



Full wwPDB X-ray Structure Validation Report ⓘ

Feb 1, 2016 – 09:50 AM GMT

PDB ID : 3JVV
Title : Crystal Structure of P. aeruginosa PilT with bound AMP-PCP
Authors : Mistic, A.M.; Satyshur, K.A.; Forest, K.T.
Deposited on : 2009-09-17
Resolution : 2.60 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

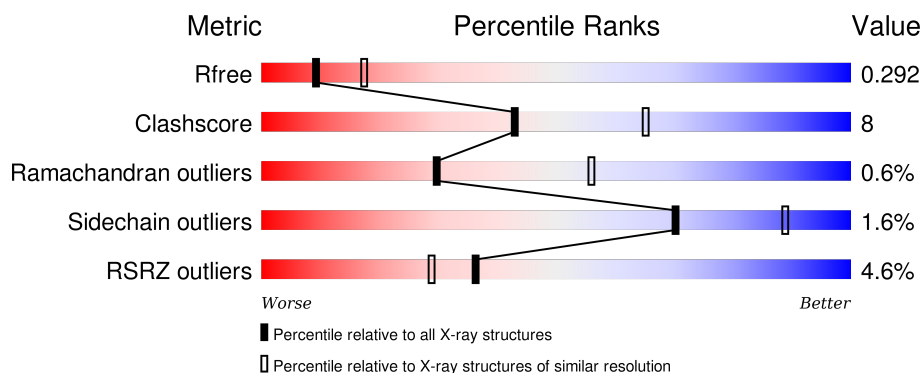
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.60 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}	91344	2328 (2.60-2.60)
Clashscore	102246	2679 (2.60-2.60)
Ramachandran outliers	100387	2635 (2.60-2.60)
Sidechain outliers	100360	2635 (2.60-2.60)
RSRZ outliers	91569	2334 (2.60-2.60)

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. 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	356	<div> <div>5%</div> <div>78% 12% • 7%</div> </div>
1	B	356	<div> <div>6%</div> <div>76% 14% • 8%</div> </div>
1	C	356	<div> <div>3%</div> <div>74% 17% • 5%</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
2	ACP	C	400	-	-	-	X

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 7939 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 Twitching mobility protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	331	Total	C	N	O	S	0	0	0
			2577	1617	458	487	15			
1	B	328	Total	C	N	O	S	0	0	0
			2551	1599	453	484	15			
1	C	337	Total	C	N	O	S	0	0	0
			2613	1641	464	493	15			

There are 36 discrepancies between the modelled and reference sequences:

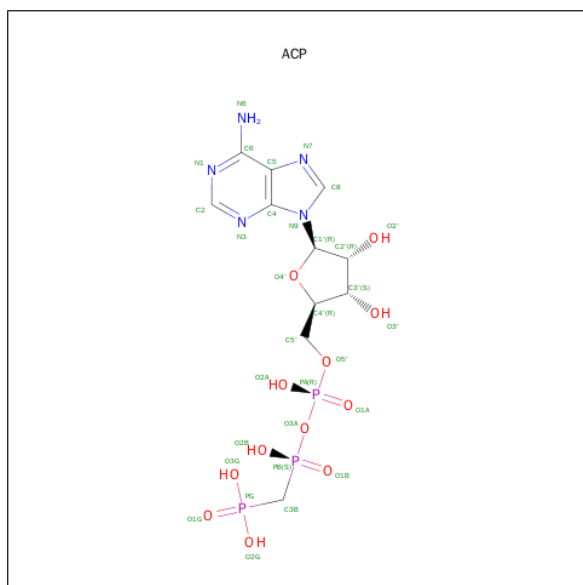
Chain	Residue	Modelled	Actual	Comment	Reference
A	345	GLY	-	EXPRESSION TAG	UNP P24559
A	346	ALA	-	EXPRESSION TAG	UNP P24559
A	347	ALA	-	EXPRESSION TAG	UNP P24559
A	348	ALA	-	EXPRESSION TAG	UNP P24559
A	349	LEU	-	EXPRESSION TAG	UNP P24559
A	350	GLU	-	EXPRESSION TAG	UNP P24559
A	351	HIS	-	EXPRESSION TAG	UNP P24559
A	352	HIS	-	EXPRESSION TAG	UNP P24559
A	353	HIS	-	EXPRESSION TAG	UNP P24559
A	354	HIS	-	EXPRESSION TAG	UNP P24559
A	355	HIS	-	EXPRESSION TAG	UNP P24559
A	356	HIS	-	EXPRESSION TAG	UNP P24559
B	345	GLY	-	EXPRESSION TAG	UNP P24559
B	346	ALA	-	EXPRESSION TAG	UNP P24559
B	347	ALA	-	EXPRESSION TAG	UNP P24559
B	348	ALA	-	EXPRESSION TAG	UNP P24559
B	349	LEU	-	EXPRESSION TAG	UNP P24559
B	350	GLU	-	EXPRESSION TAG	UNP P24559
B	351	HIS	-	EXPRESSION TAG	UNP P24559
B	352	HIS	-	EXPRESSION TAG	UNP P24559
B	353	HIS	-	EXPRESSION TAG	UNP P24559
B	354	HIS	-	EXPRESSION TAG	UNP P24559
B	355	HIS	-	EXPRESSION TAG	UNP P24559

