



wwPDB X-ray Structure Validation Summary Report ⓘ

Jun 13, 2020 – 10:18 pm BST

PDB ID : 5SXV
Title : X-ray structure of 2-bromoethanol bound to a pentameric ligand gated ion channel (ELIC) in a resting state
Authors : Chen, Q.; Kinde, M.; Cohen, A.; Xu, Y.; Tang, P.
Deposited on : 2016-08-10
Resolution : 3.40 Å(reported)

This is a wwPDB X-ray Structure Validation Summary 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	:	2.11
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)	:	2.11

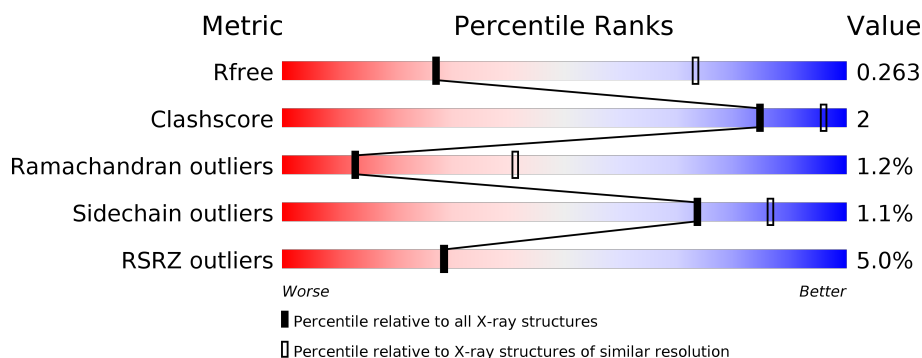
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.40 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}	130704	1026 (3.48-3.32)
Clashscore	141614	1055 (3.48-3.32)
Ramachandran outliers	138981	1038 (3.48-3.32)
Sidechain outliers	138945	1038 (3.48-3.32)
RSRZ outliers	127900	2173 (3.50-3.30)

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	322	<div> <div>6%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>• •</div> </div> </div>
1	B	322	<div> <div>3%</div> <div> <div></div> <div>86%</div> <div>9%</div> <div>• •</div> </div> </div>
1	C	322	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>6%</div> <div>• •</div> </div> </div>
1	D	322	<div> <div>5%</div> <div> <div></div> <div>88%</div> <div>7%</div> <div>• •</div> </div> </div>
1	E	322	<div> <div>4%</div> <div> <div></div> <div>87%</div> <div>9%</div> <div>•</div> </div> </div>
1	F	322	<div> <div>4%</div> <div> <div></div> <div>90%</div> <div>5%</div> <div>•</div> </div> </div>

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Mol	Chain	Length	Quality of chain
1	G	322	
1	H	322	
1	I	322	
1	J	322	

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
2	BRJ	A	401	-	-	X	X
2	BRJ	A	402	-	-	-	X
2	BRJ	A	403	-	-	-	X
2	BRJ	B	401	-	-	-	X
2	BRJ	B	402	-	-	X	X
2	BRJ	B	403	-	-	-	X
2	BRJ	C	401	-	-	-	X
2	BRJ	C	403	-	-	-	X
2	BRJ	D	403	-	-	-	X
2	BRJ	E	404	-	-	-	X
2	BRJ	F	401	-	-	-	X
2	BRJ	F	402	-	-	X	-
2	BRJ	F	403	-	-	-	X
2	BRJ	G	401	-	-	-	X
2	BRJ	G	402	-	-	-	X
2	BRJ	H	401	-	-	-	X
2	BRJ	H	403	-	-	-	X
2	BRJ	I	401	-	-	-	X
2	BRJ	I	402	-	-	-	X
2	BRJ	I	403	-	-	-	X
2	BRJ	J	401	-	-	-	X
2	BRJ	J	402	-	-	-	X

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 25418 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 Cys-loop ligand-gated ion channel.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	B	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	C	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	D	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	E	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	F	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	G	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	H	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	I	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			
1	J	308	Total	C	N	O	S	0	0	0
			2516	1639	420	451	6			

There are 20 discrepancies between the modelled and reference sequences:

