



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 6, 2026 – 05:14 AM UTC

PDB ID : 5NDX / pdb_00005ndx
Title : The bacterial orthologue of Human α -L-iduronidase does not need N-glycan post-translational modifications to be catalytically competent: Crystallography and QM/MM insights into Mucopolysaccharidosis I
Authors : Raich, L.; Valero-Gonzalez, J.; Castro-Lopez, J.; Millan, C.; Jimenez-Garcia, M.J.; Nieto, P.; Uson, I.; Hurtado-Guerrero, R.; Rovira, C.
Deposited on : 2017-03-09
Resolution : 2.20 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

<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](#) ①) 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
Buster-report	:	wwPDB partial adaption of 1.1.7 (2018)
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

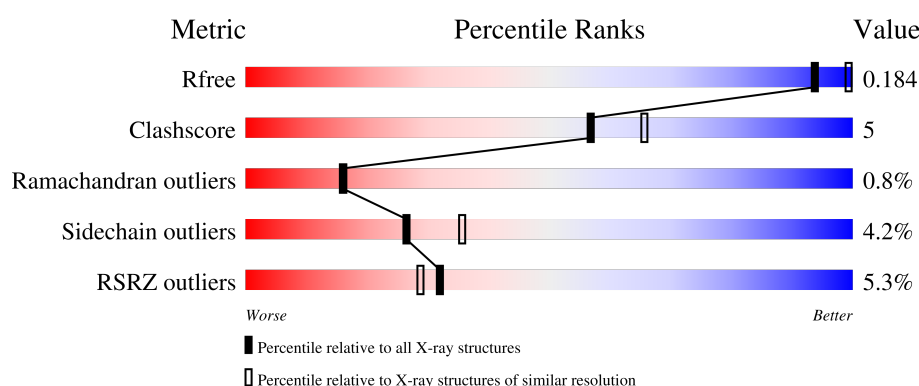
1 Overall quality at a glance

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	621	5% 84% 11% ..

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	A	702	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 5235 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.

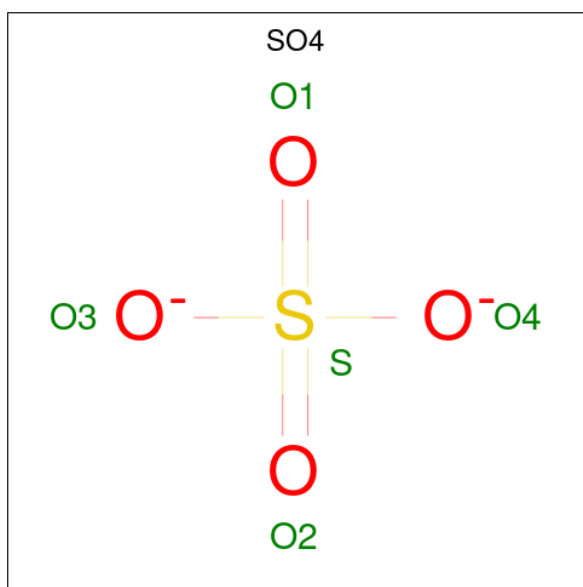
- Molecule 1 is a protein called Glycosyl hydrolase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	606	Total	C	N	O	S	0	5	0
			4746	3017	825	880	24			

There are 12 discrepancies between the modelled and reference sequences:

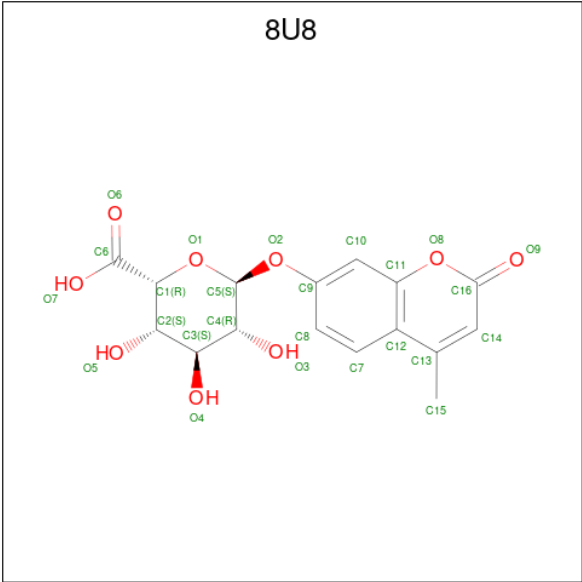
Chain	Residue	Modelled	Actual	Comment	Reference
A	65	LEU	VAL	conflict	UNP A0A1B8R7L2
A	146	GLN	GLU	engineered mutation	UNP A0A1B8R7L2
A	312	SER	ASN	conflict	UNP A0A1B8R7L2
A	355	THR	ALA	conflict	UNP A0A1B8R7L2
A	407	VAL	LEU	conflict	UNP A0A1B8R7L2
A	440	ILE	LEU	conflict	UNP A0A1B8R7L2
A	534	ALA	THR	conflict	UNP A0A1B8R7L2
A	583	SER	PRO	conflict	UNP A0A1B8R7L2
A	598	GLU	GLN	engineered mutation	UNP A0A1B8R7L2
A	607	ARG	HIS	conflict	UNP A0A1B8R7L2
A	618	LEU	VAL	conflict	UNP A0A1B8R7L2
A	619	SER	PHE	conflict	UNP A0A1B8R7L2

- 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		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		
2	A	1	Total	O	S	0	0
			5	4	1		

- Molecule 3 is (2 {R},3 {S},4 {S},5 {R},6 {S})-6-(4-methyl-2-oxidanylidene-chromen-7-yl)oxy-3,4,5-tris(oxidanyl)oxane-2-carboxylic acid (CCD ID: 8U8) (formula: C₁₆H₁₆O₉).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	C	O	0	0
			25	16	9		
3	A	1	Total	C	O	0	0
			25	16	9		

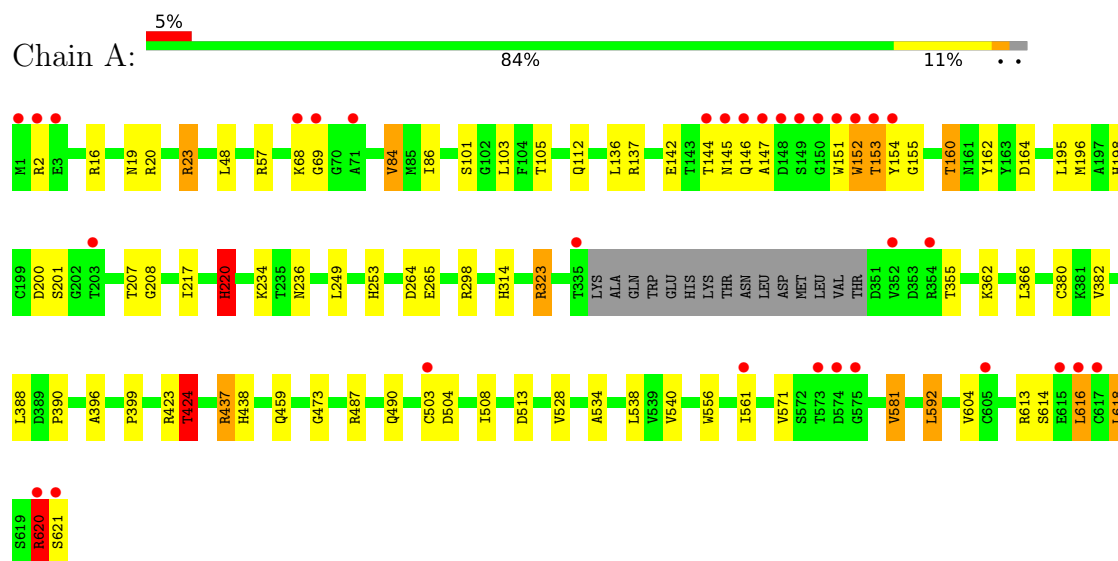
- Molecule 4 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	384	Total	O	0	0
			384	384		