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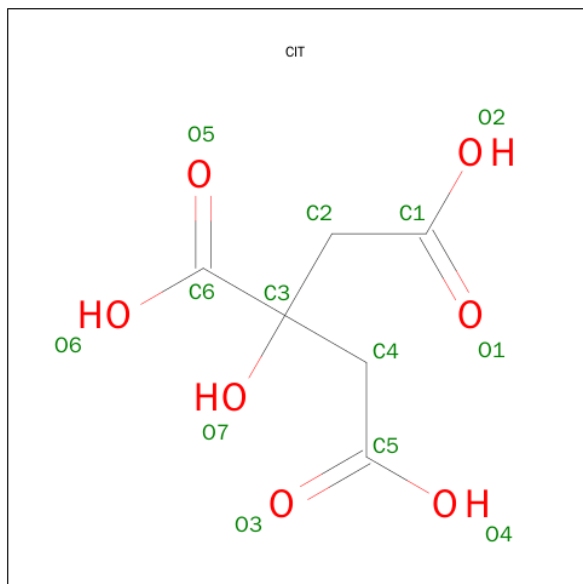
Chain	Residue	Modelled	Actual	Comment	Reference
B	356	HIS	-	EXPRESSION TAG	UNP P24559
C	345	GLY	-	EXPRESSION TAG	UNP P24559
C	346	ALA	-	EXPRESSION TAG	UNP P24559
C	347	ALA	-	EXPRESSION TAG	UNP P24559
C	348	ALA	-	EXPRESSION TAG	UNP P24559
C	349	LEU	-	EXPRESSION TAG	UNP P24559
C	350	GLU	-	EXPRESSION TAG	UNP P24559
C	351	HIS	-	EXPRESSION TAG	UNP P24559
C	352	HIS	-	EXPRESSION TAG	UNP P24559
C	353	HIS	-	EXPRESSION TAG	UNP P24559
C	354	HIS	-	EXPRESSION TAG	UNP P24559
C	355	HIS	-	EXPRESSION TAG	UNP P24559
C	356	HIS	-	EXPRESSION TAG	UNP P24559

- Molecule 2 is PHOSPHOMETHYLPHOSPHONIC ACID ADENYLATE ESTER (three-letter code: ACP) (formula: $C_{11}H_{18}N_5O_{12}P_3$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	B	1	Total Mg 1 1	0	0
3	A	1	Total Mg 1 1	0	0
3	C	1	Total Mg 1 1	0	0

- Molecule 4 is CITRIC ACID (three-letter code: CIT) (formula: $C_6H_8O_7$).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1	Total C O 13 6 7	0	0

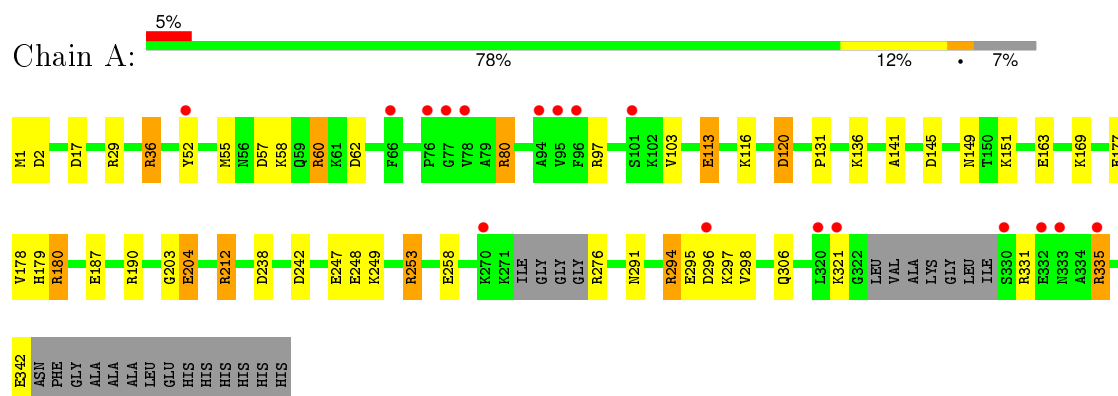
- Molecule 5 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	32	Total O 32 32	0	0
5	B	29	Total O 29 29	0	0
5	C	28	Total O 28 28	0	0