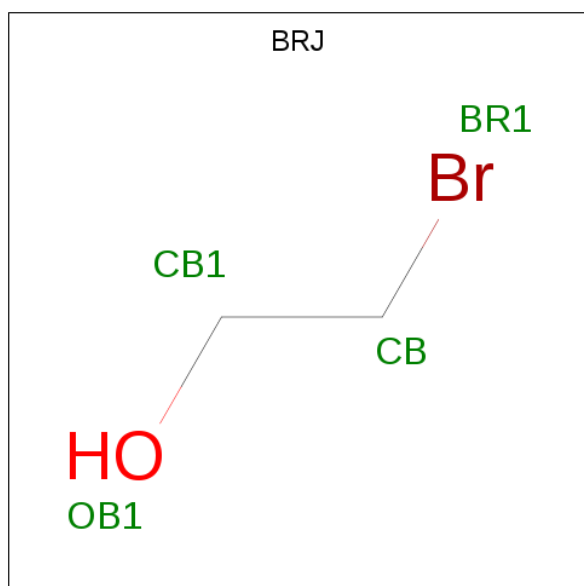
Chain	Residue	Modelled	Actual	Comment	Reference
A	164	GLY	-	insertion	UNP P0C7B7
A	289	ASN	MET	conflict	UNP P0C7B7
B	164	GLY	-	insertion	UNP P0C7B7
B	289	ASN	MET	conflict	UNP P0C7B7
C	164	GLY	-	insertion	UNP P0C7B7
C	289	ASN	MET	conflict	UNP P0C7B7
D	164	GLY	-	insertion	UNP P0C7B7
D	289	ASN	MET	conflict	UNP P0C7B7
E	164	GLY	-	insertion	UNP P0C7B7

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Chain	Residue	Modelled	Actual	Comment	Reference
E	289	ASN	MET	conflict	UNP P0C7B7
F	164	GLY	-	insertion	UNP P0C7B7
F	289	ASN	MET	conflict	UNP P0C7B7
G	164	GLY	-	insertion	UNP P0C7B7
G	289	ASN	MET	conflict	UNP P0C7B7
H	164	GLY	-	insertion	UNP P0C7B7
H	289	ASN	MET	conflict	UNP P0C7B7
I	164	GLY	-	insertion	UNP P0C7B7
I	289	ASN	MET	conflict	UNP P0C7B7
J	164	GLY	-	insertion	UNP P0C7B7
J	289	ASN	MET	conflict	UNP P0C7B7

- Molecule 2 is 2-BROMOETHANOL (three-letter code: BRJ) (formula: C_2H_5BrO).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	Br	C	O	0	0
			4	1	2	1		
2	A	1	Total	Br	C	O	0	0
			4	1	2	1		
2	A	1	Total	Br	C	O	0	0
			4	1	2	1		
2	B	1	Total	Br	C	O	0	0
			4	1	2	1		
2	B	1	Total	Br	C	O	0	0
			4	1	2	1		
2	B	1	Total	Br	C	O	0	0
			4	1	2	1		

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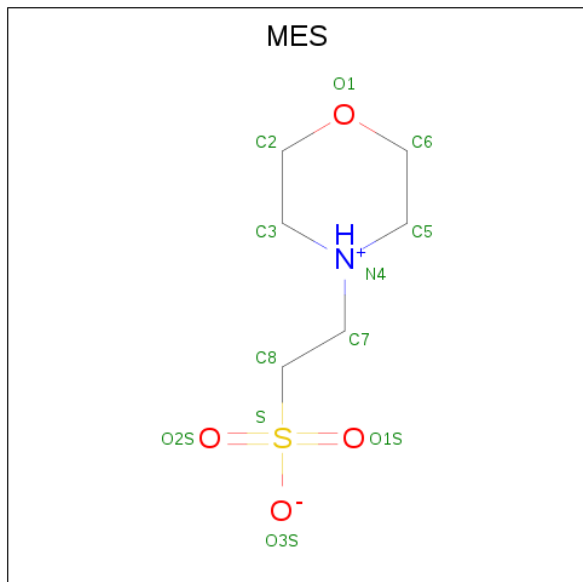
Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	C	1	Total 4	Br 1	C 2	O 1	0	0
2	C	1	Total 4	Br 1	C 2	O 1	0	0
2	C	1	Total 4	Br 1	C 2	O 1	0	0
2	D	1	Total 4	Br 1	C 2	O 1	0	0
2	D	1	Total 4	Br 1	C 2	O 1	0	0
2	D	1	Total 4	Br 1	C 2	O 1	0	0
2	E	1	Total 4	Br 1	C 2	O 1	0	0
2	E	1	Total 4	Br 1	C 2	O 1	0	0
2	E	1	Total 4	Br 1	C 2	O 1	0	0
2	E	1	Total 4	Br 1	C 2	O 1	0	0
2	F	1	Total 4	Br 1	C 2	O 1	0	0
2	F	1	Total 4	Br 1	C 2	O 1	0	0
2	F	1	Total 4	Br 1	C 2	O 1	0	0
2	G	1	Total 4	Br 1	C 2	O 1	0	0
2	G	1	Total 4	Br 1	C 2	O 1	0	0
2	G	1	Total 4	Br 1	C 2	O 1	0	0
2	G	1	Total 4	Br 1	C 2	O 1	0	0
2	H	1	Total 4	Br 1	C 2	O 1	0	0
2	H	1	Total 4	Br 1	C 2	O 1	0	0
2	H	1	Total 4	Br 1	C 2	O 1	0	0
2	I	1	Total 4	Br 1	C 2	O 1	0	0

