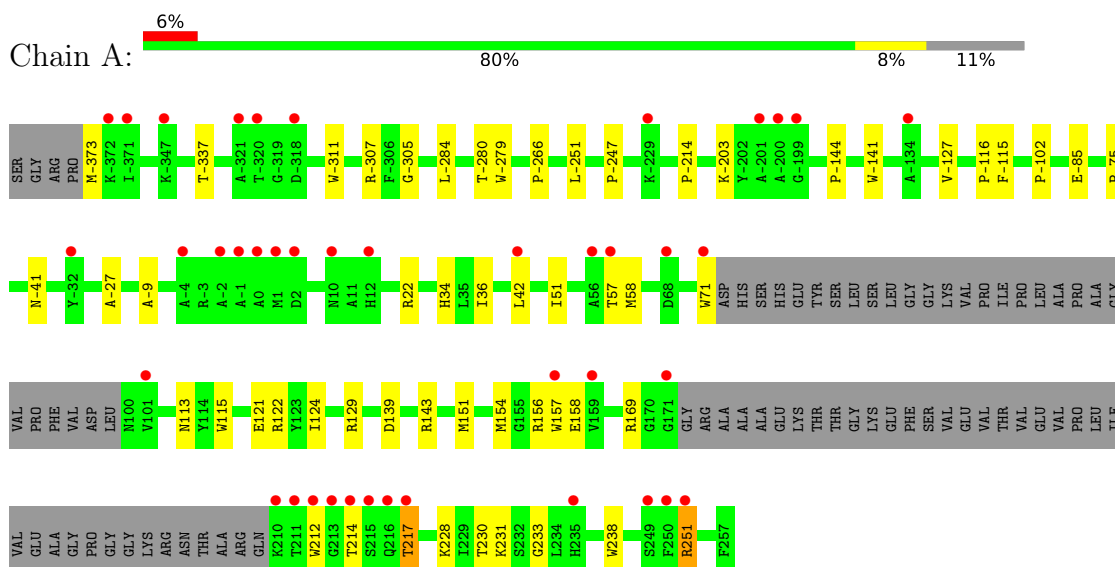
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	115	Total	O	0	0
			115	115		
3	B	47	Total	O	0	0
			47	47		

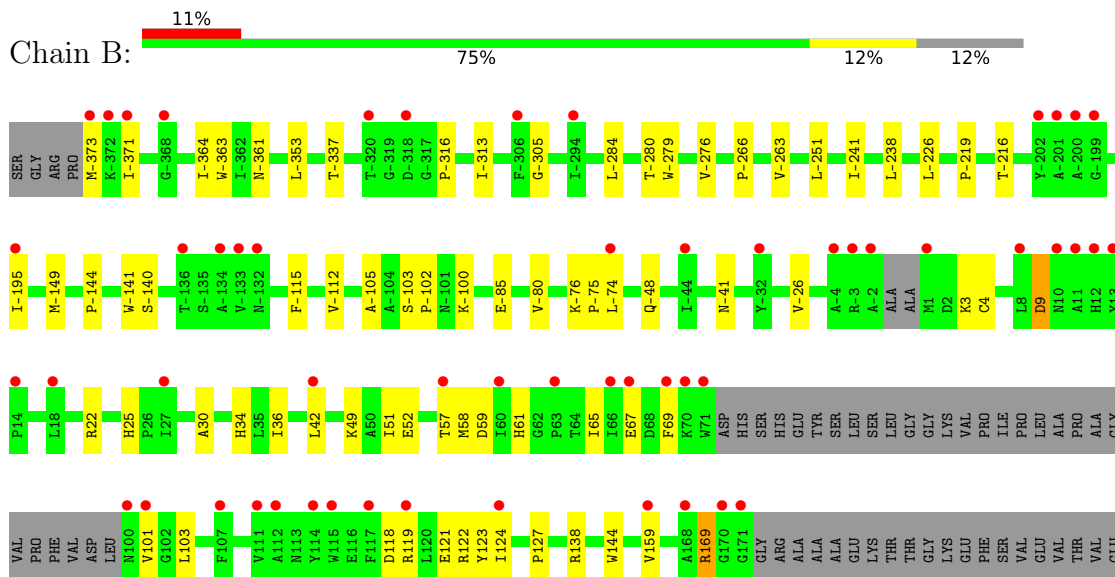
3 Residue-property plots

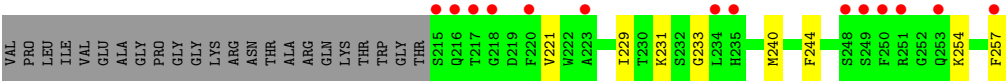
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Maltodextrin-binding protein,Gasdermin-like protein rcd-1-1



