



Full wwPDB X-ray Structure Validation Report ⓘ

Jun 5, 2017 – 08:50 PM EDT

PDB ID : 5XA9
Title : Complete structure factors and an atomic model of the calcium pump (SERCA1A) and associated phospholipids in the E2-ALF-(TG) crystals of C2 symmetry
Authors : Norimatsu, Y.; Hasegawa, K.; Shimizu, N.; Toyoshima, C.
Deposited on : 2017-03-11
Resolution : 3.20 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 : 1.7.2 (RC1), CSD as538be (2017)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20029077
Percentile statistics : 20161228.v01 (using entries in the PDB archive December 28th 2016)
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) : rb-20029077

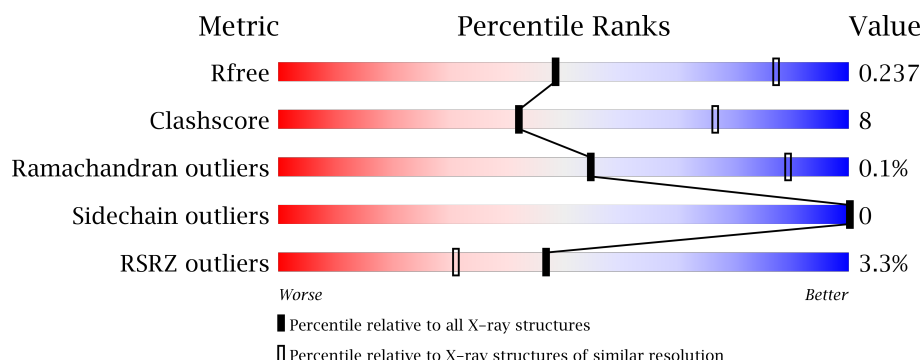
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.20 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}	100719	1015 (3.22-3.18)
Clashscore	112137	1009 (3.20-3.20)
Ramachandran outliers	110173	1118 (3.22-3.18)
Sidechain outliers	110143	1117 (3.22-3.18)
RSRZ outliers	101464	1020 (3.22-3.18)

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	995	<div> <div style="width: 3%; height: 10px; background-color: red;"></div> <div style="width: 83%; height: 10px; background-color: green;"></div> <div style="width: 17%; height: 10px; background-color: yellow;"></div> </div> <div> <div style="width: 3%;"></div> <div style="width: 83%;"></div> <div style="width: 17%;"></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
5	PCW	A	1017	-	-	-	X
5	PCW	A	1023	-	-	-	X

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Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
5	PCW	A	1029	-	-	-	X
5	PCW	A	1036	-	-	-	X

2 Entry composition [i](#)

There are 6 unique types of molecules in this entry. The entry contains 8671 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 Sarcoplasmic/endoplasmic reticulum calcium ATPase 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	995	Total	C	N	O	S	0	0	0
			7674	4878	1287	1452	57			

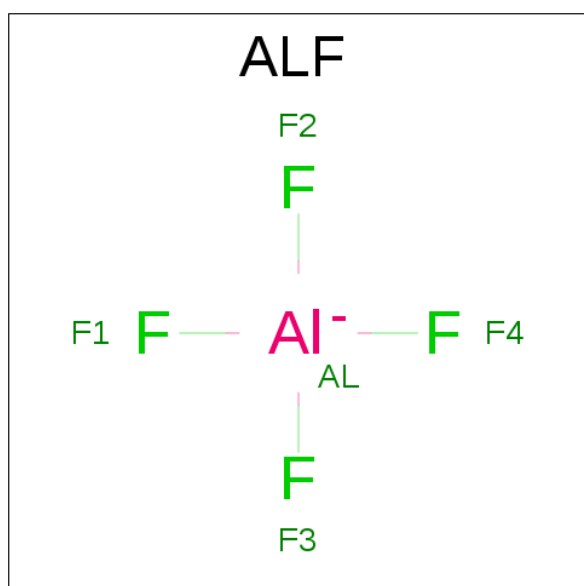
There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ACE	-	acetylation	UNP P04191

- Molecule 2 is MAGNESIUM ION (three-letter code: MG) (formula: Mg).