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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	I	1	Total	Br	C	O	0	0
			4	1	2	1		
2	I	1	Total	Br	C	O	0	0
			4	1	2	1		
2	J	1	Total	Br	C	O	0	0
			4	1	2	1		
2	J	1	Total	Br	C	O	0	0
			4	1	2	1		
2	J	1	Total	Br	C	O	0	0
			4	1	2	1		

- Molecule 3 is 2-(N-MORPHOLINO)-ETHANESULFONIC ACID (three-letter code: MES) (formula: C₆H₁₃NO₄S).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	B	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	D	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	E	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	F	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
3	G	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	H	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	I	1	Total	C	N	O	S	0	0
			12	6	1	4	1		
3	J	1	Total	C	N	O	S	0	0
			12	6	1	4	1		

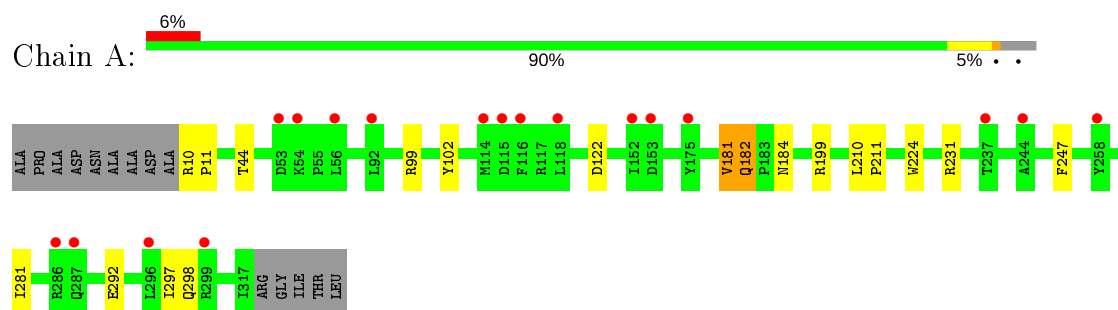
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	1	Total	O	0	0
			1	1		
4	D	4	Total	O	0	0
			4	4		
4	E	2	Total	O	0	0
			2	2		
4	H	2	Total	O	0	0
			2	2		
4	I	1	Total	O	0	0
			1	1		

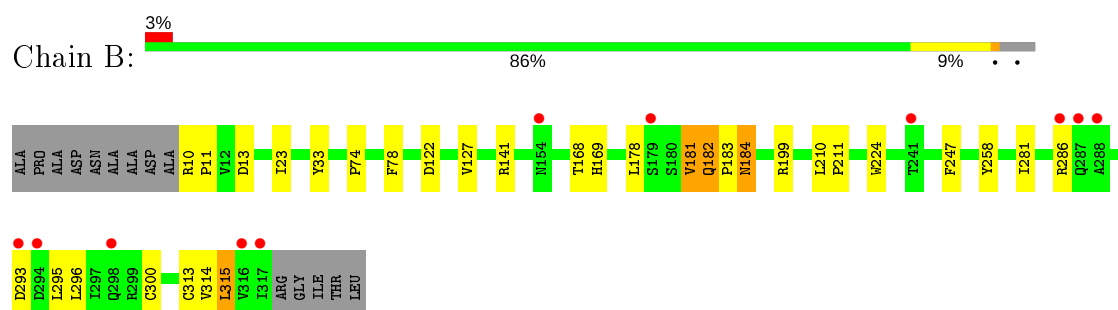
3 Residue-property plots [i](#)

These plots are drawn for all protein, RNA and DNA 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.

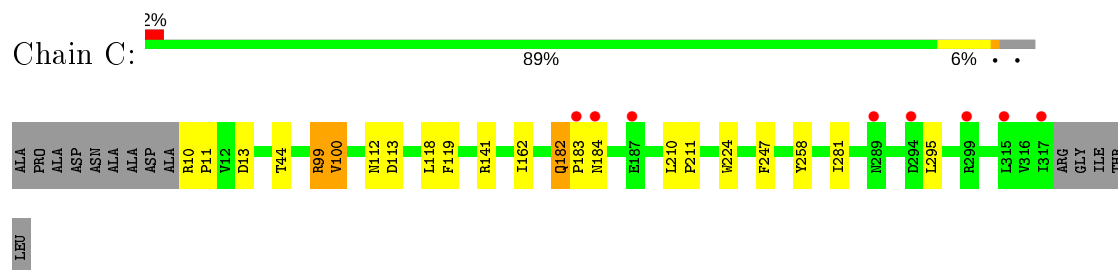
- Molecule 1: Cys-loop ligand-gated ion channel