- Molecule 1: Maltodextrin-binding protein,Gasdermin-like protein rcd-1-1





- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain C: 100%



- Molecule 2: alpha-D-glucopyranose-(1-4)-alpha-D-glucopyranose

Chain D: 100%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	81.14Å 91.91Å 105.87Å 90.00° 101.38° 90.00°	Depositor
Resolution (Å)	45.96 – 2.35 45.96 – 2.35	Depositor EDS
% Data completeness (in resolution range)	99.8 (45.96-2.35) 93.7 (45.96-2.35)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.20 (at 2.34Å)	Xtriage
Refinement program	PHENIX 1.20.1_4487	Depositor
R, R_{free}	0.216 , 0.248 0.217 , 0.248	Depositor DCC
R_{free} test set	2000 reflections (3.15%)	wwPDB-VP
Wilson B-factor (Å ²)	42.0	Xtriage
Anisotropy	0.731	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 40.6	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	8949	wwPDB-VP
Average B, all atoms (Å ²)	58.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.37% 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: 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	0.09	0/4509	0.24	0/6116
1	B	0.08	0/4455	0.23	0/6040
All	All	0.08	0/8964	0.24	0/12156

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	4396	0	4358	28	0
1	B	4345	0	4310	47	0
2	C	23	0	21	0	0
2	D	23	0	21	0	0
3	A	115	0	0	0	0
3	B	47	0	0	2	0
All	All	8949	0	8710	74	0

The all-atom clashscore is defined as the number of clashes found per 1000 atoms (including hydrogen atoms). The all-atom clashscore for this structure is 4.

