



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 10:11 AM UTC

PDB ID : 1XSI / pdb_00001xsi
Title : Structure of a Family 31 alpha glycosidase
Authors : Lovering, A.L.; Lee, S.S.; Kim, Y.W.; Withers, S.G.; Strynadka, N.C.
Deposited on : 2004-10-19
Resolution : 2.20 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 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

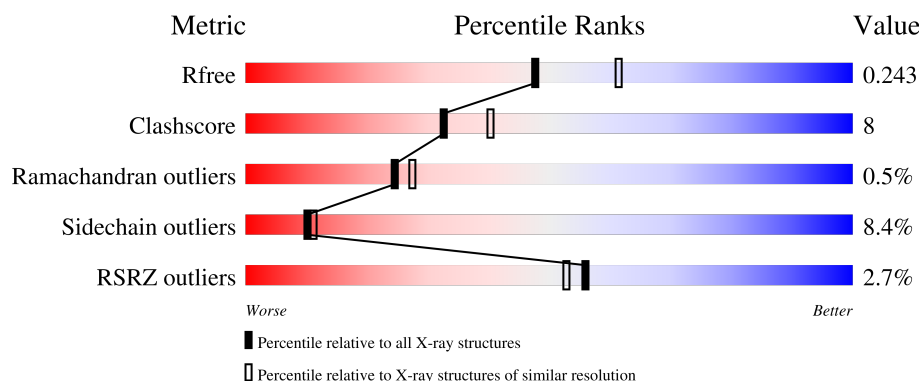
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	180053	6164 (2.20-2.20)
Clashscore	190562	6851 (2.20-2.20)
Ramachandran outliers	187476	6768 (2.20-2.20)
Sidechain outliers	187428	6769 (2.20-2.20)
RSRZ outliers	180081	6166 (2.20-2.20)

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	778	% 82% 14% ..
1	B	778	3% 77% 19% ..
1	C	778	% 79% 16% ..
1	D	778	6% 77% 18% ..
1	E	778	3% 76% 20% ..

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Mol	Chain	Length	Quality of chain
1	F	778	% 78%18% . ..

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	SO4	F	3009	-	-	X	-

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 38490 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 Putative family 31 glucosidase yicI.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	773	Total	C	N	O	S	0	0	0
			6226	3978	1069	1147	32			
1	B	773	Total	C	N	O	S	0	0	0
			6226	3978	1069	1147	32			
1	C	773	Total	C	N	O	S	0	0	0
			6226	3978	1069	1147	32			
1	D	773	Total	C	N	O	S	0	0	0
			6226	3978	1069	1147	32			
1	E	773	Total	C	N	O	S	0	0	0
			6226	3978	1069	1147	32			
1	F	773	Total	C	N	O	S	0	0	0
			6226	3978	1069	1147	32			

There are 36 discrepancies between the modelled and reference sequences:

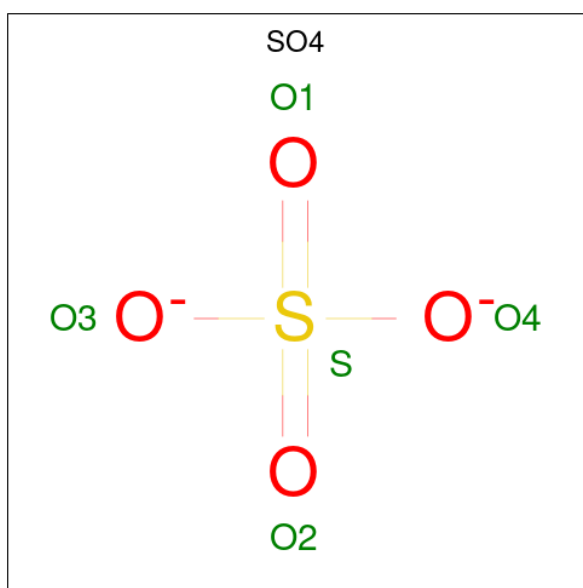
Chain	Residue	Modelled	Actual	Comment	Reference
A	773	HIS	-	expression tag	UNP P31434
A	774	HIS	-	expression tag	UNP P31434
A	775	HIS	-	expression tag	UNP P31434
A	776	HIS	-	expression tag	UNP P31434
A	777	HIS	-	expression tag	UNP P31434
A	778	HIS	-	expression tag	UNP P31434
B	773	HIS	-	expression tag	UNP P31434
B	774	HIS	-	expression tag	UNP P31434
B	775	HIS	-	expression tag	UNP P31434
B	776	HIS	-	expression tag	UNP P31434
B	777	HIS	-	expression tag	UNP P31434
B	778	HIS	-	expression tag	UNP P31434
C	773	HIS	-	expression tag	UNP P31434
C	774	HIS	-	expression tag	UNP P31434
C	775	HIS	-	expression tag	UNP P31434
C	776	HIS	-	expression tag	UNP P31434
C	777	HIS	-	expression tag	UNP P31434