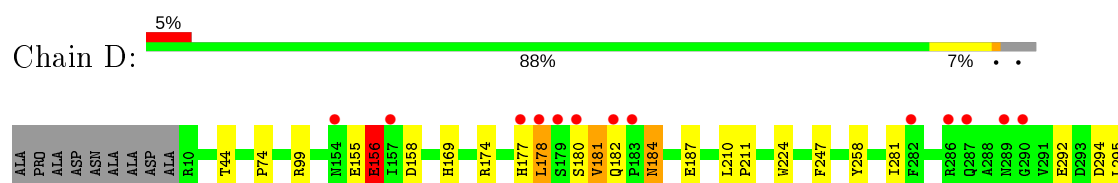
- Molecule 1: Cys-loop ligand-gated ion channel

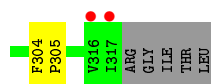


- Molecule 1: Cys-loop ligand-gated ion channel

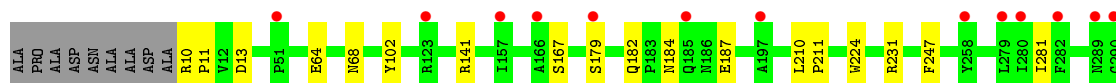
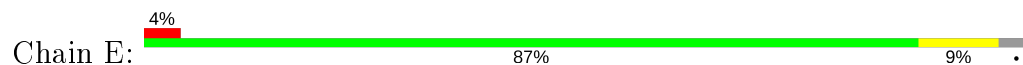


- Molecule 1: Cys-loop ligand-gated ion channel

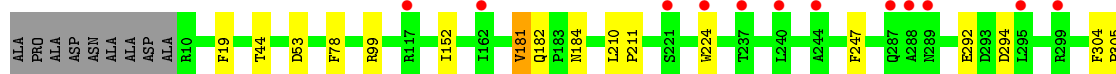
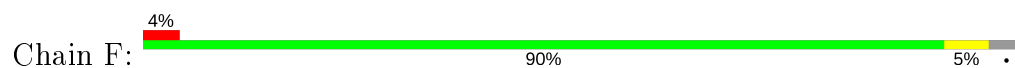




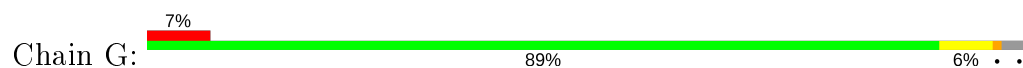
- Molecule 1: Cys-loop ligand-gated ion channel



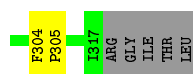
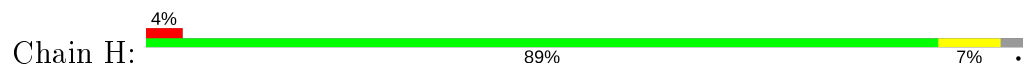
- Molecule 1: Cys-loop ligand-gated ion channel



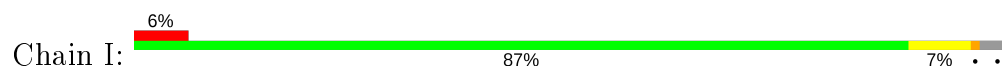
- Molecule 1: Cys-loop ligand-gated ion channel

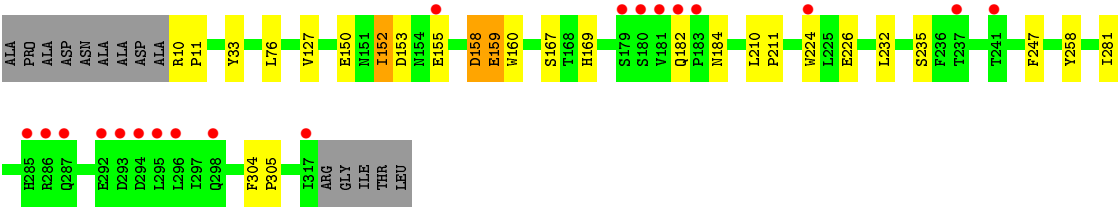


- Molecule 1: Cys-loop ligand-gated ion channel

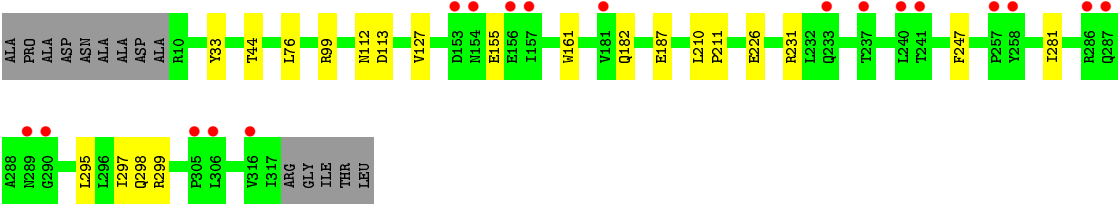
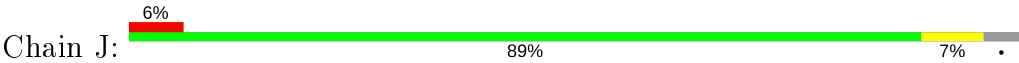