All (74) 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:121:GLU:OE1	1:B:169:ARG:NH1	2.24	0.71
1:B:3:LYS:HD2	1:B:257:PHE:HA	1.73	0.70
1:A:231:LYS:NZ	1:A:233:GLY:O	2.29	0.66
1:A:22:ARG:NH2	1:A:58:MET:O	2.29	0.66
1:A:121:GLU:OE1	1:A:169:ARG:NH1	2.29	0.65
1:A:154:MET:SD	1:B:-48:GLN:NE2	2.70	0.64
1:B:254:LYS:NZ	3:B:302:HOH:O	2.33	0.61
1:B:30:ALA:HB3	1:B:221:VAL:HG21	1.83	0.60
1:B:36:ILE:HG21	1:B:42:LEU:HD12	1.83	0.60
1:A:-373:MET:HG3	1:A:-337:THR:HG21	1.84	0.59
1:B:52:GLU:OE1	1:B:138:ARG:NH1	2.36	0.59
1:B:-251:LEU:HD11	1:B:-238:LEU:HD21	1.85	0.58
1:B:69:PHE:HB2	1:B:118:ASP:HA	1.86	0.57
1:B:127:PRO:HG2	1:B:240:MET:HE1	1.87	0.57
1:A:-251:LEU:HD21	1:A:-247:PRO:HD3	1.88	0.55
1:A:36:ILE:HG21	1:A:42:LEU:HD12	1.87	0.55
1:B:67:GLU:HG3	1:B:103:LEU:HB2	1.89	0.55
1:B:-141:TRP:HB2	1:B:-75:PRO:HG2	1.90	0.53
1:B:-80:VAL:HG12	1:B:-74:LEU:HD11	1.90	0.53
1:B:22:ARG:NH2	1:B:58:MET:O	2.43	0.52
1:A:129:ARG:NH2	1:A:238:TRP:O	2.43	0.51
1:A:139:ASP:HB3	1:A:143:ARG:NH1	2.26	0.51
1:B:-103:SER:O	1:B:-100:LYS:NZ	2.40	0.50
1:A:-214:PRO:HG3	1:A:-116:PRO:HA	1.93	0.50
1:B:119:ARG:HB3	1:B:169:ARG:HB2	1.93	0.50
1:B:-373:MET:HG3	1:B:-337:THR:HG21	1.94	0.49
1:A:-141:TRP:HB2	1:A:-75:PRO:HG2	1.95	0.48
1:B:-284:LEU:HB2	1:B:-279:TRP:NE1	2.27	0.48
1:B:9:ASP:OD1	1:B:9:ASP:N	2.46	0.48
1:A:113:ASN:HB3	1:A:212:TRP:CE2	2.49	0.48
1:B:-305:GLY:HA3	1:B:-41:ASN:O	2.14	0.48
1:B:-144:PRO:HA	1:B:-141:TRP:CE2	2.48	0.48
1:A:-280:THR:HB	1:A:-266:PRO:HB2	1.95	0.47
1:A:-27:ALA:HB2	1:A:-9:ALA:HB2	1.96	0.47
1:A:-284:LEU:HB2	1:A:-279:TRP:NE1	2.29	0.47
1:B:-102:PRO:HB3	1:B:57:THR:HB	1.97	0.47
1:B:-105:ALA:HB1	1:B:61:HIS:NE2	2.29	0.47
1:B:-195:ILE:HD11	1:B:101:VAL:HG11	1.96	0.47
1:A:-305:GLY:HA3	1:A:-41:ASN:O	2.14	0.47
1:B:-263:VAL:HG22	1:B:-112:VAL:HG22	1.96	0.46
1:B:22:ARG:NH2	1:B:59:ASP:HA	2.30	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:-364:ILE:HG21	1:B:-353:LEU:HD21	1.98	0.46
1:A:214:THR:O	1:A:217:THR:HG22	2.16	0.45
1:A:-144:PRO:HA	1:A:-141:TRP:CE2	2.52	0.45
1:B:-241:ILE:HD12	1:B:-149:MET:HE1	1.98	0.44
1:B:159:VAL:HG22	1:B:229:ILE:HB	2.00	0.44
1:B:65:ILE:HD13	1:B:121:GLU:HG2	1.98	0.44
1:B:-363:TRP:CD2	1:B:-316:PRO:HG3	2.53	0.44
1:A:-311:TRP:CD1	1:A:-307:ARG:HG3	2.52	0.43
1:B:-361:ASN:ND2	3:B:305:HOH:O	2.51	0.43
1:B:-140:SER:HB2	1:B:-75:PRO:HD3	2.00	0.43
1:B:34:HIS:CD2	1:B:51:ILE:HD11	2.54	0.43
1:B:-216:THR:HG21	1:B:-26:VAL:HG11	2.01	0.43
1:B:231:LYS:NZ	1:B:233:GLY:O	2.52	0.43
1:A:151:MET:HE3	1:A:151:MET:HB3	1.91	0.42
1:B:-226:LEU:HB2	1:B:-149:MET:HE3	2.01	0.42
1:A:251:ARG:HD2	1:A:251:ARG:HA	1.89	0.42
1:B:122:ARG:HG2	1:B:124:ILE:HG12	2.01	0.42
1:A:71:TRP:CE3	1:A:115:TRP:HA	2.54	0.42
1:B:4:CYS:HB3	1:B:244:PHE:CD1	2.54	0.42
1:B:-140:SER:HB3	1:B:-76:LYS:HD3	2.01	0.42
1:B:254:LYS:HD2	1:B:254:LYS:H	1.85	0.42
1:B:144:TRP:CZ3	1:B:159:VAL:HG12	2.55	0.42
1:A:158:GLU:HB2	1:A:230:THR:HG22	2.02	0.41
1:A:-102:PRO:HB3	1:A:57:THR:HB	2.02	0.41
1:A:228:LYS:HG2	1:A:230:THR:HG23	2.03	0.41
1:B:-280:THR:HB	1:B:-266:PRO:HB2	2.01	0.41
1:B:-276:VAL:HG21	1:B:-266:PRO:HD3	2.01	0.41
1:A:157:TRP:CD1	1:A:157:TRP:C	2.98	0.41
1:A:122:ARG:HG2	1:A:124:ILE:HG12	2.03	0.41
1:B:-219:PRO:HA	1:B:-216:THR:HG22	2.03	0.41
1:A:34:HIS:CD2	1:A:51:ILE:HD11	2.55	0.40
1:B:25:HIS:HA	1:B:49:LYS:HA	2.03	0.40
1:B:61:HIS:O	1:B:123:TYR:HA	2.21	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	559/635 (88%)	540 (97%)	19 (3%)	0	100	100
1	B	550/635 (87%)	536 (98%)	14 (2%)	0	100	100
All	All	1109/1270 (87%)	1076 (97%)	33 (3%)	0	100	100

There are no Ramachandran outliers to report.