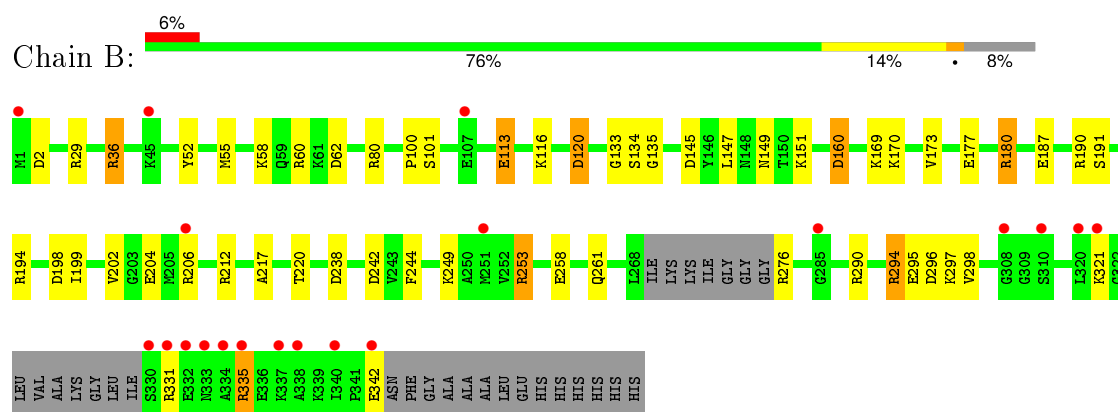
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

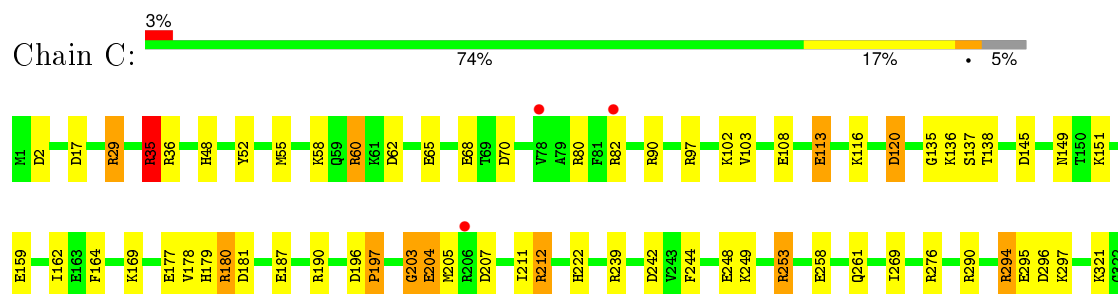
• Molecule 1: Twitching mobility protein

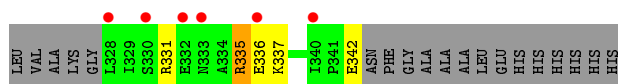


• Molecule 1: Twitching mobility protein



• Molecule 1: Twitching mobility protein





4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	108.48Å 119.55Å 185.53Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	29.12 – 2.60 29.12 – 2.60	Depositor EDS
% Data completeness (in resolution range)	94.2 (29.12-2.60) 94.3 (29.12-2.60)	Depositor EDS
R_{merge}	0.05	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.90 (at 2.61Å)	Xtriage
Refinement program	REFMAC 5.4.0067	Depositor
R, R_{free}	0.244 , 0.291 0.247 , 0.292	Depositor DCC
R_{free} test set	1757 reflections (5.24%)	DCC
Wilson B-factor (Å ²)	60.7	Xtriage
Anisotropy	0.044	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.30 , 44.6	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.51$, $\langle L^2 \rangle = 0.34$	Xtriage
Outliers	0 of 35352 reflections	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	7939	wwPDB-VP
Average B, all atoms (Å ²)	60.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.59% 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, 0.375 respectively for untwinned datasets, and 0.333, 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: MG, ACP, CIT

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	0.52	1/2614 (0.0%)	0.98	26/3523 (0.7%)
1	B	0.51	0/2588	0.98	25/3490 (0.7%)
1	C	0.55	2/2651 (0.1%)	0.97	24/3574 (0.7%)
All	All	0.53	3/7853 (0.0%)	0.98	75/10587 (0.7%)

All (3) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	1	MET	N-CA	6.41	1.59	1.46
1	C	48	HIS	CE1-NE2	6.23	1.47	1.32
1	C	48	HIS	CG-CD2	5.58	1.45	1.35