3 Residue-property plots [i](#)

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: Glycosyl hydrolase



4 Data and refinement statistics

Property	Value	Source
Space group	P 62 2 2	Depositor
Cell constants a, b, c, α , β , γ	173.03Å 173.03Å 156.69Å 90.00° 90.00° 120.00°	Depositor
Resolution (Å)	149.85 – 2.20 149.85 – 2.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (149.85-2.20) 99.8 (149.85-2.20)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.96 (at 2.19Å)	Xtriage
Refinement program	REFMAC 5.8.0155	Depositor
R, R_{free}	0.159 , 0.175 0.168 , 0.184	Depositor DCC
R_{free} test set	1939 reflections (2.76%)	wwPDB-VP
Wilson B-factor (Å ²)	41.4	Xtriage
Anisotropy	0.365	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 39.5	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	5235	wwPDB-VP
Average B, all atoms (Å ²)	47.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 2.88% 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: 8U8, SO4

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	1.03	4/4885 (0.1%)	1.09	16/6650 (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

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	A	23	ARG	CD-NE	-11.07	1.30	1.46
1	A	323	ARG	CD-NE	-8.95	1.33	1.46
1	A	528	VAL	C-O	-5.62	1.17	1.24
1	A	424	THR	CB-CG2	-5.17	1.35	1.52

All (16) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	23	ARG	NE-CZ-NH2	-13.21	107.31	119.20
1	A	23	ARG	NE-CZ-NH1	9.58	131.08	121.50
1	A	323	ARG	NE-CZ-NH2	-9.02	111.08	119.20
1	A	201	SER	N-CA-C	-8.03	97.91	109.31
1	A	23	ARG	CD-NE-CZ	7.62	135.07	124.40
1	A	84	VAL	CB-CA-C	-6.99	102.70	112.14
1	A	424	THR	CB-CA-C	-6.95	97.18	110.24
1	A	323	ARG	NE-CZ-NH1	6.74	128.24	121.50
1	A	84	VAL	N-CA-CB	6.73	119.70	110.54

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	380	CYS	CB-CA-C	-6.23	99.52	109.80
1	A	207	THR	N-CA-C	-5.89	98.24	110.80
1	A	220	HIS	CB-CA-C	-5.72	100.30	109.75
1	A	581	VAL	CB-CA-C	5.71	115.99	110.63
1	A	581	VAL	N-CA-CB	-5.39	103.27	111.57
1	A	616	LEU	CA-CB-CG	5.34	134.98	116.30
1	A	437	ARG	CB-CA-C	-5.02	101.07	109.65

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	208	GLY	Peptide

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	4746	0	4666	44	0
2	A	55	0	0	1	5
3	A	50	0	0	1	0
4	A	384	0	0	7	0
All	All	5235	0	4666	44	5

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 5.

All (44) 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:613:ARG:NH1	1:A:614:SER:O	2.00	0.95
1:A:147:ALA:HA	1:A:151:TRP:HB2	1.56	0.87
1:A:57:ARG:NH1	1:A:142:GLU:OE1	2.13	0.81
1:A:196:MET:HE2	1:A:249:LEU:HD21	1.64	0.78
1:A:620:ARG:HE	1:A:620:ARG:HA	1.54	0.72