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	451/505 (89%)	444 (98%)	7 (2%)	55	70
1	B	447/505 (88%)	441 (99%)	6 (1%)	61	76
All	All	898/1010 (89%)	885 (99%)	13 (1%)	59	73

All (13) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	-203	LYS
1	A	-127	VAL
1	A	-115	PHE
1	A	-85	GLU
1	A	156	ARG
1	A	217	THR
1	A	251	ARG
1	B	-371	ILE

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Mol	Chain	Res	Type
1	B	-313	ILE
1	B	-115	PHE
1	B	-85	GLU
1	B	9	ASP
1	B	169	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (5) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	-324	GLN
1	A	-132	ASN
1	A	-41	ASN
1	A	100	ASN
1	B	-6	ASN

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	$\# Z > 2$
2	GLC	C	1	2	12,12,12	0.18	0	17,17,17	0.28	0
2	GLC	C	2	2	11,11,12	0.38	0	15,15,17	0.47	0
2	GLC	D	1	2	12,12,12	0.20	0	17,17,17	0.33	0
2	GLC	D	2	2	11,11,12	0.35	0	15,15,17	0.48	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	GLC	C	1	2	-	0/2/22/22	0/1/1/1
2	GLC	C	2	2	-	0/2/19/22	0/1/1/1
2	GLC	D	1	2	-	0/2/22/22	0/1/1/1
2	GLC	D	2	2	-	0/2/19/22	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

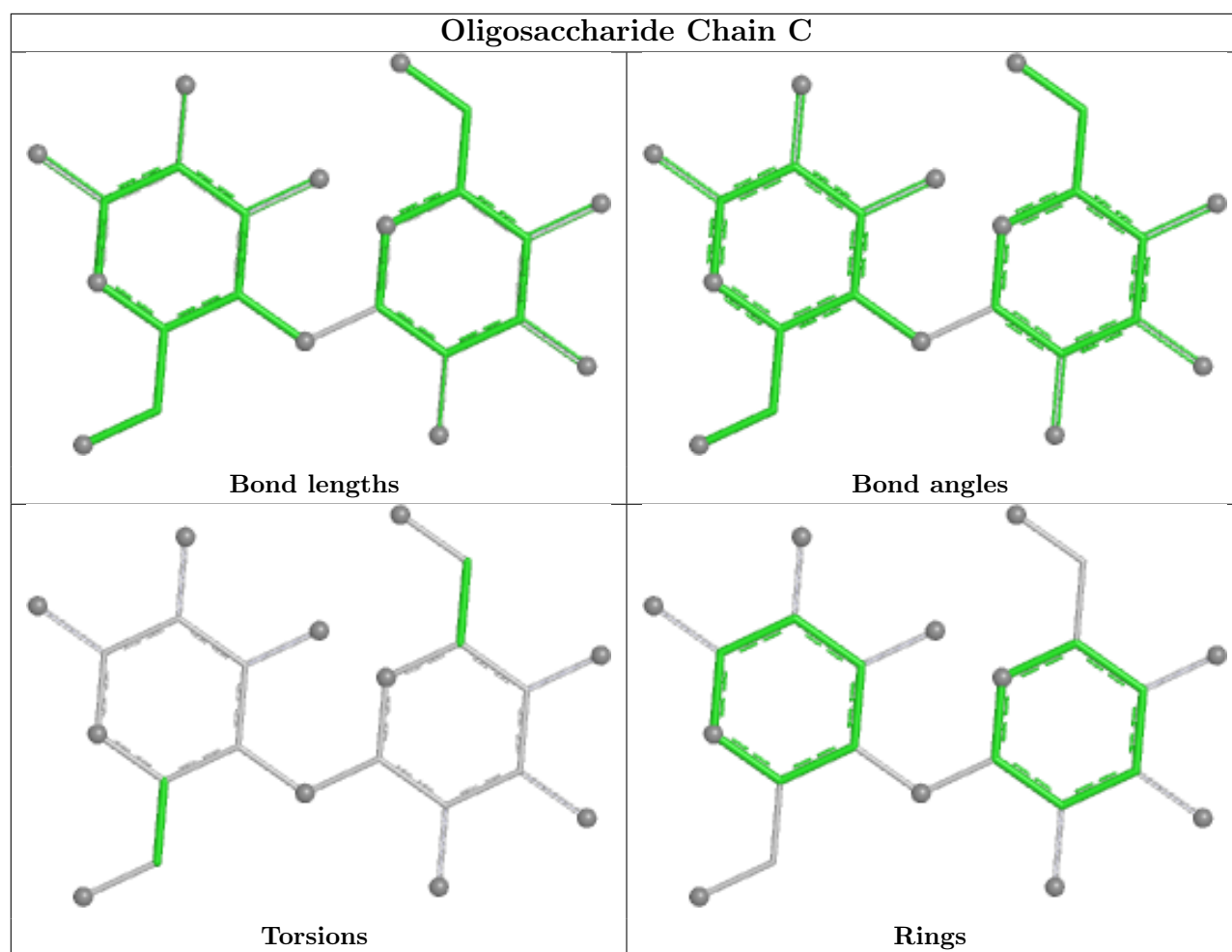
There are no chirality outliers.