- Molecule 1: Cys-loop ligand-gated ion channel





● Molecule 1: Cys-loop ligand-gated ion channel



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	105.75Å 266.94Å 111.42Å 90.00° 107.04° 90.00°	Depositor
Resolution (Å)	29.73 – 3.40 39.39 – 3.40	Depositor EDS
% Data completeness (in resolution range)	99.8 (29.73-3.40) 99.8 (39.39-3.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.28 (at 3.40Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.215 , 0.259 0.222 , 0.263	Depositor DCC
R_{free} test set	4080 reflections (5.06%)	wwPDB-VP
Wilson B-factor (Å ²)	109.6	Xtriage
Anisotropy	0.235	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.29 , 72.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.45$, $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	25418	wwPDB-VP
Average B, all atoms (Å ²)	117.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.29% 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: BRJ, MES

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	0.23	0/2584	0.41	0/3522
1	B	0.23	0/2584	0.43	0/3522
1	C	0.24	0/2584	0.43	0/3522
1	D	0.24	0/2584	0.44	0/3522
1	E	0.23	0/2584	0.42	0/3522
1	F	0.23	0/2584	0.42	0/3522
1	G	0.24	0/2584	0.42	0/3522
1	H	0.23	0/2584	0.43	1/3522 (0.0%)
1	I	0.24	0/2584	0.47	1/3522 (0.0%)
1	J	0.23	0/2584	0.42	0/3522
All	All	0.23	0/25840	0.43	2/35220 (0.0%)

There are no bond length outliers.

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	I	153	ASP	N-CA-C	-5.54	96.05	111.00
1	H	178	LEU	CA-CB-CG	5.41	127.73	115.30

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	2516	0	2490	12	0
1	B	2516	0	2490	16	0
1	C	2516	0	2490	11	0
1	D	2516	0	2490	14	0
1	E	2516	0	2490	11	0
1	F	2516	0	2490	10	0
1	G	2516	0	2490	14	0
1	H	2516	0	2490	11	0
1	I	2516	0	2490	13	0
1	J	2516	0	2490	11	0
2	A	12	0	9	2	0
2	B	12	0	9	4	0
2	C	12	0	9	1	0
2	D	12	0	9	1	0
2	E	16	0	12	0	0
2	F	12	0	9	2	0
2	G	16	0	12	1	0
2	H	12	0	9	1	0
2	I	12	0	9	0	0
2	J	12	0	9	1	0
3	B	24	0	26	0	0
3	D	24	0	26	0	0
3	E	12	0	13	0	0
3	F	12	0	13	0	0
3	G	12	0	13	0	0
3	H	12	0	13	0	0
3	I	12	0	13	0	0
3	J	12	0	13	0	0
4	B	1	0	0	0	0
4	D	4	0	0	0	0
4	E	2	0	0	0	0
4	H	2	0	0	0	0
4	I	1	0	0	0	0
All	All	25418	0	25126	114	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 2.

The worst 5 of 114 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:A:231:ARG:NH2	1:A:292:GLU:OE2	2.17	0.78

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:13:ASP:OD1	1:C:141:ARG:NH2	2.18	0.77
1:E:231:ARG:NH2	1:E:292:GLU:OE2	2.20	0.74
1:C:182:GLN:O	1:C:184:ASN:N	2.21	0.74
1:G:231:ARG:NH2	1:G:292:GLU:OE2	2.21	0.73

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	306/322 (95%)	281 (92%)	23 (8%)	2 (1%)	22	55
1	B	306/322 (95%)	282 (92%)	17 (6%)	7 (2%)	6	28
1	C	306/322 (95%)	278 (91%)	22 (7%)	6 (2%)	7	30
1	D	306/322 (95%)	280 (92%)	22 (7%)	4 (1%)	12	39
1	E	306/322 (95%)	275 (90%)	26 (8%)	5 (2%)	9	34
1	F	306/322 (95%)	281 (92%)	22 (7%)	3 (1%)	15	46
1	G	306/322 (95%)	281 (92%)	22 (7%)	3 (1%)	15	46
1	H	306/322 (95%)	280 (92%)	23 (8%)	3 (1%)	15	46
1	I	306/322 (95%)	276 (90%)	29 (10%)	1 (0%)	41	72
1	J	306/322 (95%)	276 (90%)	27 (9%)	3 (1%)	15	46
All	All	3060/3220 (95%)	2790 (91%)	233 (8%)	37 (1%)	13	41

5 of 37 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	181	VAL
1	B	183	PRO
1	B	286	ARG

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Mol	Chain	Res	Type
1	B	314	VAL
1	C	99	ARG