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Chain	Residue	Modelled	Actual	Comment	Reference
C	778	HIS	-	expression tag	UNP P31434
D	773	HIS	-	expression tag	UNP P31434
D	774	HIS	-	expression tag	UNP P31434
D	775	HIS	-	expression tag	UNP P31434
D	776	HIS	-	expression tag	UNP P31434
D	777	HIS	-	expression tag	UNP P31434
D	778	HIS	-	expression tag	UNP P31434
E	773	HIS	-	expression tag	UNP P31434
E	774	HIS	-	expression tag	UNP P31434
E	775	HIS	-	expression tag	UNP P31434
E	776	HIS	-	expression tag	UNP P31434
E	777	HIS	-	expression tag	UNP P31434
E	778	HIS	-	expression tag	UNP P31434
F	773	HIS	-	expression tag	UNP P31434
F	774	HIS	-	expression tag	UNP P31434
F	775	HIS	-	expression tag	UNP P31434
F	776	HIS	-	expression tag	UNP P31434
F	777	HIS	-	expression tag	UNP P31434
F	778	HIS	-	expression tag	UNP P31434

- Molecule 2 is SULFATE ION (CCD ID: SO4) (formula: O₄S).



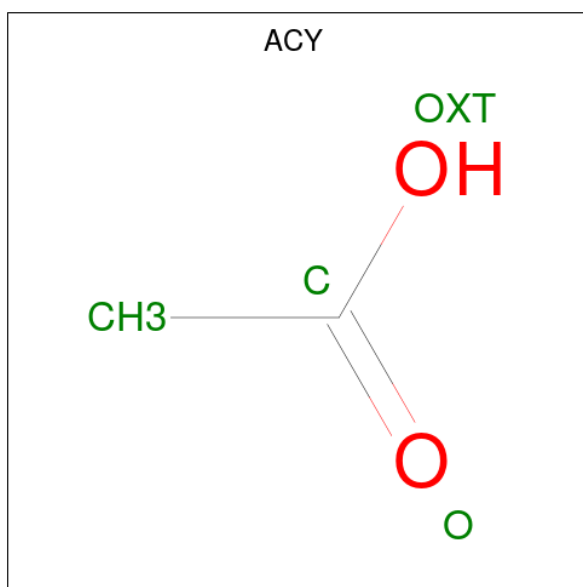
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

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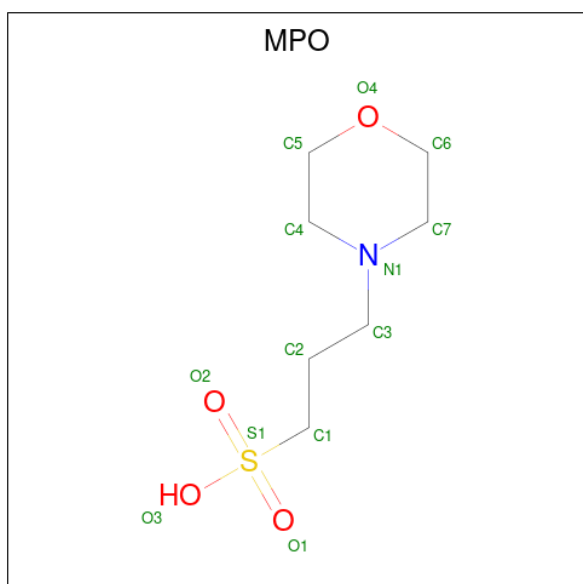
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
2	A	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	B	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	C	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	D	1	Total	O	S	0	0
			5	4	1		
2	E	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		
2	F	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is ACETIC ACID (CCD ID: ACY) (formula: C₂H₄O₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			4	2	2		
3	E	1	Total	C	O	0	0
			4	2	2		
3	F	1	Total	C	O	0	0
			4	2	2		

- Molecule 4 is 3[N-MORPHOLINO]PROPANE SULFONIC ACID (CCD ID: MPO) (formula: $C_7H_{15}NO_4S$).