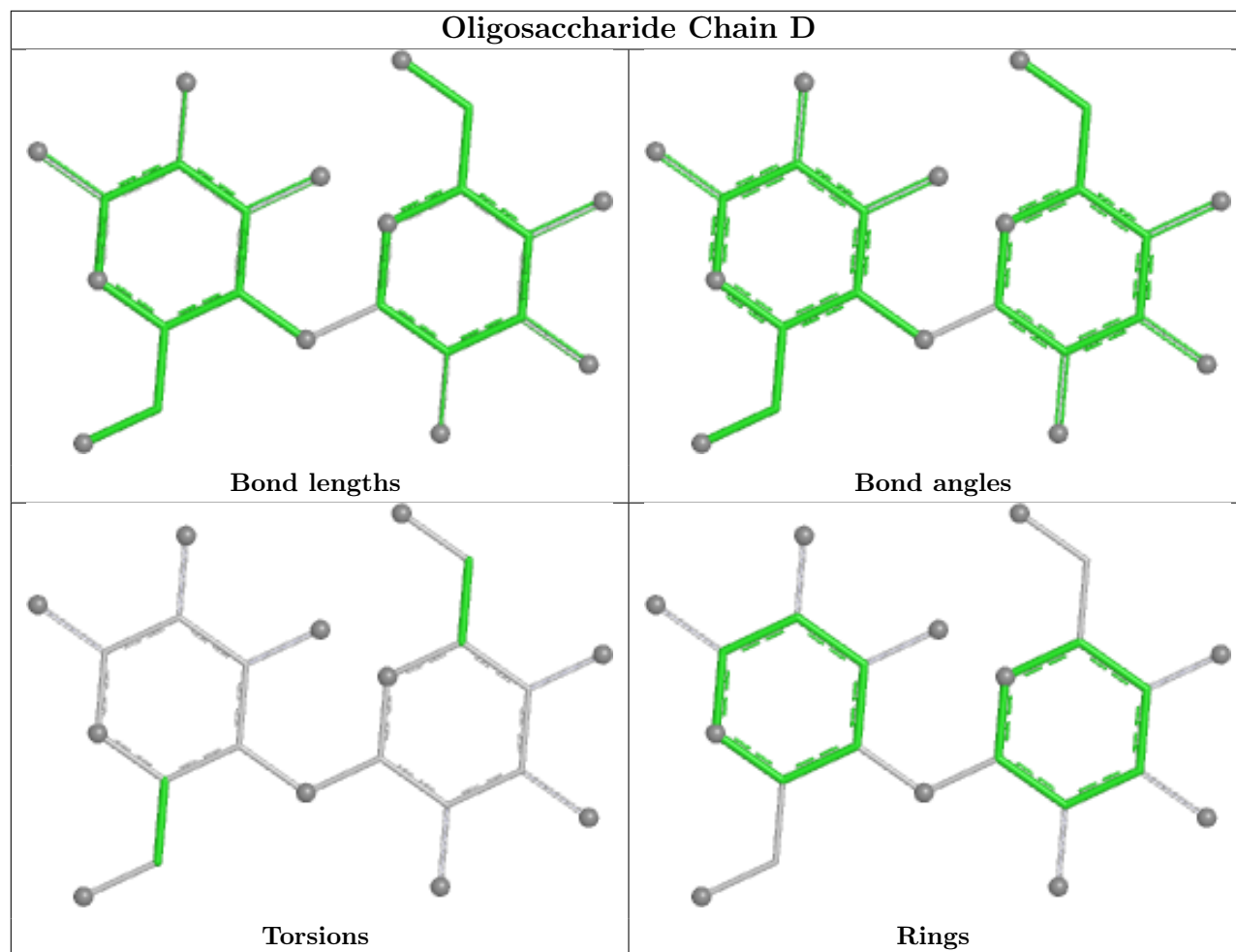
There are no torsion outliers.