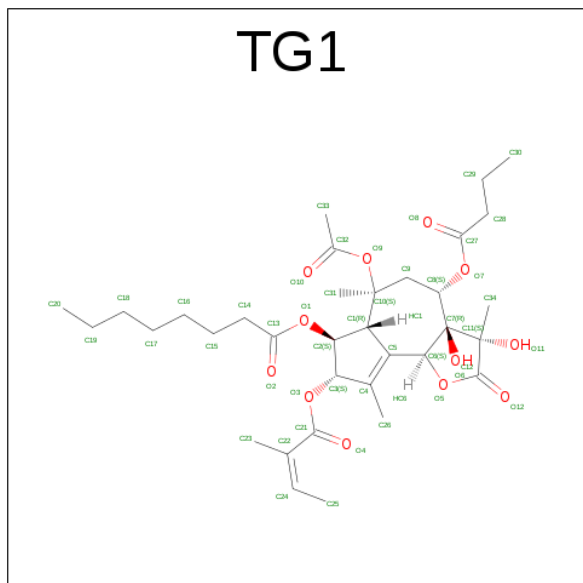
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	1	Total	Mg	0	0
			1	1		

- Molecule 3 is TETRAFLUOROALUMINATE ION (three-letter code: ALF) (formula: AlF_4).



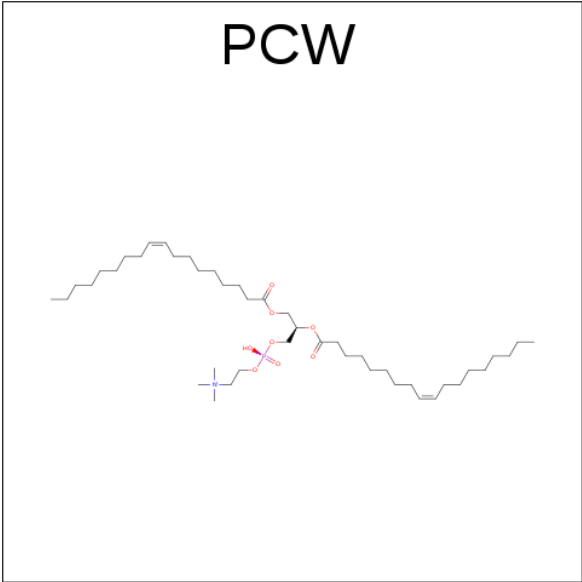
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Al	F	0	0
			5	1	4		

- Molecule 4 is OCTANOIC ACID [3S-[3ALPHA, 3ABETA, 4ALPHA, 6BETA, 6ABETA, 7BETA, 8ALPHA(Z), 9BAPHA]]-6-(ACETYLOXY)-2,3,-3A,4,5,6,6A,7,8,9B-DECAHYDRO-3,3A-DIHYDROXY-3,6,9-TRIMETHYL-8-[(2-METHYL-1-OXO-2-BUTENYL)OXY]-2-OXO-4-(1-OXOBUTOXY)-AZULENO[4,5-B]FURAN-7-YL ESTER (three-letter code: TG1) (formula: C₃₄H₅₀O₁₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	A	1	Total	C	O	0	0
			46	34	12		

- Molecule 5 is 1,2-DIOLEOYL-SN-GLYCERO-3-PHOSPHOCHOLINE (three-letter code: PCW) (formula: C₄₄H₈₅NO₈P).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		

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Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		
5	A	1	Total	C	N	O	P	0	0
			22	12	1	8	1		

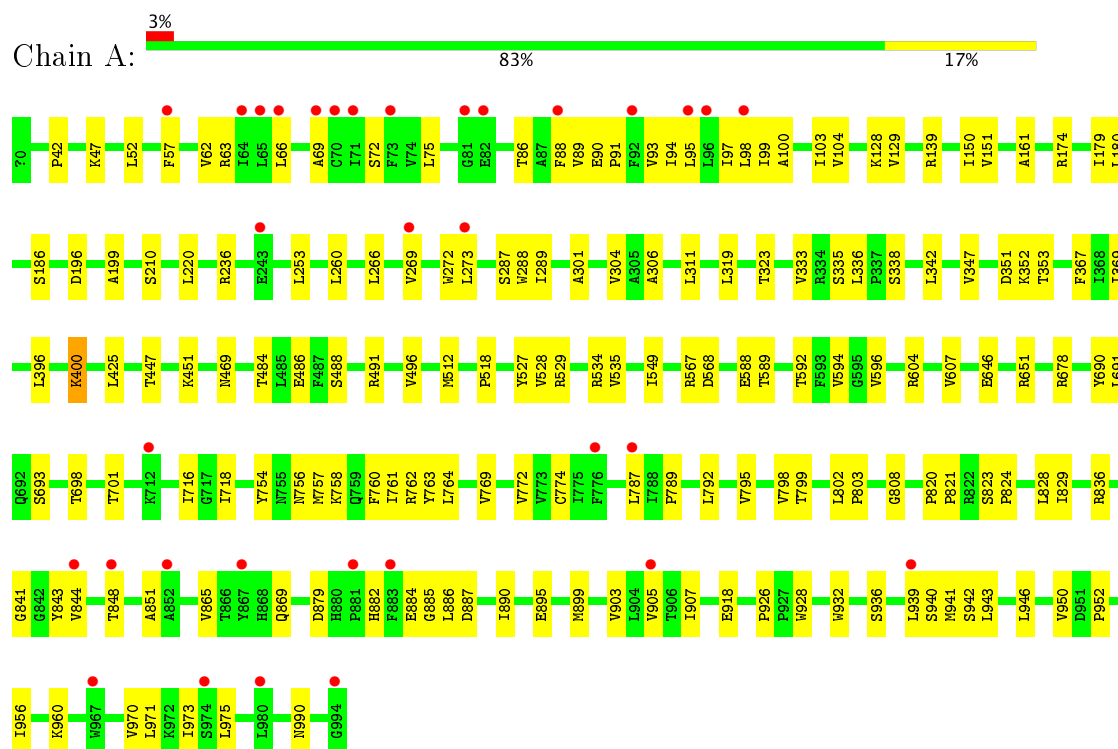
- Molecule 6 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	197	Total 197	O 197	0	0