Mol	Chain	Residues	Atoms					ZeroOcc	AltConf
4	B	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	C	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	D	1	Total	C	N	O	S	0	0
			13	7	1	4	1		
4	E	1	Total	C	N	O	S	0	0
			13	7	1	4	1		

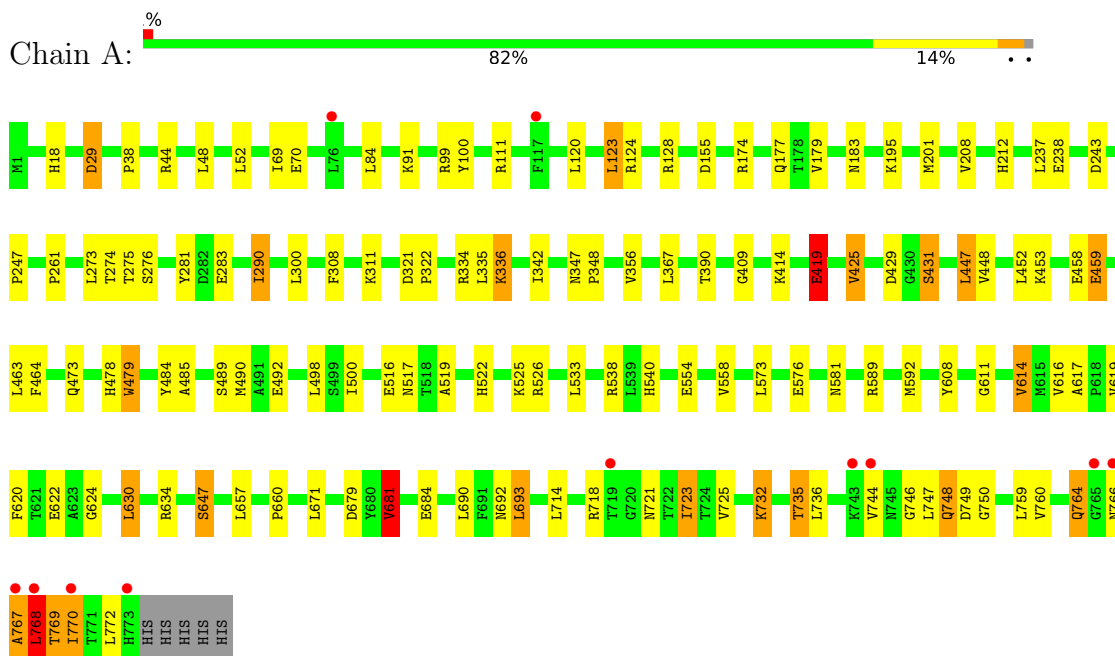
- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	170	Total	O	0	0
			170	170		
5	B	140	Total	O	0	0
			140	140		
5	C	189	Total	O	0	0
			189	189		
5	D	162	Total	O	0	0
			162	162		
5	E	152	Total	O	0	0
			152	152		
5	F	167	Total	O	0	0
			167	167		