There are no ring outliers.

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 oligosaccharide.





5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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 [i](#)

6.1 Protein, DNA and RNA chains [i](#)

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	565/635 (88%)	0.65	41 (7%) 21 24	38, 51, 78, 123	0
1	B	558/635 (87%)	0.92	69 (12%) 8 9	43, 58, 88, 122	0
All	All	1123/1270 (88%)	0.79	110 (9%) 13 15	38, 55, 85, 123	0

All (110) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	-2	ALA	6.5
1	A	250	PHE	5.0
1	B	171	GLY	4.9
1	B	250	PHE	4.5
1	B	-371	ILE	4.5
1	A	0	ALA	4.5
1	A	101	VAL	4.4
1	A	-1	ALA	4.3
1	A	71	TRP	4.3
1	B	101	VAL	3.9
1	A	214	THR	3.6
1	A	-2	ALA	3.6
1	B	-4	ALA	3.6
1	B	220	PHE	3.6
1	B	-199	GLY	3.5
1	A	-200	ALA	3.4
1	B	234	LEU	3.4
1	B	1	MET	3.4
1	A	213	GLY	3.4
1	A	216	GLN	3.4
1	B	12	HIS	3.3
1	B	-202	TYR	3.2
1	B	115	TRP	3.2
1	A	171	GLY	3.1

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Mol	Chain	Res	Type	RSRZ
1	A	1	MET	3.1
1	B	218	GLY	3.1
1	B	217	THR	3.0
1	A	211	THR	3.0
1	A	249	SER	3.0
1	B	248	SER	3.0
1	A	157	TRP	3.0
1	A	-201	ALA	2.9
1	A	212	TRP	2.9
1	B	159	VAL	2.9
1	B	66	ILE	2.9
1	B	-134	ALA	2.9
1	B	-201	ALA	2.8
1	B	168	ALA	2.8
1	B	100	ASN	2.8
1	B	-32	TYR	2.8
1	B	-200	ALA	2.8
1	B	249	SER	2.7
1	A	-199	GLY	2.7
1	A	159	VAL	2.7
1	A	215	SER	2.7
1	A	-371	ILE	2.7
1	B	253	GLN	2.6
1	B	-373	MET	2.6
1	A	-32	TYR	2.6
1	A	-347	LYS	2.6
1	A	210	LYS	2.6
1	B	216	GLN	2.5
1	B	71	TRP	2.5
1	B	257	PHE	2.5
1	B	-133	VAL	2.5
1	B	67	GLU	2.5
1	B	112	ALA	2.5
1	A	217	THR	2.4
1	B	57	THR	2.4
1	B	251	ARG	2.4
1	B	111	VAL	2.4
1	B	18	LEU	2.4
1	B	42	LEU	2.4
1	B	117	PHE	2.4
1	B	124	ILE	2.4
1	B	235	HIS	2.4