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: Sarcoplasmic/endoplasmic reticulum calcium ATPase 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	177.40Å 70.10Å 141.90Å 90.00° 107.00° 90.00°	Depositor
Resolution (Å)	135.70 – 3.20 135.70 – 3.20	Depositor EDS
% Data completeness (in resolution range)	100.0 (135.70-3.20) 100.0 (135.70-3.20)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	6.50 (at 3.19Å)	Xtriage
Refinement program	PHENIX 1.9_1692	Depositor
R, R_{free}	0.215 , 0.235 0.224 , 0.237	Depositor DCC
R_{free} test set	1380 reflections (5.21%)	DCC
Wilson B-factor (Å ²)	110.0	Xtriage
Anisotropy	0.145	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.28 , 99.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.90	EDS
Total number of atoms	8671	wwPDB-VP
Average B, all atoms (Å ²)	148.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.70% 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: ALF, MG, TG1, PCW, ACE

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	0.25	0/7813	0.40	1/10594 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed($^{\circ}$)	Ideal($^{\circ}$)
1	A	400	LYS	CB-CA-C	5.20	120.81	110.40

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	7674	0	7767	133	0
2	A	1	0	0	0	0
3	A	5	0	0	1	0
4	A	46	0	50	2	0
5	A	748	0	612	9	0
6	A	197	0	0	2	0
All	All	8671	0	8429	133	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 (133) 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:886:LEU:HG	1:A:887:ASP:N	1.51	1.18
1:A:75:LEU:HD21	5:A:1017:PCW:C32	1.81	1.11
1:A:886:LEU:CG	1:A:887:ASP:H	1.61	1.09
1:A:90:GLU:HG2	1:A:91:PRO:HD3	1.37	1.02
1:A:90:GLU:CG	1:A:91:PRO:HD3	1.90	1.02
1:A:99:ILE:O	1:A:103:ILE:HG12	1.67	0.94
1:A:93:VAL:HG12	1:A:97:ILE:HD11	1.50	0.92
1:A:529:ARG:NH1	6:A:1101:HOH:O	2.07	0.88
1:A:90:GLU:O	1:A:94:ILE:HG13	1.76	0.86
1:A:72:SER:HB3	1:A:91:PRO:HG3	1.57	0.84
1:A:89:VAL:O	1:A:93:VAL:HG23	1.76	0.84
1:A:941:MET:HE3	1:A:941:MET:HA	1.58	0.84
1:A:772:VAL:HG21	4:A:1003:TG1:H24	1.63	0.80
1:A:57:PHE:HE1	1:A:98:LEU:HG	1.45	0.80
1:A:486:GLU:O	1:A:491:ARG:NH2	2.16	0.79
1:A:88:PHE:HE1	5:A:1013:PCW:H2	1.46	0.78
1:A:88:PHE:CE1	5:A:1013:PCW:H2	2.20	0.76
1:A:62:VAL:HG13	1:A:98:LEU:HD11	1.67	0.75