All (75) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	60	ARG	NE-CZ-NH1	-15.38	112.61	120.30
1	B	212	ARG	NE-CZ-NH1	-14.14	113.23	120.30
1	C	253	ARG	NE-CZ-NH1	13.91	127.25	120.30
1	C	29	ARG	NE-CZ-NH2	-13.88	113.36	120.30
1	C	253	ARG	NE-CZ-NH2	-13.87	113.37	120.30
1	A	190	ARG	NE-CZ-NH2	-13.47	113.56	120.30
1	B	331	ARG	NE-CZ-NH1	-13.36	113.62	120.30
1	C	29	ARG	NE-CZ-NH1	12.64	126.62	120.30
1	A	36	ARG	NE-CZ-NH2	-12.43	114.08	120.30
1	B	331	ARG	NE-CZ-NH2	12.40	126.50	120.30
1	A	60	ARG	NE-CZ-NH2	12.19	126.39	120.30
1	B	335	ARG	NE-CZ-NH1	12.15	126.37	120.30
1	B	212	ARG	NE-CZ-NH2	11.54	126.07	120.30
1	B	335	ARG	NE-CZ-NH2	-11.25	114.67	120.30
1	A	36	ARG	NE-CZ-NH1	10.87	125.73	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	80	ARG	NE-CZ-NH2	-10.26	115.17	120.30
1	A	190	ARG	NE-CZ-NH1	9.74	125.17	120.30
1	A	276	ARG	NE-CZ-NH1	-9.56	115.52	120.30
1	C	180	ARG	NE-CZ-NH2	-9.54	115.53	120.30
1	A	294	ARG	NE-CZ-NH2	9.15	124.88	120.30
1	A	276	ARG	NE-CZ-NH2	9.15	124.87	120.30
1	C	294	ARG	NE-CZ-NH2	-8.75	115.93	120.30
1	A	29	ARG	NE-CZ-NH1	-8.60	116.00	120.30
1	C	36	ARG	NE-CZ-NH1	-8.58	116.01	120.30
1	C	294	ARG	NE-CZ-NH1	8.57	124.59	120.30
1	A	294	ARG	NE-CZ-NH1	-8.53	116.04	120.30
1	B	294	ARG	NE-CZ-NH1	8.49	124.55	120.30
1	B	294	ARG	NE-CZ-NH2	-8.45	116.07	120.30
1	B	190	ARG	NE-CZ-NH1	-8.12	116.24	120.30
1	B	80	ARG	NE-CZ-NH1	7.94	124.27	120.30
1	C	180	ARG	NE-CZ-NH1	7.70	124.15	120.30
1	C	190	ARG	NE-CZ-NH1	-7.68	116.46	120.30
1	C	36	ARG	NE-CZ-NH2	7.52	124.06	120.30
1	A	80	ARG	NE-CZ-NH1	-7.40	116.60	120.30
1	C	80	ARG	NE-CZ-NH1	-7.29	116.66	120.30
1	B	29	ARG	NE-CZ-NH1	-7.23	116.68	120.30
1	A	212	ARG	NE-CZ-NH2	-7.19	116.70	120.30
1	B	190	ARG	NE-CZ-NH2	7.16	123.88	120.30
1	B	253	ARG	NE-CZ-NH1	-6.97	116.81	120.30
1	A	253	ARG	NE-CZ-NH1	-6.83	116.88	120.30
1	A	212	ARG	NE-CZ-NH1	6.81	123.70	120.30
1	A	80	ARG	NE-CZ-NH2	6.80	123.70	120.30
1	A	180	ARG	NE-CZ-NH1	-6.76	116.92	120.30
1	A	335	ARG	NE-CZ-NH1	-6.73	116.93	120.30
1	C	253	ARG	CD-NE-CZ	6.69	132.96	123.60
1	B	36	ARG	NE-CZ-NH1	-6.62	116.99	120.30
1	C	335	ARG	NE-CZ-NH1	-6.51	117.04	120.30
1	C	212	ARG	NE-CZ-NH2	-6.36	117.12	120.30
1	B	160	ASP	CB-CG-OD1	6.31	123.97	118.30
1	B	36	ARG	NE-CZ-NH2	6.29	123.44	120.30
1	C	212	ARG	NE-CZ-NH1	6.28	123.44	120.30
1	C	29	ARG	CD-NE-CZ	6.25	132.35	123.60
1	C	35	ARG	CG-CD-NE	6.01	124.41	111.80
1	C	80	ARG	NE-CZ-NH2	6.01	123.30	120.30
1	B	180	ARG	NE-CZ-NH1	-6.00	117.30	120.30
1	A	60	ARG	CD-NE-CZ	5.99	131.99	123.60
1	C	190	ARG	NE-CZ-NH2	5.96	123.28	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	331	ARG	NE-CZ-NH2	-5.92	117.34	120.30
1	B	331	ARG	CD-NE-CZ	5.91	131.88	123.60
1	C	331	ARG	NE-CZ-NH2	-5.84	117.38	120.30
1	A	29	ARG	NE-CZ-NH2	5.82	123.21	120.30
1	B	29	ARG	NE-CZ-NH2	5.80	123.20	120.30
1	C	60	ARG	NE-CZ-NH2	-5.71	117.44	120.30
1	A	190	ARG	CD-NE-CZ	5.66	131.52	123.60
1	B	253	ARG	NE-CZ-NH2	5.57	123.08	120.30
1	B	276	ARG	NE-CZ-NH2	-5.53	117.53	120.30
1	B	212	ARG	CD-NE-CZ	5.51	131.32	123.60
1	A	335	ARG	NE-CZ-NH2	5.42	123.01	120.30
1	B	335	ARG	CD-NE-CZ	5.41	131.18	123.60
1	A	180	ARG	NE-CZ-NH2	5.38	122.99	120.30
1	A	331	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	C	276	ARG	NE-CZ-NH2	-5.20	117.70	120.30
1	C	335	ARG	NE-CZ-NH2	5.17	122.89	120.30
1	B	276	ARG	NE-CZ-NH1	5.08	122.84	120.30
1	A	36	ARG	CD-NE-CZ	5.03	130.64	123.60