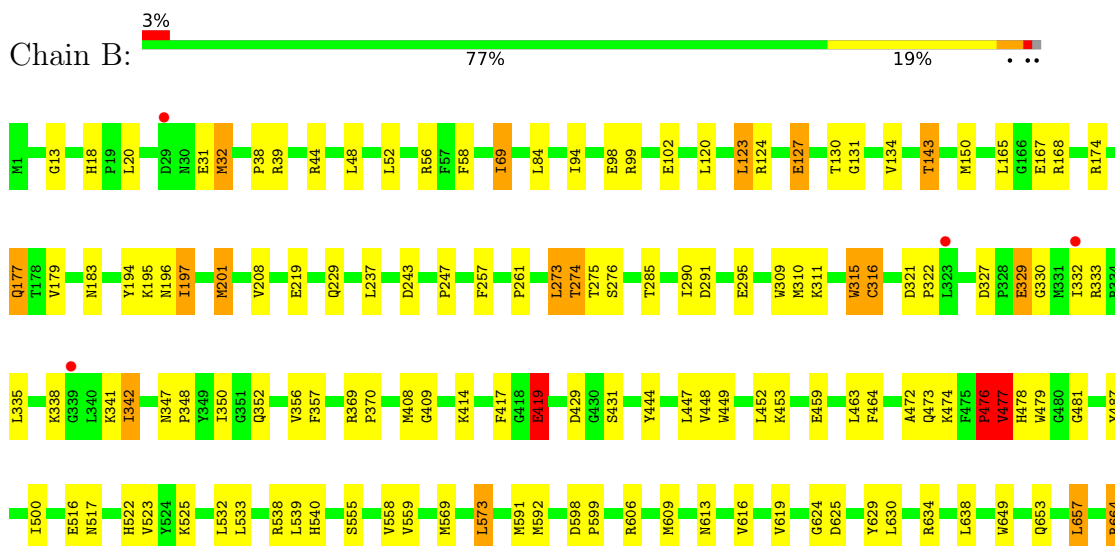
3 Residue-property plots

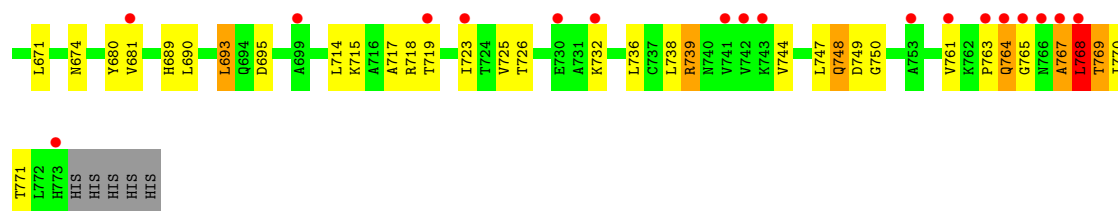
These plots are drawn for all protein, RNA, DNA and oligosaccharide chains in the entry. The first graphic for a chain summarises the proportions of the various outlier classes displayed in the second graphic. The second graphic shows the sequence view annotated by issues in geometry and electron density. 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: Putative family 31 glucosidase yicI

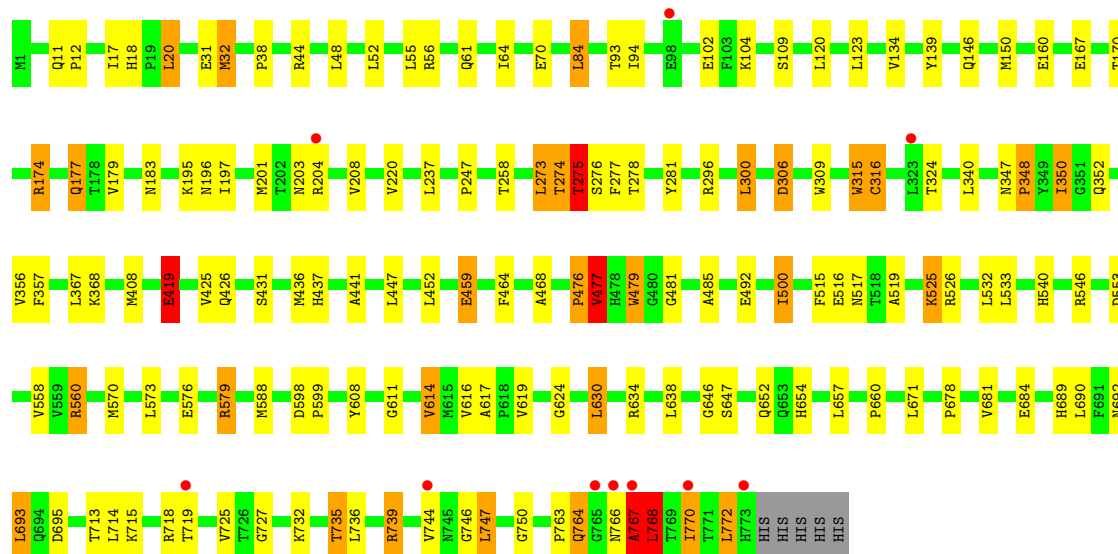
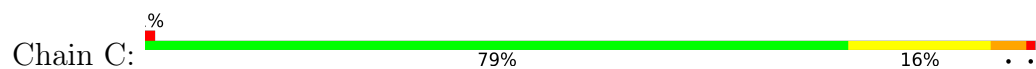


• Molecule 1: Putative family 31 glucosidase yicI

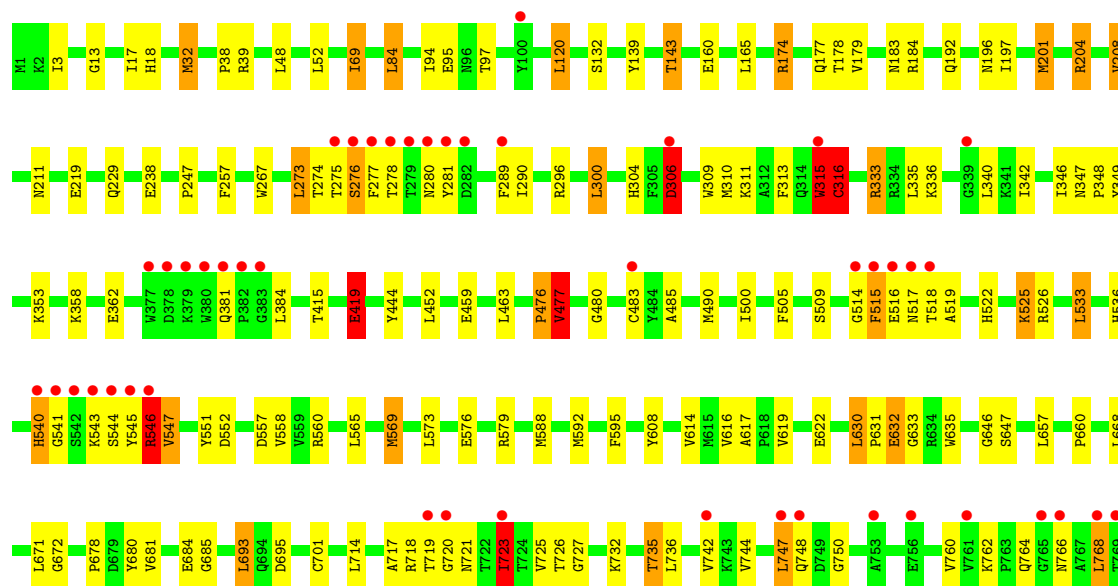
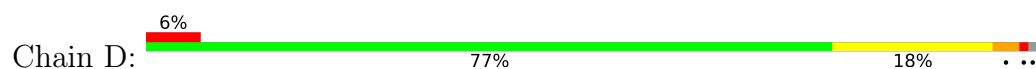