1:A:396:LEU:HA	1:A:400:LYS:O	1.88	0.73
1:A:90:GLU:CG	1:A:91:PRO:CD	2.67	0.73
1:A:512:MET:HB2	1:A:567:ARG:HB3	1.70	0.72
1:A:260:LEU:HD11	1:A:306:ALA:HB1	1.73	0.71
1:A:886:LEU:HG	1:A:887:ASP:H	0.68	0.71
1:A:72:SER:CB	1:A:91:PRO:HG3	2.21	0.70
1:A:266:LEU:HD21	5:A:1004:PCW:C12	2.22	0.70
1:A:90:GLU:HG3	1:A:91:PRO:HD3	1.72	0.69
1:A:90:GLU:HG3	1:A:91:PRO:CD	2.23	0.69
1:A:529:ARG:NH2	6:A:1102:HOH:O	2.19	0.67
1:A:304:VAL:HG23	1:A:792:LEU:HD12	1.80	0.64
1:A:941:MET:CE	1:A:941:MET:HA	2.22	0.63
1:A:69:ALA:HA	1:A:94:ILE:HD12	1.79	0.63
1:A:66:LEU:HD13	1:A:98:LEU:CD2	2.30	0.62
1:A:851:ALA:HB1	1:A:899:MET:HG3	1.81	0.61
1:A:798:VAL:CG1	1:A:943:LEU:HD13	2.32	0.60
1:A:488:SER:HB3	1:A:491:ARG:HE	1.67	0.60
1:A:802:LEU:C	1:A:936:SER:OG	2.39	0.60
1:A:94:ILE:HA	1:A:97:ILE:HD12	1.83	0.60
1:A:491:ARG:NH1	1:A:588:GLU:OE1	2.35	0.60
1:A:63:ARG:HD3	5:A:1027:PCW:C12	2.32	0.60
1:A:266:LEU:HD13	5:A:1025:PCW:C12	2.32	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:646:GLU:OE2	1:A:651:ARG:NH1	2.35	0.59
1:A:129:VAL:HG12	1:A:151:VAL:HG22	1.84	0.59
1:A:352:LYS:NZ	1:A:353:THR:OG1	2.36	0.58
1:A:761:ILE:HG21	1:A:828:LEU:HD13	1.85	0.58
1:A:57:PHE:CE1	1:A:98:LEU:HG	2.34	0.58
1:A:941:MET:HE3	1:A:941:MET:CA	2.32	0.57
1:A:93:VAL:O	1:A:97:ILE:HG13	2.05	0.57
1:A:86:THR:HG21	1:A:956:ILE:HG22	1.85	0.57
1:A:529:ARG:HG3	1:A:594:VAL:HG22	1.86	0.57
1:A:604:ARG:HB2	1:A:607:VAL:HG23	1.86	0.56
1:A:269:VAL:O	1:A:273:LEU:HG	2.06	0.56
1:A:887:ASP:HB3	1:A:890:ILE:HD11	1.88	0.56
1:A:762:ARG:HG2	1:A:829:ILE:HD11	1.86	0.56
1:A:950:VAL:HG12	1:A:952:PRO:HD2	1.88	0.56
1:A:369:ILE:HG13	1:A:528:VAL:HG13	1.89	0.55
1:A:529:ARG:HG2	1:A:592:THR:HG22	1.89	0.55
1:A:529:ARG:NH2	1:A:568:ASP:OD2	2.41	0.54
1:A:939:LEU:O	1:A:943:LEU:HG	2.08	0.53
1:A:342:LEU:HD13	1:A:716:ILE:HG21	1.89	0.53
1:A:757:MET:HA	1:A:760:PHE:CE2	2.43	0.53
1:A:179:ILE:HG13	1:A:180:LEU:HG	1.91	0.52
1:A:844:VAL:HG22	1:A:907:ILE:HG21	1.91	0.52
1:A:760:PHE:HA	1:A:763:TYR:HB3	1.92	0.52
1:A:88:PHE:O	1:A:91:PRO:HD2	2.10	0.52
1:A:425:LEU:O	1:A:469:ASN:ND2	2.36	0.52
1:A:66:LEU:HD13	1:A:98:LEU:HD21	1.92	0.51
1:A:304:VAL:CG2	1:A:792:LEU:HD12	2.40	0.51
1:A:798:VAL:HG11	1:A:943:LEU:HD13	1.93	0.51
1:A:174:ARG:HB3	1:A:186:SER:HB3	1.92	0.51
1:A:803:PRO:N	1:A:936:SER:OG	2.44	0.51