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	276/284 (97%)	275 (100%)	1 (0%)	91	95
1	B	276/284 (97%)	272 (99%)	4 (1%)	67	83
1	C	276/284 (97%)	274 (99%)	2 (1%)	84	92
1	D	276/284 (97%)	271 (98%)	5 (2%)	59	79
1	E	276/284 (97%)	273 (99%)	3 (1%)	73	86
1	F	276/284 (97%)	275 (100%)	1 (0%)	91	95
1	G	276/284 (97%)	274 (99%)	2 (1%)	84	92
1	H	276/284 (97%)	273 (99%)	3 (1%)	73	86
1	I	276/284 (97%)	267 (97%)	9 (3%)	38	66
1	J	276/284 (97%)	275 (100%)	1 (0%)	91	95
All	All	2760/2840 (97%)	2729 (99%)	31 (1%)	73	86

5 of 31 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	247	PHE
1	G	317	ILE
1	I	247	PHE
1	F	247	PHE
1	H	178	LEU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 ⓘ

There are no carbohydrates in this entry.

5.6 Ligand geometry ⓘ

42 ligands are modelled in this entry.

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

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\# Z > 2$	Counts	RMSZ	$\# Z > 2$
2	BRJ	E	404	-	3,3,3	0.34	0	2,2,2	1.00	0
2	BRJ	G	404	-	3,3,3	0.36	0	2,2,2	0.64	0
2	BRJ	B	402	-	3,3,3	0.37	0	2,2,2	0.49	0
2	BRJ	D	401	-	3,3,3	0.36	0	2,2,2	0.65	0
2	BRJ	C	401	-	3,3,3	0.40	0	2,2,2	0.22	0
2	BRJ	D	402	-	3,3,3	0.38	0	2,2,2	0.27	0
3	MES	D	405	-	12,12,12	2.18	1 (8%)	14,16,16	1.75	3 (21%)
2	BRJ	J	402	-	3,3,3	0.39	0	2,2,2	0.50	0
2	BRJ	A	402	-	3,3,3	0.36	0	2,2,2	0.34	0
2	BRJ	F	403	-	3,3,3	0.37	0	2,2,2	0.67	0
2	BRJ	D	403	-	3,3,3	0.38	0	2,2,2	0.93	0
2	BRJ	H	403	-	3,3,3	0.38	0	2,2,2	0.44	0
3	MES	D	404	-	12,12,12	2.24	1 (8%)	14,16,16	1.61	3 (21%)
2	BRJ	C	403	-	3,3,3	0.36	0	2,2,2	0.51	0
2	BRJ	I	403	-	3,3,3	0.35	0	2,2,2	0.71	0
3	MES	I	404	-	12,12,12	2.12	1 (8%)	14,16,16	1.83	2 (14%)
2	BRJ	F	401	-	3,3,3	0.37	0	2,2,2	0.52	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
2	BRJ	G	402	-	3,3,3	0.37	0	2,2,2	0.55	0
2	BRJ	I	401	-	3,3,3	0.37	0	2,2,2	0.41	0
2	BRJ	B	403	-	3,3,3	0.34	0	2,2,2	0.60	0
2	BRJ	I	402	-	3,3,3	0.35	0	2,2,2	0.71	0
3	MES	H	404	-	12,12,12	2.21	1 (8%)	14,16,16	1.61	4 (28%)
2	BRJ	F	402	-	3,3,3	0.37	0	2,2,2	0.49	0
2	BRJ	E	403	-	3,3,3	0.38	0	2,2,2	0.51	0
3	MES	J	404	-	12,12,12	2.24	1 (8%)	14,16,16	1.60	3 (21%)
2	BRJ	B	401	-	3,3,3	0.40	0	2,2,2	0.29	0
2	BRJ	A	401	-	3,3,3	0.38	0	2,2,2	0.66	0
3	MES	G	405	-	12,12,12	2.21	1 (8%)	14,16,16	1.55	3 (21%)
2	BRJ	H	401	-	3,3,3	0.39	0	2,2,2	0.41	0
2	BRJ	G	401	-	3,3,3	0.38	0	2,2,2	0.67	0
2	BRJ	J	401	-	3,3,3	0.37	0	2,2,2	0.78	0
3	MES	B	404	-	12,12,12	2.13	1 (8%)	14,16,16	1.84	2 (14%)
3	MES	B	405	-	12,12,12	2.27	1 (8%)	14,16,16	1.68	5 (35%)
2	BRJ	J	403	-	3,3,3	0.36	0	2,2,2	0.81	0
2	BRJ	H	402	-	3,3,3	0.38	0	2,2,2	0.59	0
2	BRJ	E	401	-	3,3,3	0.35	0	2,2,2	0.73	0
3	MES	E	405	-	12,12,12	2.22	1 (8%)	14,16,16	1.68	2 (14%)
2	BRJ	E	402	-	3,3,3	0.41	0	2,2,2	0.29	0
2	BRJ	C	402	-	3,3,3	0.35	0	2,2,2	0.75	0
2	BRJ	A	403	-	3,3,3	0.37	0	2,2,2	0.55	0
3	MES	F	404	-	12,12,12	2.28	1 (8%)	14,16,16	1.55	3 (21%)
2	BRJ	G	403	-	3,3,3	0.35	0	2,2,2	0.64	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	BRJ	E	404	-	-	0/1/1/1	-
2	BRJ	G	404	-	-	0/1/1/1	-
2	BRJ	B	402	-	-	0/1/1/1	-
2	BRJ	D	401	-	-	0/1/1/1	-
2	BRJ	C	401	-	-	0/1/1/1	-
2	BRJ	D	402	-	-	0/1/1/1	-
3	MES	D	405	-	-	3/6/14/14	0/1/1/1
2	BRJ	J	402	-	-	0/1/1/1	-
2	BRJ	A	402	-	-	0/1/1/1	-