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:20:ARG:O	1:A:23:ARG:HD3	1.92	0.68
1:A:423:ARG:HD3	1:A:513:ASP:OD1	1.93	0.67
1:A:105:THR:H	1:A:112:GLN:HE22	1.43	0.67
1:A:160:THR:HG23	4:A:806:HOH:O	1.95	0.65
1:A:19:ASN:HB3	4:A:1046:HOH:O	1.97	0.64
1:A:160:THR:HG21	4:A:1140:HOH:O	2.02	0.59
1:A:236:ASN:HD22	1:A:298:ARG:HH11	1.49	0.58
1:A:101:SER:HB2	1:A:103:LEU:HD13	1.85	0.58
1:A:220:HIS:ND1	1:A:264:ASP:OD1	2.33	0.58
1:A:504:ASP:N	1:A:504:ASP:OD1	2.38	0.55
1:A:137:ARG:NH2	4:A:802:HOH:O	2.39	0.54
1:A:196:MET:HE2	1:A:249:LEU:CD2	2.34	0.54
1:A:2:ARG:O	1:A:424:THR:HG23	2.07	0.53
1:A:323:ARG:HD3	4:A:1007:HOH:O	2.08	0.52
1:A:164:ASP:OD1	1:A:198:HIS:HE1	1.92	0.52
1:A:196:MET:HE1	1:A:217:ILE:CD1	2.40	0.51
1:A:487:ARG:CZ	1:A:592:LEU:HD22	2.39	0.51
1:A:16:ARG:NE	2:A:710:SO4:O3	2.33	0.51
1:A:236:ASN:ND2	1:A:298:ARG:HH11	2.09	0.51
1:A:620:ARG:HA	1:A:620:ARG:NE	2.24	0.49
1:A:48:LEU:HD11	1:A:366:LEU:HD11	1.94	0.49
1:A:540:VAL:HG21	1:A:621:SER:HA	1.96	0.48
1:A:437:ARG:NH2	4:A:809:HOH:O	2.47	0.47
1:A:538:LEU:HB2	1:A:618[A]:LEU:HD12	1.96	0.47
1:A:390:PRO:HB3	1:A:396:ALA:HB2	1.98	0.46
1:A:459:GLN:O	1:A:473:GLY:HA2	2.17	0.45
1:A:438:HIS:CD2	1:A:503:CYS:SG	3.10	0.45
1:A:146:GLN:O	1:A:147:ALA:HB3	2.17	0.44
1:A:20:ARG:HB2	1:A:23:ARG:HD2	2.00	0.44
1:A:618[A]:LEU:HD23	4:A:1058:HOH:O	2.18	0.43
1:A:265:GLU:OE1	3:A:712:8U8:C5	2.67	0.43
1:A:534:ALA:HB2	1:A:616:LEU:HB3	2.02	0.42
1:A:144:THR:HB	1:A:162:TYR:OH	2.20	0.41
1:A:362:LYS:H	1:A:490:GLN:NE2	2.18	0.41
1:A:145:ASN:O	1:A:146:GLN:C	2.63	0.41
1:A:153:THR:O	1:A:155:GLY:N	2.44	0.41
1:A:508:ILE:HD12	1:A:508:ILE:C	2.46	0.41
1:A:200:ASP:OD2	1:A:253:HIS:HD2	2.04	0.40
1:A:556:TRP:CE2	1:A:604:VAL:HG11	2.57	0.40

All (5) 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)
2:A:702:SO4:O1	2:A:702:SO4:O4[4_665]	1.19	1.01
2:A:702:SO4:O3	2:A:702:SO4:O4[4_665]	1.34	0.86
2:A:702:SO4:S	2:A:702:SO4:O1[4_665]	1.41	0.79
2:A:702:SO4:O1	2:A:702:SO4:O3[4_665]	1.52	0.68
2:A:702:SO4:S	2:A:702:SO4:O3[4_665]	1.53	0.67

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	607/621 (98%)	579 (95%)	23 (4%)	5 (1%)	16 16

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	152	TRP
1	A	154	TYR
1	A	620	ARG
1	A	399	PRO
1	A	69	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	508/517 (98%)	485 (96%)	23 (4%)	24 33

All (23) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	68	LYS
1	A	84	VAL
1	A	86	ILE
1	A	136	LEU
1	A	152	TRP
1	A	153	THR
1	A	160	THR
1	A	195	LEU
1	A	220	HIS
1	A	234	LYS
1	A	314	HIS
1	A	355	THR
1	A	382	VAL
1	A	388	LEU
1	A	424	THR
1	A	561[A]	ILE
1	A	561[B]	ILE
1	A	571	VAL
1	A	581	VAL
1	A	592	LEU
1	A	618[A]	LEU
1	A	618[B]	LEU
1	A	620	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (9) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	112	GLN
1	A	146	GLN
1	A	198	HIS
1	A	236	ASN
1	A	253	HIS
1	A	269	GLN
1	A	438	HIS
1	A	490	GLN
1	A	496	HIS

5.3.3 RNA ⓘ

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](#)