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	2577	0	2628	37	1
1	B	2551	0	2591	43	0
1	C	2613	0	2671	57	1
2	A	31	0	14	1	0
2	B	31	0	13	0	0
2	C	31	0	14	2	0
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
4	A	13	0	5	0	0
5	A	32	0	0	4	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
5	B	29	0	0	6	0
5	C	28	0	0	6	0
All	All	7939	0	7936	129	1

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 (129) 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:36:ARG:NH1	5:A:366:HOH:O	2.14	0.81
1:A:321:LYS:NZ	1:A:342:GLU:OE2	2.18	0.75
1:C:321:LYS:NZ	1:C:342:GLU:OE2	2.20	0.73
1:C:65:GLU:O	5:C:363:HOH:O	2.05	0.73
1:B:194:ARG:HE	1:C:82:ARG:HH21	1.36	0.72
1:B:100:PRO:HA	5:B:373:HOH:O	1.88	0.72
1:B:321:LYS:NZ	1:B:342:GLU:OE2	2.20	0.69
1:B:238:ASP:HB2	5:B:368:HOH:O	1.92	0.68
1:A:298:VAL:HG12	5:A:365:HOH:O	1.93	0.68
1:C:222:HIS:HA	5:C:372:HOH:O	1.96	0.65
1:B:194:ARG:HE	1:C:82:ARG:NH2	1.95	0.64
1:B:170:LYS:O	5:B:376:HOH:O	2.15	0.64
1:B:173:VAL:O	1:C:90:ARG:NH2	2.29	0.64
1:B:100:PRO:CA	5:B:373:HOH:O	2.43	0.64
1:C:35:ARG:HG2	1:C:35:ARG:HH21	1.63	0.62
1:B:194:ARG:NE	1:C:82:ARG:NH2	2.47	0.62
1:A:80:ARG:NH1	1:A:163:GLU:O	2.33	0.61
1:C:102:LYS:NZ	1:C:108:GLU:OE2	2.33	0.61
1:A:145:ASP:OD1	1:A:169:LYS:NZ	2.31	0.60
1:C:120:ASP:OD1	1:C:151:LYS:HE3	2.01	0.60
1:C:180:ARG:HD2	1:C:181:ASP:OD1	2.01	0.60
1:B:258:GLU:OE2	1:B:294:ARG:NH1	2.31	0.60
1:C:97:ARG:HG3	5:C:371:HOH:O	2.02	0.60
1:B:335:ARG:HD2	1:B:342:GLU:O	2.02	0.59
1:B:58:LYS:NZ	1:B:62:ASP:OD2	2.36	0.59
1:A:58:LYS:NZ	1:A:62:ASP:OD2	2.36	0.59
1:C:70:ASP:OD2	5:C:376:HOH:O	2.17	0.58
1:C:103:VAL:HG12	1:C:164:PHE:CD1	2.38	0.58
1:B:145:ASP:OD1	1:B:169:LYS:NZ	2.26	0.57
1:A:120:ASP:OD1	1:A:151:LYS:HE3	2.04	0.57
1:C:55:MET:O	1:C:60:ARG:NH1	2.37	0.57