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Mol	Chain	Res	Type	RSRZ
1	B	11	ALA	2.4
1	A	235	HIS	2.4
1	A	2	ASP	2.3
1	B	-318	ASP	2.3
1	A	56	ALA	2.3
1	B	-372	LYS	2.3
1	B	13	TYR	2.3
1	B	215	SER	2.3
1	B	10	ASN	2.3
1	B	114	TYR	2.3
1	B	223	ALA	2.3
1	B	69	PHE	2.2
1	B	-320	THR	2.2
1	A	-134	ALA	2.2
1	B	14	PRO	2.2
1	B	-368	GLY	2.2
1	A	-4	ALA	2.2
1	A	251	ARG	2.2
1	B	-306	PHE	2.2
1	B	-132	ASN	2.2
1	B	-195	ILE	2.1
1	B	8	LEU	2.1
1	B	107	PHE	2.1
1	B	60	ILE	2.1
1	B	119	ARG	2.1
1	B	-136	THR	2.1
1	B	70	LYS	2.1
1	A	42	LEU	2.1
1	A	10	ASN	2.1
1	A	12	HIS	2.1
1	B	27	ILE	2.1
1	B	63	PRO	2.1
1	B	-3	ARG	2.1
1	B	-74	LEU	2.0
1	B	170	GLY	2.0
1	A	-229	LYS	2.0
1	A	-320	THR	2.0
1	A	57	THR	2.0
1	A	-321	ALA	2.0
1	A	-318	ASP	2.0
1	A	68	ASP	2.0
1	B	-294	ILE	2.0

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Mol	Chain	Res	Type	RSRZ
1	B	-44	ILE	2.0
1	A	-372	LYS	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](#)

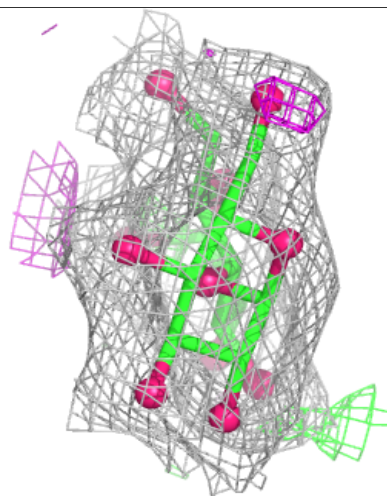
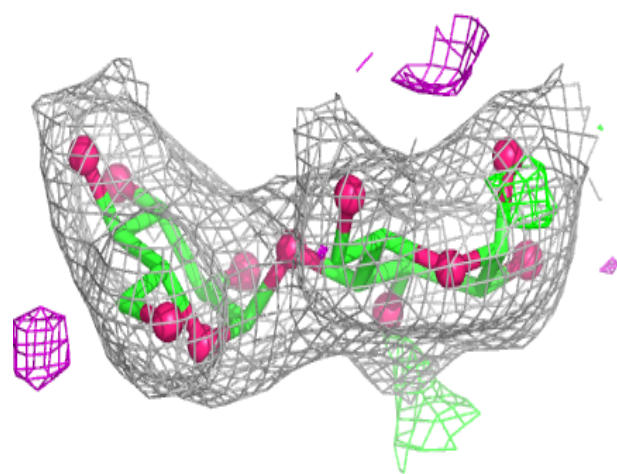
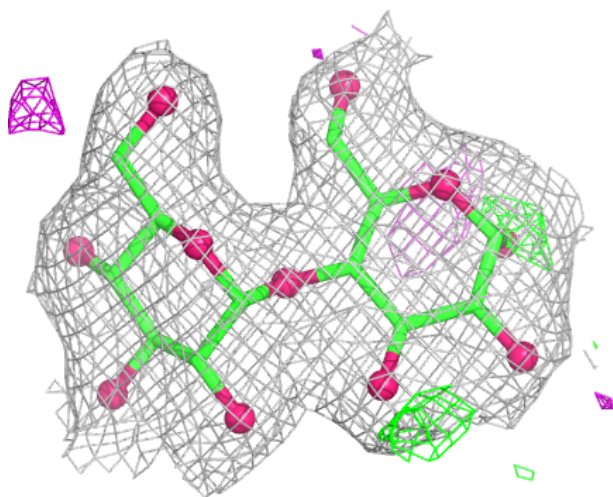
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q < 0.9' lists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