1:A:787:LEU:HD11	1:A:848:THR:HG21	1.94	0.50
1:A:843:TYR:OH	1:A:973:ILE:O	2.25	0.50
1:A:301:ALA:HA	1:A:789:PRO:HB3	1.94	0.50
1:A:100:ALA:O	1:A:104:VAL:HG23	2.12	0.50
1:A:941:MET:CA	1:A:941:MET:CE	2.85	0.49
1:A:990:ASN:O	5:A:1010:PCW:H63	2.13	0.49
1:A:253:LEU:HD23	4:A:1003:TG1:H301	1.94	0.49
1:A:311:LEU:HD13	1:A:764:LEU:HD12	1.94	0.49
1:A:289:ILE:O	5:A:1017:PCW:O2P	2.31	0.49
1:A:971:LEU:N	1:A:971:LEU:HD23	2.28	0.48
1:A:701:THR:HG22	1:A:718:ILE:HB	1.95	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:787:LEU:CD1	1:A:848:THR:HG21	2.43	0.48
1:A:518:PRO:HB3	1:A:549:ILE:HD13	1.95	0.48
1:A:287:SER:OG	1:A:288:TRP:N	2.47	0.48
1:A:971:LEU:O	1:A:975:LEU:HB2	2.15	0.47
1:A:304:VAL:HG23	1:A:792:LEU:CD1	2.43	0.47
1:A:940:SER:HA	1:A:943:LEU:HD12	1.97	0.47
1:A:528:VAL:N	1:A:535:VAL:O	2.48	0.47
1:A:66:LEU:HD13	1:A:98:LEU:HD23	1.97	0.47
1:A:754:TYR:O	1:A:758:LYS:N	2.46	0.47
1:A:323:THR:HG23	1:A:333:VAL:HB	1.97	0.46
1:A:347:VAL:HB	1:A:698:THR:HG22	1.97	0.46
1:A:47:LYS:HB3	1:A:52:LEU:HD11	1.96	0.46
1:A:678:ARG:O	1:A:678:ARG:HG2	2.16	0.46
1:A:690:TYR:O	1:A:693:SER:OG	2.26	0.46
1:A:484:THR:HB	1:A:496:VAL:HG12	1.98	0.45
1:A:942:SER:O	1:A:946:LEU:N	2.44	0.45
1:A:567:ARG:NE	1:A:589:THR:O	2.51	0.44
1:A:347:VAL:HG11	1:A:691:LEU:HD13	1.99	0.44
1:A:150:ILE:HG22	1:A:220:LEU:HD11	2.00	0.44
1:A:529:ARG:HD3	1:A:592:THR:HG21	1.99	0.43
1:A:836:ARG:NH1	1:A:918:GLU:O	2.31	0.43
1:A:335:SER:O	1:A:338:SER:OG	2.28	0.43
1:A:351:ASP:OD2	3:A:1002:ALF:F2	2.26	0.43
1:A:903:VAL:HA	1:A:970:VAL:HG13	2.01	0.43
1:A:62:VAL:HG13	1:A:98:LEU:CD1	2.44	0.43
1:A:756:ASN:HB3	1:A:808:GLY:HA2	2.00	0.42
1:A:774:CYS:SG	1:A:848:THR:HG21	2.60	0.42
1:A:128:LYS:HG2	1:A:139:ARG:HG2	2.00	0.42
1:A:447:THR:HG22	1:A:451:LYS:HE3	2.02	0.42
1:A:196:ASP:HB3	1:A:199:ALA:HB2	2.01	0.42
1:A:272:TRP:HE3	1:A:273:LEU:HD23	1.84	0.42
1:A:527:TYR:CG	1:A:534:ARG:HD3	2.55	0.42
1:A:802:LEU:HB2	1:A:803:PRO:HD3	2.01	0.42
1:A:865:VAL:HG13	1:A:869:GLN:HG3	2.02	0.42
1:A:72:SER:C	1:A:91:PRO:HG3	2.40	0.41
1:A:879:ASP:OD1	1:A:882:HIS:HB3	2.20	0.41
1:A:795:VAL:HA	1:A:799:THR:HB	2.01	0.41
1:A:820:PRO:HA	1:A:821:PRO:HD3	1.95	0.41
1:A:95:LEU:HA	1:A:95:LEU:HD12	1.75	0.41
1:A:367:PHE:CE1	1:A:596:VAL:HB	2.56	0.41
1:A:161:ALA:HA	1:A:210:SER:HB2	2.03	0.41