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:145:ASP:OD1	1:C:169:LYS:NZ	2.34	0.57
1:C:82:ARG:NE	5:C:376:HOH:O	2.26	0.56
1:A:212:ARG:HD3	1:A:248:GLU:OE2	2.06	0.56
1:A:247:GLU:HG3	5:A:376:HOH:O	2.05	0.55
1:B:191:SER:OG	1:C:68:GLU:OE1	2.20	0.55
1:C:258:GLU:OE2	1:C:294:ARG:NH1	2.31	0.55
1:C:58:LYS:NZ	1:C:62:ASP:OD2	2.39	0.54
1:A:149:ASN:OD1	1:A:169:LYS:HD2	2.08	0.54
1:C:103:VAL:HG12	1:C:164:PHE:HD1	1.72	0.54
1:C:295:GLU:OE1	1:C:297:LYS:NZ	2.25	0.54
1:B:198:ASP:OD2	1:C:29:ARG:NH2	2.38	0.53
1:B:187:GLU:N	1:B:187:GLU:CD	2.62	0.53
1:B:194:ARG:HD2	1:C:82:ARG:CZ	2.39	0.53
1:A:177:GLU:OE2	1:A:180:ARG:NH2	2.42	0.53
1:A:187:GLU:CD	1:A:187:GLU:N	2.63	0.53
1:B:120:ASP:OD1	1:B:151:LYS:HE3	2.09	0.52
1:C:187:GLU:CD	1:C:187:GLU:N	2.64	0.52
1:C:203:GLY:O	1:C:204:GLU:HB3	2.10	0.52
1:C:177:GLU:OE2	1:C:180:ARG:NH2	2.44	0.51
1:B:160:ASP:OD2	1:B:206:ARG:NH2	2.40	0.51
1:B:55:MET:O	1:B:60:ARG:NH1	2.44	0.51
1:B:149:ASN:OD1	1:B:169:LYS:HD2	2.11	0.50
1:A:57:ASP:OD1	1:A:60:ARG:NH2	2.44	0.50
1:A:103:VAL:HG13	1:A:141:ALA:HB1	1.94	0.50
1:A:253:ARG:CZ	1:A:296:ASP:CG	2.79	0.50
1:A:335:ARG:NE	1:A:342:GLU:O	2.40	0.49
1:A:169:LYS:O	1:B:36:ARG:NH1	2.45	0.49
1:C:253:ARG:CZ	1:C:296:ASP:CG	2.81	0.49
1:A:17:ASP:OD1	1:A:97:ARG:NE	2.35	0.49
1:B:177:GLU:OE2	1:B:180:ARG:NH2	2.45	0.49
1:B:113:GLU:OE2	1:B:116:LYS:NZ	2.46	0.49
1:B:253:ARG:CZ	1:B:296:ASP:CG	2.81	0.48
1:A:291:ASN:OD1	1:A:294:ARG:NH2	2.46	0.48
1:A:295:GLU:OE1	1:A:297:LYS:NZ	2.24	0.48
1:A:242:ASP:O	1:A:249:LYS:NZ	2.47	0.48
1:C:212:ARG:HD3	1:C:248:GLU:OE2	2.13	0.47
1:B:101:SER:N	5:B:373:HOH:O	2.48	0.47
1:A:131:PRO:O	1:A:136:LYS:NZ	2.48	0.47
1:B:238:ASP:OD1	1:B:298:VAL:HG11	2.15	0.46
1:C:120:ASP:OD1	1:C:151:LYS:CE	2.62	0.46
1:A:204:GLU:O	5:A:383:HOH:O	2.20	0.46

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:17:ASP:OD1	1:C:97:ARG:HG2	2.16	0.46
1:A:55:MET:O	1:A:60:ARG:NH1	2.49	0.46
1:C:335:ARG:NE	1:C:342:GLU:O	2.43	0.46
1:C:269:ILE:HG12	1:C:337:LYS:HD2	1.98	0.46
1:B:120:ASP:OD1	1:B:151:LYS:CE	2.64	0.45
1:C:149:ASN:OD1	1:C:169:LYS:HD2	2.15	0.45
1:C:253:ARG:NH1	1:C:296:ASP:OD2	2.50	0.45
1:C:159:GLU:HB2	1:C:162:ILE:HA	1.98	0.45
1:A:253:ARG:NH1	1:A:296:ASP:CG	2.70	0.45
1:C:336:GLU:CD	1:C:337:LYS:NZ	2.70	0.45
1:A:120:ASP:OD1	1:A:151:LYS:CE	2.64	0.45
1:C:336:GLU:OE2	1:C:337:LYS:NZ	2.50	0.45
1:B:187:GLU:H	1:B:187:GLU:CD	2.19	0.44
1:A:113:GLU:OE2	1:A:116:LYS:NZ	2.50	0.44
1:A:145:ASP:CG	1:A:169:LYS:HZ1	2.20	0.44
1:B:261:GLN:OE1	1:B:290:ARG:NH1	2.51	0.44
1:C:178:VAL:O	1:C:179:HIS:HB2	2.17	0.44
1:C:138:THR:OG1	2:C:400:ACP:O2A	2.36	0.44
1:C:113:GLU:OE2	1:C:116:LYS:NZ	2.51	0.44
1:B:217:ALA:O	1:B:220:THR:HG22	2.18	0.44
1:C:97:ARG:HD2	5:C:378:HOH:O	2.18	0.43
1:C:253:ARG:NH1	1:C:296:ASP:CG	2.70	0.43
1:C:159:GLU:CB	1:C:162:ILE:HA	2.48	0.43
1:B:52:TYR:O	1:B:60:ARG:NH1	2.49	0.43
1:C:269:ILE:HG12	1:C:337:LYS:CD	2.48	0.43
1:C:35:ARG:CG	1:C:35:ARG:HH21	2.32	0.43
1:B:113:GLU:OE1	1:B:116:LYS:NZ	2.49	0.43
1:A:187:GLU:CD	1:A:187:GLU:H	2.22	0.43
1:B:244:PHE:O	1:B:249:LYS:NZ	2.37	0.43
1:A:238:ASP:OD1	1:A:298:VAL:HG11	2.19	0.43
1:B:295:GLU:OE1	1:B:297:LYS:NZ	2.29	0.43
1:A:253:ARG:NH1	1:A:296:ASP:OD2	2.52	0.42
1:B:133:GLY:O	1:B:135:GLY:N	2.52	0.42
1:B:58:LYS:NZ	1:B:62:ASP:OD1	2.52	0.42
1:B:242:ASP:O	1:B:249:LYS:NZ	2.52	0.42
1:A:178:VAL:O	1:A:179:HIS:HB2	2.20	0.42
1:A:52:TYR:C	1:A:52:TYR:CD1	2.92	0.42
1:A:113:GLU:OE1	1:A:116:LYS:NZ	2.52	0.42
1:B:147:LEU:HD13	1:B:199:ILE:HD13	2.02	0.42
1:A:58:LYS:NZ	1:A:62:ASP:OD1	2.53	0.42
1:C:187:GLU:CD	1:C:187:GLU:H	2.23	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:204:GLU:OE1	1:B:206:ARG:NH2	2.52	0.41
1:C:196:ASP:N	1:C:197:PRO:HD3	2.35	0.41
1:C:336:GLU:OE1	1:C:337:LYS:NZ	2.47	0.41
1:B:194:ARG:HD2	1:C:82:ARG:NH2	2.36	0.41
1:C:135:GLY:O	1:C:136:LYS:C	2.58	0.41
1:C:242:ASP:O	1:C:249:LYS:NZ	2.54	0.41
1:C:261:GLN:OE1	1:C:290:ARG:NH1	2.53	0.41
2:A:400:ACP:O1A	2:A:400:ACP:H3B2	2.21	0.41
1:A:335:ARG:NH1	1:A:342:GLU:O	2.52	0.41
1:A:258:GLU:CD	1:A:294:ARG:HH11	2.23	0.41
1:B:194:ARG:CD	1:C:82:ARG:NH2	2.84	0.41
2:C:400:ACP:O1A	2:C:400:ACP:H3B1	2.22	0.40
1:B:202:VAL:O	5:B:374:HOH:O	2.21	0.40
1:C:244:PHE:O	1:C:249:LYS:NZ	2.32	0.40
1:C:205:MET:O	1:C:211:ILE:HD11	2.21	0.40
1:C:58:LYS:NZ	1:C:62:ASP:OD1	2.53	0.40