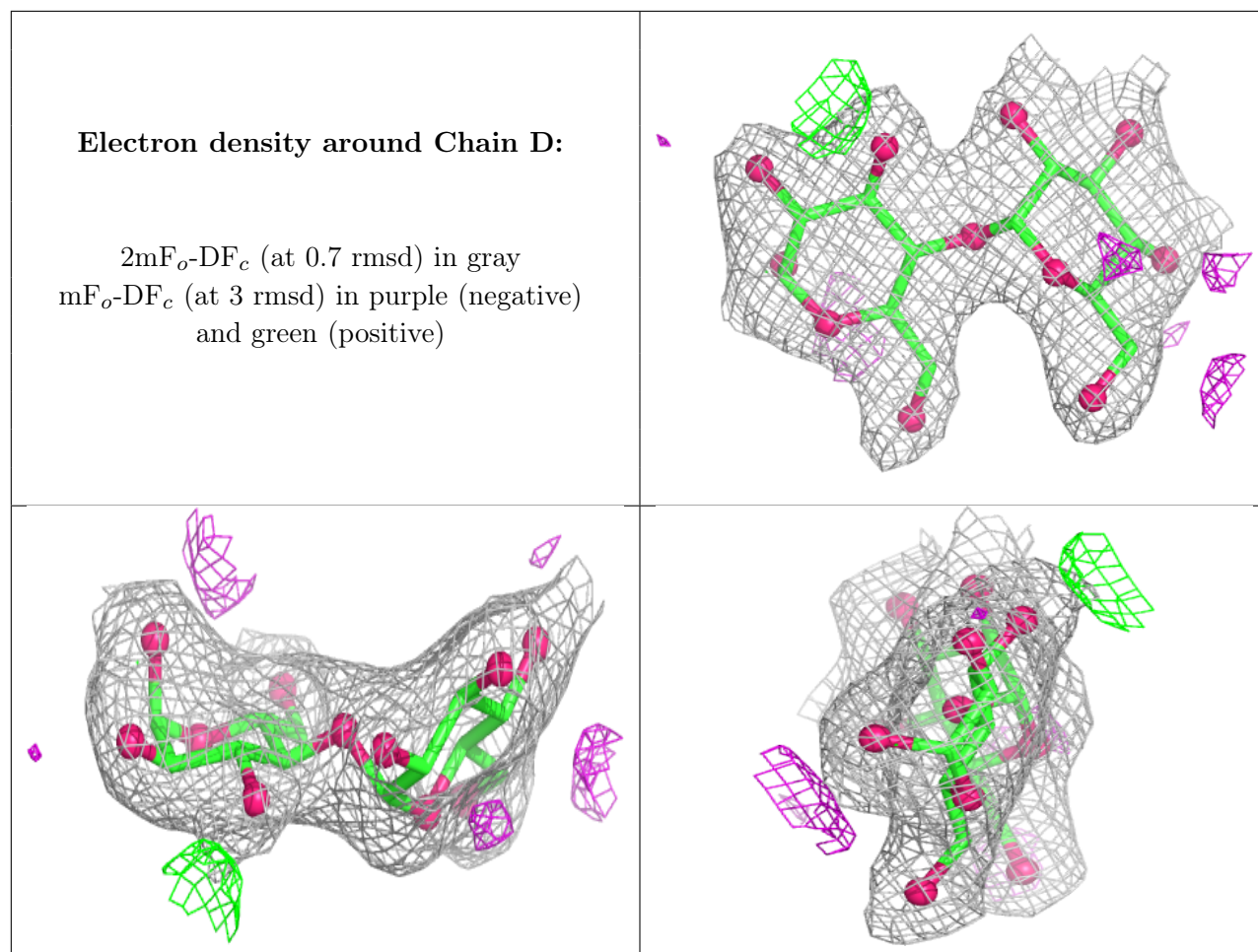
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	GLC	D	1	12/12	0.90	0.10	45,52,56,61	0
2	GLC	C	1	12/12	0.91	0.11	42,47,49,56	0
2	GLC	D	2	11/12	0.94	0.08	41,46,53,54	0
2	GLC	C	2	11/12	0.95	0.07	40,42,42,47	0

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 [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.