• Molecule 1: Putative family 31 glucosidase yicI

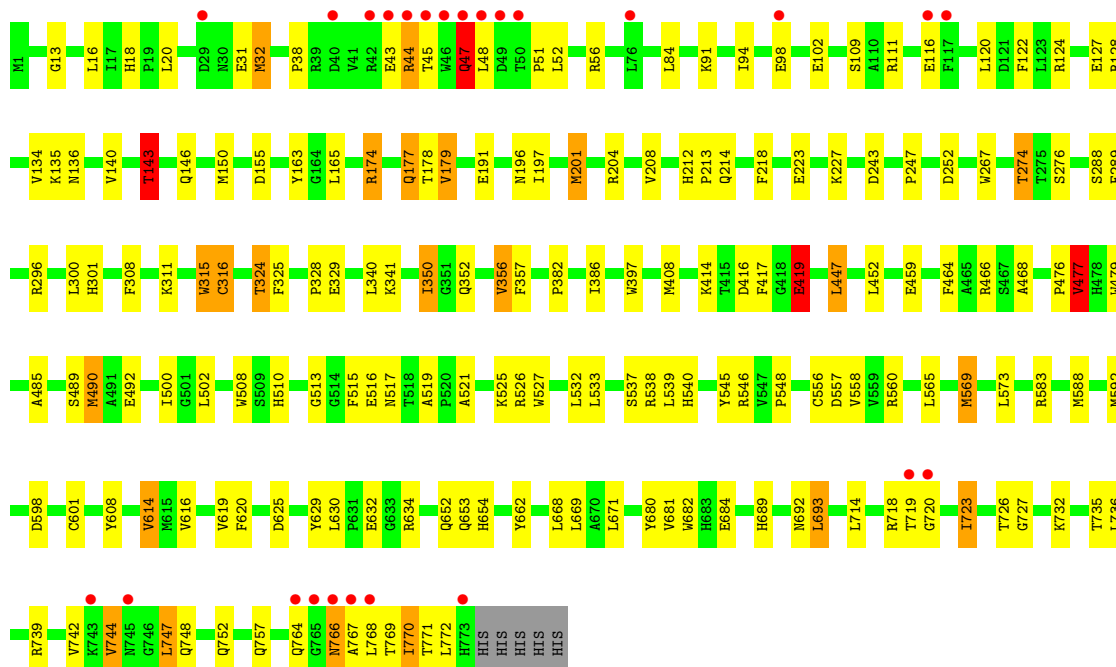
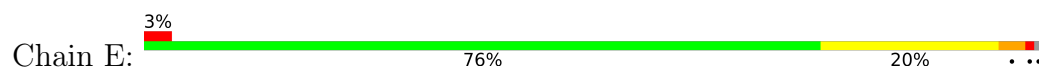