All (1) symmetry-related close contacts are listed below. The label for Atom-2 includes the symmetry operator and encoded unit-cell translations to be applied.

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:306:GLN:O	1:C:60:ARG:NH2[5_545]	2.03	0.17

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	325/356 (91%)	309 (95%)	14 (4%)	2 (1%)	30	56
1	B	322/356 (90%)	307 (95%)	14 (4%)	1 (0%)	46	72
1	C	333/356 (94%)	314 (94%)	16 (5%)	3 (1%)	21	42
All	All	980/1068 (92%)	930 (95%)	44 (4%)	6 (1%)	30	56

All (6) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	134	SER
1	A	204	GLU
1	C	204	GLU
1	C	197	PRO
1	C	203	GLY
1	A	203	GLY

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	283/299 (95%)	280 (99%)	3 (1%)	80	93
1	B	280/299 (94%)	277 (99%)	3 (1%)	80	93
1	C	286/299 (96%)	278 (97%)	8 (3%)	51	78
All	All	849/897 (95%)	835 (98%)	14 (2%)	70	89

All (14) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	2	ASP
1	A	113	GLU
1	A	120	ASP
1	B	2	ASP
1	B	113	GLU
1	B	120	ASP
1	C	2	ASP
1	C	35	ARG
1	C	52	TYR
1	C	113	GLU
1	C	120	ASP
1	C	137	SER
1	C	207	ASP
1	C	239	ARG

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

5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

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

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

5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 7 ligands modelled in this entry, 3 are monoatomic - leaving 4 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	CIT	A	357	-	3,12,12	1.50	0	3,17,17	2.73	2 (66%)
2	ACP	A	400	3	25,33,33	1.19	3 (12%)	31,52,52	2.21	8 (25%)
2	ACP	B	400	3	25,33,33	1.12	2 (8%)	31,52,52	2.07	7 (22%)
2	ACP	C	400	3	25,33,33	1.30	2 (8%)	31,52,52	1.76	6 (19%)

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	CIT	A	357	-	-	0/6/16/16	0/0/0/0
2	ACP	A	400	3	-	0/15/38/38	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	ACP	B	400	3	-	0/15/38/38	0/3/3/3
2	ACP	C	400	3	-	0/15/38/38	0/3/3/3

All (7) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	B	400	ACP	PB-O2B	-2.22	1.50	1.56
2	A	400	ACP	PB-O2B	-2.08	1.51	1.56
2	A	400	ACP	PB-O3A	2.87	1.61	1.58
2	B	400	ACP	C5-C4	3.05	1.47	1.40
2	A	400	ACP	C5-C4	3.22	1.47	1.40
2	C	400	ACP	C5-C4	3.26	1.47	1.40
2	C	400	ACP	PB-O3A	3.42	1.62	1.58