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:823:SER:HA	1:A:824:PRO:HD3	1.93	0.41
1:A:926:PRO:HB3	1:A:928:TRP:CE2	2.56	0.41
1:A:769:VAL:HG12	1:A:841:GLY:HA3	2.01	0.41
1:A:932:TRP:HE1	5:A:1007:PCW:H51	1.85	0.41
1:A:319:LEU:HD23	1:A:336:LEU:HB3	2.03	0.40
1:A:57:PHE:HA	1:A:62:VAL:HG11	2.02	0.40
1:A:884:GLU:O	1:A:886:LEU:N	2.53	0.40
1:A:42:PRO:HG2	1:A:236:ARG:CZ	2.51	0.40
1:A:895:GLU:HG3	1:A:960:LYS:HD3	2.04	0.40
1:A:758:LYS:HE2	1:A:762:ARG:NH2	2.36	0.40
1:A:799:THR:HG21	1:A:905:VAL:HG22	2.02	0.40

There are no symmetry-related clashes.

5.3 Torsion angles [i](#)

5.3.1 Protein backbone [i](#)

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

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

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles
1	A	993/995 (100%)	925 (93%)	67 (7%)	1 (0%)	55 89

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	885	GLY

5.3.2 Protein sidechains [i](#)

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	840/840 (100%)	840 (100%)	0	100	100

There are no protein residues with a non-rotameric sidechain to report.

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 ⓘ

Of 37 ligands modelled in this entry, 1 is monoatomic - leaving 36 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
3	ALF	A	1002	-	0,4,4	0.00	-	0,6,6	0.00	-
4	TG1	A	1003	-	43,48,48	2.03	8 (18%)	47,72,72	3.57	12 (25%)
5	PCW	A	1004	-	21,21,53	0.67	0	26,29,61	0.98	0
5	PCW	A	1005	-	21,21,53	0.71	0	26,29,61	0.99	1 (3%)
5	PCW	A	1006	-	21,21,53	0.85	1 (4%)	26,29,61	0.99	1 (3%)
5	PCW	A	1007	-	21,21,53	0.83	1 (4%)	26,29,61	0.97	0
5	PCW	A	1008	-	21,21,53	0.85	1 (4%)	26,29,61	0.90	0
5	PCW	A	1009	-	21,21,53	0.98	0	26,29,61	0.98	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
5	PCW	A	1010	-	21,21,53	0.86	0	26,29,61	0.98	0
5	PCW	A	1011	-	21,21,53	0.70	0	26,29,61	0.92	0
5	PCW	A	1012	-	21,21,53	0.77	0	26,29,61	0.95	0
5	PCW	A	1013	-	21,21,53	0.86	1 (4%)	26,29,61	0.92	0
5	PCW	A	1014	-	21,21,53	0.91	0	26,29,61	0.95	0
5	PCW	A	1015	-	21,21,53	0.85	0	26,29,61	0.88	0
5	PCW	A	1016	-	21,21,53	0.84	0	26,29,61	1.04	1 (3%)
5	PCW	A	1017	-	21,21,53	0.86	0	26,29,61	0.95	0
5	PCW	A	1018	-	21,21,53	0.79	0	26,29,61	0.96	0
5	PCW	A	1019	-	21,21,53	0.91	0	26,29,61	0.92	0
5	PCW	A	1020	-	21,21,53	0.72	0	26,29,61	0.94	0
5	PCW	A	1021	-	21,21,53	0.66	0	26,29,61	0.89	0
5	PCW	A	1022	-	21,21,53	0.99	0	26,29,61	1.03	1 (3%)
5	PCW	A	1023	-	21,21,53	0.90	0	26,29,61	1.22	1 (3%)
5	PCW	A	1024	-	21,21,53	0.75	0	26,29,61	0.90	0
5	PCW	A	1025	-	21,21,53	0.69	0	26,29,61	0.93	0
5	PCW	A	1026	-	21,21,53	0.79	0	26,29,61	0.93	0
5	PCW	A	1027	-	21,21,53	0.75	0	26,29,61	0.88	0
5	PCW	A	1028	-	21,21,53	0.67	0	26,29,61	0.95	0
5	PCW	A	1029	-	21,21,53	0.67	0	26,29,61	0.89	0
5	PCW	A	1030	-	21,21,53	1.04	2 (9%)	26,29,61	0.96	0
5	PCW	A	1031	-	21,21,53	0.72	0	26,29,61	0.90	0
5	PCW	A	1032	-	21,21,53	0.93	0	26,29,61	0.97	0
5	PCW	A	1033	-	21,21,53	0.76	0	26,29,61	0.92	0
5	PCW	A	1034	-	21,21,53	0.95	1 (4%)	26,29,61	0.95	0
5	PCW	A	1035	-	21,21,53	0.88	0	26,29,61	0.97	0
5	PCW	A	1036	-	21,21,53	1.05	1 (4%)	26,29,61	0.97	0
5	PCW	A	1037	-	21,21,53	0.99	0	26,29,61	2.45	2 (7%)

In the following table, the Chirals column lists the number of chiral outliers, the number of chiral centers analysed, the number of these observed in the model and the number defined in the chemical component dictionary. Similar counts are reported in the Torsion and Rings columns. '-' means no outliers of that kind were identified.