• Molecule 1: Putative family 31 glucosidase yicI

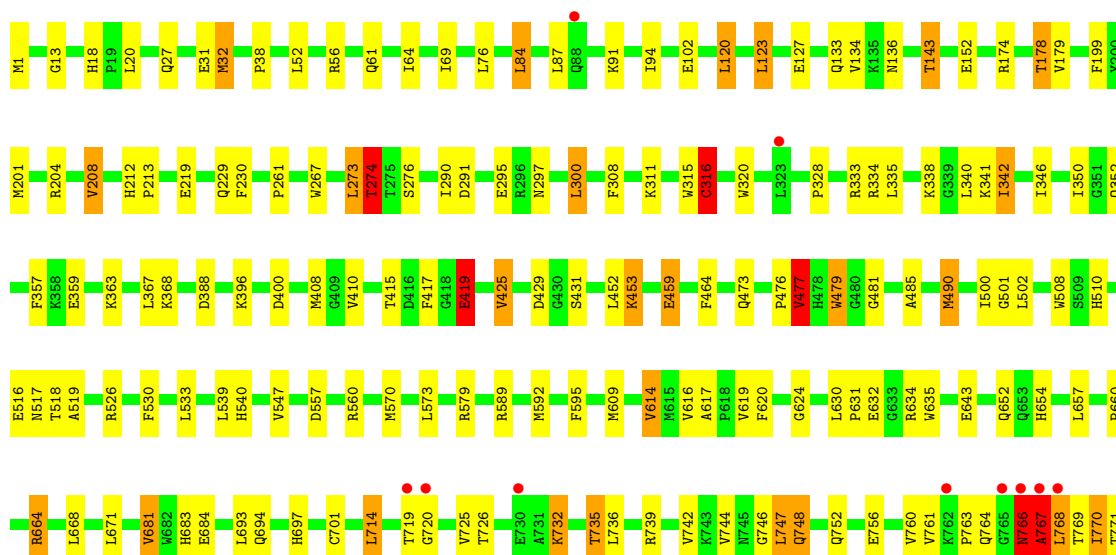
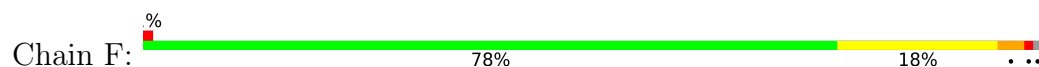




- Molecule 1: Putative family 31 glucosidase yicI



- Molecule 1: Putative family 31 glucosidase yicI



L772	HIS
H773	HIS
	HIS
	HIS
	HIS
	HIS

4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	161.69Å 174.93Å 209.51Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	30.00 – 2.20 30.00 – 2.20	Depositor EDS
% Data completeness (in resolution range)	98.9 (30.00-2.20) 98.7 (30.00-2.20)	Depositor EDS
R_{merge}	0.07	Depositor
R_{sym}	0.07	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.16 (at 2.20Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.200 , 0.239 0.208 , 0.243	Depositor DCC
R_{free} test set	14939 reflections (5.05%)	wwPDB-VP
Wilson B-factor (Å ²)	31.3	Xtriage
Anisotropy	0.714	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 23.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.34$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	38490	wwPDB-VP
Average B, all atoms (Å ²)	34.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.55% 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: SO4, MPO, ACY

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	1.05	2/6409 (0.0%)	1.12	11/8711 (0.1%)
1	B	1.01	7/6409 (0.1%)	1.10	11/8711 (0.1%)
1	C	1.05	3/6409 (0.0%)	1.13	21/8711 (0.2%)
1	D	1.06	9/6409 (0.1%)	1.14	21/8711 (0.2%)
1	E	1.02	6/6409 (0.1%)	1.11	22/8711 (0.3%)
1	F	1.09	9/6409 (0.1%)	1.14	25/8711 (0.3%)
All	All	1.05	36/38454 (0.1%)	1.12	111/52266 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand. A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	A	0	1
1	B	1	1
1	C	2	1
1	D	1	2
1	E	2	1
1	F	2	0
All	All	8	6

The worst 5 of 36 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	32	MET	SD-CE	-13.99	1.44	1.79
1	F	32	MET	SD-CE	-10.56	1.53	1.79
1	D	32	MET	SD-CE	-10.52	1.53	1.79
1	D	490	MET	SD-CE	-9.41	1.56	1.79
1	D	306	ASP	CB-CG	8.19	1.72	1.52

The worst 5 of 111 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	767	ALA	N-CA-C	-13.27	97.71	114.56
1	C	315	TRP	CA-C-N	11.11	138.74	122.74
1	C	315	TRP	C-N-CA	11.11	138.74	122.74
1	E	316	CYS	N-CA-C	10.79	126.31	111.74
1	E	315	TRP	CA-C-N	10.47	136.96	122.19

5 of 8 chirality outliers are listed below:

Mol	Chain	Res	Type	Atom
1	B	477	VAL	CA
1	C	316	CYS	CA
1	C	477	VAL	CA
1	D	477	VAL	CA
1	E	316	CYS	CA

5 of 6 planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	766	ASN	Peptide
1	B	476	PRO	Peptide
1	C	476	PRO	Peptide
1	D	315	TRP	Peptide
1	D	476	PRO	Peptide

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	6226	0	5934	80	0
1	B	6226	0	5934	94	0
1	C	6226	0	5934	113	0
1	D	6226	0	5934	99	0
1	E	6226	0	5934	103	0
1	F	6226	0	5934	95	0
2	A	15	0	0	0	0
2	B	25	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
2	C	10	0	0	0	0
2	D	10	0	0	0	0
2	E	5	0	0	1	0
2	F	25	0	0	4	0
3	A	4	0	3	0	0
3	E	4	0	3	0	0
3	F	4	0	3	0	0
4	B	13	0	15	0	0
4	C	13	0	15	0	0
4	D	13	0	15	0	0
4	E	13	0	15	0	0
5	A	170	0	0	2	0
5	B	140	0	0	4	0
5	C	189	0	0	1	0
5	D	162	0	0	2	0
5	E	152	0	0	7	0
5	F	167	0	0	2	0
All	All	38490	0	35673	581	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.