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	BRJ	F	403	-	-	0/1/1/1	-
2	BRJ	D	403	-	-	0/1/1/1	-
2	BRJ	H	403	-	-	0/1/1/1	-
3	MES	D	404	-	-	2/6/14/14	0/1/1/1
2	BRJ	C	403	-	-	0/1/1/1	-
2	BRJ	I	403	-	-	0/1/1/1	-
3	MES	I	404	-	-	5/6/14/14	0/1/1/1
2	BRJ	F	401	-	-	0/1/1/1	-
2	BRJ	G	402	-	-	0/1/1/1	-
2	BRJ	I	401	-	-	0/1/1/1	-
2	BRJ	B	403	-	-	0/1/1/1	-
2	BRJ	I	402	-	-	0/1/1/1	-
3	MES	H	404	-	-	4/6/14/14	0/1/1/1
2	BRJ	F	402	-	-	0/1/1/1	-
2	BRJ	E	403	-	-	0/1/1/1	-
3	MES	J	404	-	-	0/6/14/14	0/1/1/1
2	BRJ	B	401	-	-	0/1/1/1	-
2	BRJ	A	401	-	-	0/1/1/1	-
3	MES	G	405	-	-	2/6/14/14	0/1/1/1
2	BRJ	H	401	-	-	0/1/1/1	-
2	BRJ	G	401	-	-	0/1/1/1	-
2	BRJ	J	401	-	-	0/1/1/1	-
3	MES	B	404	-	-	5/6/14/14	0/1/1/1
3	MES	B	405	-	-	2/6/14/14	0/1/1/1
2	BRJ	J	403	-	-	0/1/1/1	-
2	BRJ	H	402	-	-	0/1/1/1	-
2	BRJ	E	401	-	-	0/1/1/1	-
3	MES	E	405	-	-	6/6/14/14	0/1/1/1
2	BRJ	E	402	-	-	0/1/1/1	-
2	BRJ	C	402	-	-	0/1/1/1	-
2	BRJ	A	403	-	-	0/1/1/1	-
3	MES	F	404	-	-	4/6/14/14	0/1/1/1
2	BRJ	G	403	-	-	0/1/1/1	-

The worst 5 of 10 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	F	404	MES	C8-S	-7.64	1.66	1.77
3	B	405	MES	C8-S	-7.59	1.66	1.77
3	J	404	MES	C8-S	-7.50	1.66	1.77
3	D	404	MES	C8-S	-7.49	1.66	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	H	404	MES	C8-S	-7.39	1.67	1.77

The worst 5 of 30 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	B	404	MES	O2S-S-C8	4.48	112.31	106.92
3	I	404	MES	O2S-S-C8	4.35	112.16	106.92
3	E	405	MES	O1S-S-C8	4.25	112.03	106.92
3	D	405	MES	O3S-S-C8	3.84	111.98	105.77
3	F	404	MES	O2S-S-C8	2.95	110.47	106.92

There are no chirality outliers.

5 of 33 torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	D	405	MES	C7-C8-S-O2S
3	D	405	MES	C7-C8-S-O3S
3	D	404	MES	C8-C7-N4-C3
3	I	404	MES	C7-C8-S-O1S
3	I	404	MES	C7-C8-S-O3S

There are no ring outliers.

10 monomers are involved in 13 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	B	402	BRJ	2	0
2	D	401	BRJ	1	0
2	C	403	BRJ	1	0
2	G	402	BRJ	1	0
2	B	403	BRJ	1	0
2	F	402	BRJ	2	0
2	B	401	BRJ	1	0
2	A	401	BRJ	2	0
2	H	401	BRJ	1	0
2	J	401	BRJ	1	0

5.7 Other polymers ⓘ

There are no such residues in this entry.