All (23) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	400	ACP	N3-C2-N1	-7.00	123.53	128.89
2	A	400	ACP	PA-O3A-PB	-6.31	115.00	132.73
2	A	400	ACP	N3-C2-N1	-6.30	124.07	128.89
2	C	400	ACP	N3-C2-N1	-6.13	124.20	128.89
2	B	400	ACP	PA-O3A-PB	-5.81	116.41	132.73
2	A	400	ACP	C2'-C1'-N9	-4.25	107.81	114.29
4	A	357	CIT	C3-C2-C1	-3.91	108.70	114.96
2	C	400	ACP	PA-O3A-PB	-3.43	123.09	132.73
2	C	400	ACP	O1G-PG-C3B	-2.92	104.46	111.13
2	A	400	ACP	O1G-PG-C3B	-2.92	104.47	111.13
2	B	400	ACP	C2'-C1'-N9	-2.69	110.18	114.29
4	A	357	CIT	C3-C4-C5	-2.54	110.89	114.96
2	A	400	ACP	C4-C5-N7	-2.52	107.16	109.48
2	B	400	ACP	C4-C5-N7	-2.52	107.16	109.48
2	C	400	ACP	C4-C5-N7	-2.38	107.29	109.48
2	A	400	ACP	C4'-O4'-C1'	-2.32	107.17	109.72
2	B	400	ACP	O2G-PG-C3B	-2.12	101.26	106.40
2	B	400	ACP	O3G-PG-O2G	2.27	114.78	108.13
2	B	400	ACP	O2B-PB-O1B	2.27	117.26	110.12
2	A	400	ACP	O4'-C4'-C3'	2.43	110.05	105.15
2	C	400	ACP	O3G-PG-O2G	2.66	115.91	108.13
2	C	400	ACP	O2B-PB-O1B	2.89	119.21	110.12
2	A	400	ACP	O2B-PB-O1B	3.06	119.75	110.12

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

2 monomers are involved in 3 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	400	ACP	1	0
2	C	400	ACP	2	0

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	331/356 (92%)	0.20	17 (5%)	32 25	38, 58, 89, 118	0
1	B	328/356 (92%)	0.21	20 (6%)	25 18	34, 57, 94, 121	0
1	C	337/356 (94%)	0.10	9 (2%)	58 51	35, 58, 86, 101	0
All	All	996/1068 (93%)	0.17	46 (4%)	36 29	34, 58, 89, 121	0

All (46) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	330	SER	7.2
1	B	321	LYS	6.7
1	A	333	ASN	6.0
1	B	331	ARG	5.8
1	B	332	GLU	5.0
1	A	332	GLU	4.8
1	A	52	TYR	4.0
1	A	270	LYS	4.0
1	B	330	SER	3.7
1	C	336	GLU	3.6
1	A	320	LEU	3.5
1	A	321	LYS	3.3
1	B	320	LEU	3.2
1	B	206	ARG	3.1
1	A	94	ALA	3.1
1	B	334	ALA	2.9
1	B	251	MET	2.9
1	C	332	GLU	2.9
1	B	337	LYS	2.8
1	A	78	VAL	2.8
1	B	335	ARG	2.7
1	B	285	GLY	2.7
1	C	330	SER	2.7

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Mol	Chain	Res	Type	RSRZ
1	A	296	ASP	2.6
1	A	95	VAL	2.6
1	A	101	SER	2.6
1	A	335	ARG	2.6
1	B	310	SER	2.6
1	B	1	MET	2.5
1	B	338	ALA	2.5
1	C	333	ASN	2.5
1	B	45	LYS	2.5
1	C	206	ARG	2.5
1	B	342	GLU	2.4
1	C	328	LEU	2.4
1	C	82	ARG	2.3
1	B	333	ASN	2.3
1	A	77	GLY	2.3
1	B	107	GLU	2.2
1	B	308	GLY	2.2
1	A	96	PHE	2.2
1	C	78	VAL	2.1
1	C	340	ILE	2.1
1	A	66	PHE	2.1
1	A	76	PRO	2.1
1	B	340	ILE	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](#)

There are no carbohydrates in this entry.

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. LLDF column lists the quality of electron density of the group with respect to its neighbouring residues in protein, DNA or RNA chains. 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	LLDF	B-factors(\AA^2)	Q<0.9
2	ACP	C	400	31/31	0.89	0.27	3.05	68,71,71,72	0
4	CIT	A	357	13/13	0.91	0.14	-0.23	53,54,58,58	0
2	ACP	A	400	31/31	0.93	0.16	-0.47	67,72,73,73	0
2	ACP	B	400	31/31	0.94	0.13	-0.98	58,62,63,63	0
3	MG	B	401	1/1	0.97	0.11	-	44,44,44,44	0
3	MG	C	401	1/1	0.65	0.23	-	64,64,64,64	0
3	MG	A	401	1/1	0.85	0.15	-	55,55,55,55	0

6.5 Other polymers [i](#)

There are no such residues in this entry.