The worst 5 of 581 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:F:274:THR:HG22	1:F:276:SER:H	0.98	1.10
1:B:274:THR:HG22	1:B:276:SER:H	1.13	1.10
1:D:32:MET:HE2	1:D:94:ILE:HG23	1.23	1.08
1:E:274:THR:HG21	1:E:540:HIS:ND1	1.68	1.08
1:C:93:THR:HG22	1:C:104:LYS:HB3	1.36	1.07

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	771/778 (99%)	744 (96%)	25 (3%)	2 (0%)	36	42
1	B	771/778 (99%)	731 (95%)	37 (5%)	3 (0%)	30	34
1	C	771/778 (99%)	740 (96%)	27 (4%)	4 (0%)	24	27
1	D	771/778 (99%)	733 (95%)	32 (4%)	6 (1%)	16	16
1	E	771/778 (99%)	738 (96%)	29 (4%)	4 (0%)	24	27
1	F	771/778 (99%)	739 (96%)	26 (3%)	6 (1%)	16	16
All	All	4626/4668 (99%)	4425 (96%)	176 (4%)	25 (0%)	24	27

5 of 25 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	768	LEU
1	B	767	ALA
1	C	766	ASN
1	C	768	LEU
1	E	768	LEU

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	659/665 (99%)	610 (93%)	49 (7%)	13	14
1	B	659/665 (99%)	605 (92%)	54 (8%)	10	12
1	C	659/665 (99%)	610 (93%)	49 (7%)	13	14
1	D	659/665 (99%)	599 (91%)	60 (9%)	9	9
1	E	659/665 (99%)	597 (91%)	62 (9%)	8	9
1	F	659/665 (99%)	600 (91%)	59 (9%)	9	9
All	All	3954/3990 (99%)	3621 (92%)	333 (8%)	10	11

5 of 333 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	208	VAL
1	F	179	VAL
1	E	356	VAL
1	E	719	THR
1	F	425	VAL

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 84 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	47	GLN
1	F	73	GLN
1	E	133	GLN
1	E	697	HIS
1	F	177	GLN

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

25 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
3	ACY	A	2003	-	3,3,3	0.96	0	3,3,3	1.09	0
2	SO4	F	3005	-	4,4,4	0.57	0	6,6,6	0.89	0
2	SO4	B	3016	-	4,4,4	0.35	0	6,6,6	0.32	0
2	SO4	F	3003	-	4,4,4	0.29	0	6,6,6	0.55	0
3	ACY	E	2001	-	3,3,3	1.22	0	3,3,3	0.66	0
2	SO4	C	3012	-	4,4,4	0.38	0	6,6,6	0.63	0
4	MPO	B	1001	-	13,13,13	1.82	2 (15%)	17,17,17	1.48	2 (11%)
2	SO4	B	3010	-	4,4,4	0.30	0	6,6,6	0.43	0
2	SO4	F	3002	-	4,4,4	0.24	0	6,6,6	0.41	0
2	SO4	F	3001	-	4,4,4	0.36	0	6,6,6	0.21	0
2	SO4	B	3008	-	4,4,4	0.29	0	6,6,6	0.39	0
3	ACY	F	2002	-	3,3,3	0.90	0	3,3,3	1.23	0
2	SO4	D	3011	-	4,4,4	0.30	0	6,6,6	0.41	0
2	SO4	A	3018	-	4,4,4	0.30	0	6,6,6	0.11	0
2	SO4	E	3006	-	4,4,4	0.22	0	6,6,6	0.45	0
2	SO4	D	3004	-	4,4,4	0.39	0	6,6,6	0.42	0
2	SO4	F	3009	-	4,4,4	0.41	0	6,6,6	0.43	0
2	SO4	C	3007	-	4,4,4	0.18	0	6,6,6	0.15	0
4	MPO	E	1004	-	13,13,13	1.77	2 (15%)	17,17,17	1.10	1 (5%)
2	SO4	B	3015	-	4,4,4	0.36	0	6,6,6	0.22	0
2	SO4	A	3017	-	4,4,4	0.27	0	6,6,6	0.44	0
4	MPO	C	1002	-	13,13,13	1.41	1 (7%)	17,17,17	1.28	2 (11%)
2	SO4	A	3014	-	4,4,4	0.27	0	6,6,6	0.33	0
2	SO4	B	3013	-	4,4,4	0.30	0	6,6,6	0.36	0
4	MPO	D	1003	-	13,13,13	1.28	1 (7%)	17,17,17	1.42	3 (17%)