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	ALF	A	1002	-	-	0/0/0/0	0/0/0/0
4	TG1	A	1003	-	-	0/33/99/99	0/3/3/3
5	PCW	A	1004	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1005	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1006	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1007	-	-	0/23/23/57	0/0/0/0

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PCW	A	1008	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1009	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1010	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1011	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1012	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1013	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1014	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1015	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1016	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1017	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1018	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1019	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1020	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1021	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1022	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1023	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1024	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1025	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1026	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1027	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1028	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1029	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1030	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1031	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1032	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1033	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1034	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1035	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1036	-	-	0/23/23/57	0/0/0/0
5	PCW	A	1037	-	-	0/23/23/57	0/0/0/0

All (16) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1003	TG1	O7-C8	-2.20	1.42	1.46
5	A	1007	PCW	C3-C2	2.07	1.56	1.50
5	A	1030	PCW	P-O2P	2.10	1.58	1.50
5	A	1030	PCW	C3-C2	2.13	1.56	1.50
5	A	1013	PCW	C3-C2	2.13	1.56	1.50
5	A	1008	PCW	C5-C4	2.13	1.58	1.51
5	A	1006	PCW	C3-C2	2.14	1.56	1.50
5	A	1034	PCW	C3-C2	2.15	1.56	1.50

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	A	1003	TG1	O3-C21	2.19	1.39	1.34
5	A	1036	PCW	C3-C2	2.19	1.56	1.50
4	A	1003	TG1	C9-C8	3.05	1.55	1.52
4	A	1003	TG1	C24-C22	3.44	1.53	1.30
4	A	1003	TG1	C1-C5	3.88	1.57	1.51
4	A	1003	TG1	O5-C12	4.19	1.42	1.35
4	A	1003	TG1	C11-C7	4.86	1.61	1.55
4	A	1003	TG1	O12-C12	7.24	1.37	1.20

All (19) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	A	1003	TG1	O12-C12-C11	-17.29	111.82	128.28
5	A	1037	PCW	O11-C11-C12	-11.37	83.02	124.82
4	A	1003	TG1	O5-C12-O12	-11.29	106.05	121.63
4	A	1003	TG1	O9-C32-C33	-4.40	101.88	110.73
4	A	1003	TG1	C26-C4-C5	-4.00	119.40	129.77
4	A	1003	TG1	C23-C22-C24	-3.92	106.20	123.38
4	A	1003	TG1	O5-C12-C11	-3.47	105.09	110.15
4	A	1003	TG1	O3-C21-O4	-3.23	116.86	123.31
5	A	1037	PCW	O3-C11-C12	-2.75	100.06	112.44
4	A	1003	TG1	C23-C22-C21	-2.75	108.91	116.01
4	A	1003	TG1	O9-C32-O10	-2.64	118.32	123.56
5	A	1005	PCW	C2-O2-C31	2.03	121.86	117.94
4	A	1003	TG1	O11-C11-C12	2.21	112.46	105.94
5	A	1006	PCW	C2-O2-C31	2.22	122.22	117.94
4	A	1003	TG1	C10-C9-C8	2.33	125.58	117.21
5	A	1023	PCW	C8-N-C7	2.33	114.89	108.98
5	A	1022	PCW	C2-O2-C31	2.56	122.88	117.94
5	A	1016	PCW	C2-O2-C31	2.81	123.38	117.94
4	A	1003	TG1	C10-O9-C32	6.72	138.78	121.83

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 12 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	A	1002	ALF	1	0
4	A	1003	TG1	2	0
5	A	1004	PCW	1	0

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Mol	Chain	Res	Type	Clashes	Symm-Clashes
5	A	1007	PCW	1	0
5	A	1010	PCW	1	0
5	A	1013	PCW	2	0
5	A	1017	PCW	2	0
5	A	1025	PCW	1	0
5	A	1027	PCW	1	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	994/995 (99%)	0.05	33 (3%) 47 31	62, 114, 245, 480	0