5.8 Polymer linkage issues ⓘ

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	308/322 (95%)	0.19	18 (5%) 23 24	85, 117, 163, 197	0
1	B	308/322 (95%)	0.13	11 (3%) 42 42	75, 105, 177, 215	0
1	C	308/322 (95%)	0.10	8 (2%) 56 54	71, 107, 176, 196	0
1	D	308/322 (95%)	0.16	15 (4%) 29 29	60, 102, 177, 201	0
1	E	308/322 (95%)	0.19	14 (4%) 33 33	75, 114, 176, 206	0
1	F	308/322 (95%)	0.18	14 (4%) 33 33	76, 119, 173, 205	0
1	G	308/322 (95%)	0.15	23 (7%) 14 16	67, 107, 165, 196	0
1	H	308/322 (95%)	0.25	14 (4%) 33 33	75, 110, 174, 214	0
1	I	308/322 (95%)	0.22	19 (6%) 20 21	73, 112, 171, 213	0
1	J	308/322 (95%)	0.26	18 (5%) 23 24	81, 119, 186, 210	0
All	All	3080/3220 (95%)	0.18	154 (5%) 28 29	60, 111, 177, 215	0

The worst 5 of 154 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	H	288	ALA	6.3
1	I	287	GLN	6.0
1	H	289	ASN	5.8
1	D	154	ASN	5.6
1	H	181	VAL	5.3

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

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

6.3 Carbohydrates ⓘ

There are no carbohydrates in this entry.

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
2	BRJ	C	401	4/4	0.34	0.97	107,125,131,186	0
2	BRJ	B	403	4/4	0.35	0.83	99,100,124,181	0
2	BRJ	E	404	4/4	0.42	0.58	141,144,162,171	0
2	BRJ	C	403	4/4	0.52	0.49	117,118,121,168	0
2	BRJ	F	403	4/4	0.55	0.51	107,115,120,160	0
2	BRJ	H	401	4/4	0.57	0.86	104,108,114,177	0
2	BRJ	H	403	4/4	0.58	0.78	122,124,143,156	0
2	BRJ	G	401	4/4	0.58	0.69	144,155,157,186	0
2	BRJ	F	401	4/4	0.61	0.55	94,100,122,131	0
2	BRJ	F	402	4/4	0.61	0.33	96,100,106,150	0
2	BRJ	A	403	4/4	0.63	0.61	120,129,133,166	0
2	BRJ	J	402	4/4	0.64	0.71	104,116,118,173	0
2	BRJ	D	403	4/4	0.66	0.57	131,146,148,150	0
2	BRJ	A	401	4/4	0.67	0.45	112,120,122,174	0
2	BRJ	I	401	4/4	0.67	0.55	99,103,116,181	0
2	BRJ	J	401	4/4	0.69	0.66	97,112,113,155	0
2	BRJ	I	403	4/4	0.69	0.71	134,134,142,152	0
2	BRJ	B	401	4/4	0.70	0.61	90,104,114,168	0
2	BRJ	G	402	4/4	0.74	1.00	106,115,121,159	0
3	MES	I	404	12/12	0.76	0.34	150,161,172,189	0
2	BRJ	A	402	4/4	0.76	0.40	123,130,132,134	0
2	BRJ	I	402	4/4	0.77	0.64	119,127,128,130	0
2	BRJ	B	402	4/4	0.78	0.42	120,120,123,160	0
2	BRJ	G	404	4/4	0.79	0.34	88,88,103,146	0
2	BRJ	H	402	4/4	0.80	0.39	103,104,112,128	0
2	BRJ	E	402	4/4	0.81	0.50	110,122,122,175	0
2	BRJ	E	401	4/4	0.82	0.57	136,142,150,151	0
3	MES	B	404	12/12	0.82	0.22	136,150,169,183	0
2	BRJ	D	402	4/4	0.82	0.32	94,100,111,135	0
2	BRJ	C	402	4/4	0.83	0.42	111,119,140,144	0
3	MES	J	404	12/12	0.83	0.34	157,173,186,195	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
3	MES	D	404	12/12	0.84	0.22	133,146,165,170	0
2	BRJ	J	403	4/4	0.85	0.44	125,133,134,143	0
2	BRJ	G	403	4/4	0.85	0.67	101,110,115,119	0
3	MES	E	405	12/12	0.86	0.19	133,157,173,175	0
3	MES	D	405	12/12	0.87	0.20	131,145,152,160	0
2	BRJ	E	403	4/4	0.88	0.32	135,136,144,146	0
3	MES	H	404	12/12	0.88	0.20	125,136,162,172	0
3	MES	B	405	12/12	0.89	0.11	122,137,156,159	0
3	MES	F	404	12/12	0.91	0.13	137,148,163,176	0
2	BRJ	D	401	4/4	0.92	0.52	94,103,136,140	0
3	MES	G	405	12/12	0.94	0.11	114,138,150,164	0

6.5 Other polymers [i](#)

There are no such residues in this entry.