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	MPO	D	1003	-	-	4/7/15/15	0/1/1/1
4	MPO	B	1001	-	-	0/7/15/15	0/1/1/1
4	MPO	E	1004	-	-	1/7/15/15	0/1/1/1
4	MPO	C	1002	-	-	0/7/15/15	0/1/1/1

The worst 5 of 6 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	1001	MPO	C1-S1	5.42	1.85	1.77

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Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	E	1004	MPO	C1-S1	4.50	1.83	1.77
4	C	1002	MPO	C1-S1	4.16	1.83	1.77
4	D	1003	MPO	C1-S1	3.59	1.82	1.77
4	B	1001	MPO	O2-S1	2.25	1.51	1.45

The worst 5 of 8 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
4	B	1001	MPO	O1-S1-C1	3.15	111.49	106.73
4	D	1003	MPO	O4-C6-C7	-3.10	105.10	111.77
4	E	1004	MPO	O2-S1-C1	2.38	110.33	106.73
4	D	1003	MPO	C7-N1-C4	2.37	113.95	108.84
4	C	1002	MPO	C5-C4-N1	-2.26	106.69	110.12

There are no chirality outliers.

All (5) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	D	1003	MPO	C2-C3-N1-C7
4	D	1003	MPO	C2-C3-N1-C4
4	D	1003	MPO	C2-C1-S1-O2
4	D	1003	MPO	C2-C1-S1-O3
4	E	1004	MPO	C1-C2-C3-N1

There are no ring outliers.

3 monomers are involved in 5 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	F	3005	SO4	1	0
2	E	3006	SO4	1	0
2	F	3009	SO4	3	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 [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	773/778 (99%)	-0.25	11 (1%) 73 71	18, 29, 47, 71	0
1	B	773/778 (99%)	0.12	22 (2%) 55 52	23, 36, 60, 81	0
1	C	773/778 (99%)	-0.21	10 (1%) 75 73	20, 30, 47, 75	0
1	D	773/778 (99%)	0.07	48 (6%) 26 23	19, 32, 64, 78	0
1	E	773/778 (99%)	-0.07	25 (3%) 50 47	20, 33, 57, 89	0
1	F	773/778 (99%)	-0.16	11 (1%) 73 71	21, 31, 50, 69	0
All	All	4638/4668 (99%)	-0.08	127 (2%) 56 53	18, 32, 55, 89	0

The worst 5 of 127 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	278	THR	7.0
1	D	545	TYR	5.9
1	B	766	ASN	5.7
1	D	275	THR	5.7
1	F	773	HIS	5.7

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 oligosaccharides 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. 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	SO4	B	3015	5/5	0.65	0.13	79,81,82,82	0
2	SO4	A	3014	5/5	0.70	0.13	78,79,80,82	0
2	SO4	B	3016	5/5	0.71	0.15	72,72,73,75	0
2	SO4	D	3011	5/5	0.74	0.12	86,87,88,88	0
2	SO4	A	3018	5/5	0.75	0.12	84,85,85,86	0
3	ACY	A	2003	4/4	0.75	0.18	40,40,42,42	0
2	SO4	F	3009	5/5	0.76	0.16	64,66,68,69	0
3	ACY	F	2002	4/4	0.76	0.19	46,46,47,48	0
2	SO4	B	3013	5/5	0.77	0.11	77,78,79,80	0
3	ACY	E	2001	4/4	0.79	0.15	38,39,41,41	0
2	SO4	B	3010	5/5	0.82	0.12	76,77,77,78	0
2	SO4	C	3012	5/5	0.84	0.15	66,66,69,70	0
2	SO4	F	3005	5/5	0.85	0.16	50,53,56,56	0
2	SO4	F	3001	5/5	0.86	0.16	65,66,67,68	0
2	SO4	A	3017	5/5	0.86	0.13	73,75,77,78	0
2	SO4	F	3003	5/5	0.89	0.17	57,57,59,60	0
2	SO4	B	3008	5/5	0.89	0.16	59,61,62,63	0
4	MPO	B	1001	13/13	0.89	0.15	46,54,64,66	0
2	SO4	D	3004	5/5	0.90	0.12	65,65,66,67	0
4	MPO	E	1004	13/13	0.90	0.14	51,53,58,58	0
2	SO4	F	3002	5/5	0.91	0.12	60,63,65,66	0
4	MPO	C	1002	13/13	0.92	0.11	43,48,53,55	0
4	MPO	D	1003	13/13	0.93	0.11	43,52,58,58	0
2	SO4	C	3007	5/5	0.94	0.15	61,62,63,63	0
2	SO4	E	3006	5/5	0.94	0.15	56,58,59,62	0

6.5 Other polymers [i](#)

There are no such residues in this entry.