All (33) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	881	PRO	11.0
1	A	243	GLU	8.6
1	A	96	LEU	6.4
1	A	81	GLY	4.9
1	A	92	PHE	4.9
1	A	974	SER	4.4
1	A	852	ALA	4.1
1	A	82	GLU	3.9
1	A	776	PHE	3.8
1	A	73	PHE	3.8
1	A	939	LEU	3.8
1	A	95	LEU	3.8
1	A	905	VAL	3.7
1	A	65	LEU	3.4
1	A	70	CYS	3.4
1	A	848	THR	3.4
1	A	967	TRP	3.3
1	A	994	GLY	2.9
1	A	69	ALA	2.9
1	A	57	PHE	2.9
1	A	844	VAL	2.8
1	A	980	LEU	2.6
1	A	883	PHE	2.5
1	A	98	LEU	2.4
1	A	269	VAL	2.4
1	A	787	LEU	2.3
1	A	273	LEU	2.2

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Mol	Chain	Res	Type	RSRZ
1	A	71	ILE	2.2
1	A	867	TYR	2.2
1	A	88	PHE	2.2
1	A	66	LEU	2.1
1	A	712	LYS	2.1
1	A	64	ILE	2.1

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(Å ²)	Q<0.9
5	PCW	A	1017	22/54	0.13	0.92	5.07	274,274,274,274	0
5	PCW	A	1029	22/54	0.70	0.45	4.63	257,257,257,257	0
5	PCW	A	1036	22/54	0.42	0.50	4.39	250,250,250,250	0
5	PCW	A	1014	22/54	0.72	0.36	1.29	283,283,283,283	0
4	TG1	A	1003	46/46	0.90	0.39	1.02	199,203,205,206	0
5	PCW	A	1023	22/54	0.48	0.51	0.86	260,260,260,260	0
3	ALF	A	1002	5/5	0.97	0.19	-0.40	58,61,66,79	0
2	MG	A	1001	1/1	0.96	0.16	-1.34	67,67,67,67	0
5	PCW	A	1033	22/54	0.27	1.25	-	256,256,256,256	0
5	PCW	A	1021	22/54	0.74	0.25	-	255,255,255,255	0
5	PCW	A	1028	22/54	0.62	0.35	-	268,268,268,268	0
5	PCW	A	1006	22/54	0.29	1.16	-	297,297,297,297	0
5	PCW	A	1030	22/54	0.18	0.89	-	285,285,285,285	0
5	PCW	A	1032	22/54	0.43	0.84	-	266,266,266,266	0
5	PCW	A	1027	22/54	0.32	0.82	-	296,296,296,296	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	LLDF	B-factors(\AA^2)	Q<0.9
5	PCW	A	1026	22/54	0.52	0.42	-	220,220,220,220	0
5	PCW	A	1018	22/54	0.67	0.55	-	300,300,300,300	0
5	PCW	A	1022	22/54	0.37	0.60	-	273,273,273,273	0
5	PCW	A	1016	22/54	0.11	0.94	-	315,315,315,315	0
5	PCW	A	1012	22/54	0.51	0.38	-	274,274,274,274	0
5	PCW	A	1019	22/54	0.47	0.38	-	264,264,264,264	0
5	PCW	A	1013	22/54	0.32	0.40	-	272,272,272,272	0
5	PCW	A	1034	22/54	0.33	1.54	-	262,262,262,262	0
5	PCW	A	1011	22/54	0.53	0.43	-	253,253,253,253	0
5	PCW	A	1010	22/54	0.40	0.86	-	272,272,272,272	0
5	PCW	A	1020	22/54	0.62	0.25	-	268,268,268,268	0
5	PCW	A	1015	22/54	0.56	0.35	-	287,287,287,287	0
5	PCW	A	1035	22/54	0.50	1.01	-	241,241,241,241	0
5	PCW	A	1037	22/54	-0.09	1.72	-	292,292,292,292	0
5	PCW	A	1004	22/54	0.46	0.58	-	281,281,281,281	0
5	PCW	A	1025	22/54	0.68	0.42	-	275,275,275,275	0
5	PCW	A	1009	22/54	0.48	0.63	-	278,278,278,278	0
5	PCW	A	1007	22/54	0.59	0.37	-	259,259,259,259	0
5	PCW	A	1008	22/54	0.44	0.32	-	279,279,279,279	0
5	PCW	A	1024	22/54	0.21	0.63	-	263,263,263,263	0
5	PCW	A	1005	22/54	0.58	0.45	-	260,260,260,260	0
5	PCW	A	1031	22/54	0.44	0.53	-	255,255,255,255	0

6.5 Other polymers

There are no such residues in this entry.