13 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	SO4	A	702	-	4,4,4	0.45	0	6,6,6	0.54	0
3	8U8	A	713	-	27,27,27	1.79	7 (25%)	39,40,40	1.56	7 (17%)
2	SO4	A	709	-	4,4,4	0.52	0	6,6,6	0.18	0
2	SO4	A	706	-	4,4,4	0.45	0	6,6,6	0.07	0
2	SO4	A	707	-	4,4,4	0.46	0	6,6,6	0.23	0
2	SO4	A	704	-	4,4,4	0.45	0	6,6,6	0.15	0
3	8U8	A	712	-	27,27,27	2.40	11 (40%)	39,40,40	2.55	15 (38%)
2	SO4	A	701	-	4,4,4	0.45	0	6,6,6	0.45	0
2	SO4	A	703	-	4,4,4	0.47	0	6,6,6	0.17	0
2	SO4	A	710	-	4,4,4	0.63	0	6,6,6	0.34	0
2	SO4	A	711	-	4,4,4	0.64	0	6,6,6	0.28	0
2	SO4	A	708	-	4,4,4	0.62	0	6,6,6	0.15	0
2	SO4	A	705	-	4,4,4	0.44	0	6,6,6	0.19	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
3	8U8	A	713	-	-	1/8/28/28	0/3/3/3

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
3	8U8	A	712	-	-	2/8/28/28	0/3/3/3

All (18) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
3	A	713	8U8	C15-C13	-5.32	1.40	1.50
3	A	712	8U8	C1-C6	-5.06	1.42	1.53
3	A	712	8U8	O2-C5	4.86	1.48	1.41
3	A	712	8U8	C15-C13	-4.50	1.41	1.50
3	A	712	8U8	C5-C4	4.29	1.65	1.52
3	A	712	8U8	C14-C13	3.80	1.40	1.35
3	A	713	8U8	C12-C13	-3.31	1.40	1.45
3	A	713	8U8	C14-C13	3.15	1.39	1.35
3	A	713	8U8	O2-C5	2.93	1.45	1.41
3	A	712	8U8	O1-C1	-2.80	1.38	1.43
3	A	712	8U8	C3-C2	2.79	1.59	1.52
3	A	713	8U8	C14-C16	-2.49	1.39	1.44
3	A	712	8U8	O3-C4	2.45	1.49	1.43
3	A	712	8U8	O7-C6	-2.40	1.23	1.30
3	A	712	8U8	C12-C13	-2.18	1.42	1.45
3	A	713	8U8	C1-C6	2.12	1.57	1.53
3	A	713	8U8	O8-C11	-2.06	1.35	1.38
3	A	712	8U8	C14-C16	-2.01	1.40	1.44

All (22) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	712	8U8	O2-C5-C4	8.96	120.22	107.16
3	A	712	8U8	O9-C16-C14	-4.62	116.62	125.92
3	A	712	8U8	C9-O2-C5	4.60	124.30	117.82
3	A	712	8U8	O8-C16-O9	4.39	122.10	116.40
3	A	712	8U8	O1-C1-C2	3.78	116.95	109.48
3	A	712	8U8	C5-O1-C1	3.68	118.26	112.23
3	A	713	8U8	C5-O1-C1	3.65	118.22	112.23
3	A	713	8U8	C16-C14-C13	-3.48	120.11	123.06
3	A	712	8U8	O8-C16-C14	3.34	121.23	117.16
3	A	713	8U8	O9-C16-C14	-3.33	119.23	125.92
3	A	712	8U8	C16-C14-C13	-3.18	120.36	123.06
3	A	712	8U8	O3-C4-C5	2.95	117.10	110.08
3	A	712	8U8	C15-C13-C12	2.94	123.26	119.94
3	A	713	8U8	O8-C16-O9	2.75	119.97	116.40
3	A	713	8U8	O1-C5-O2	-2.74	101.40	108.42

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
3	A	713	8U8	O8-C16-C14	2.71	120.46	117.16
3	A	712	8U8	C11-C12-C13	2.57	120.54	118.58
3	A	712	8U8	C3-C2-C1	2.43	113.48	109.30
3	A	713	8U8	O2-C5-C4	2.42	110.69	107.16
3	A	712	8U8	O8-C11-C12	-2.12	119.64	121.57
3	A	712	8U8	O8-C11-C10	2.10	118.81	115.83
3	A	712	8U8	C15-C13-C14	-2.05	118.53	120.98

There are no chirality outliers.

All (3) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
3	A	712	8U8	C4-C5-O2-C9
3	A	712	8U8	O1-C5-O2-C9
3	A	713	8U8	C2-C1-C6-O7

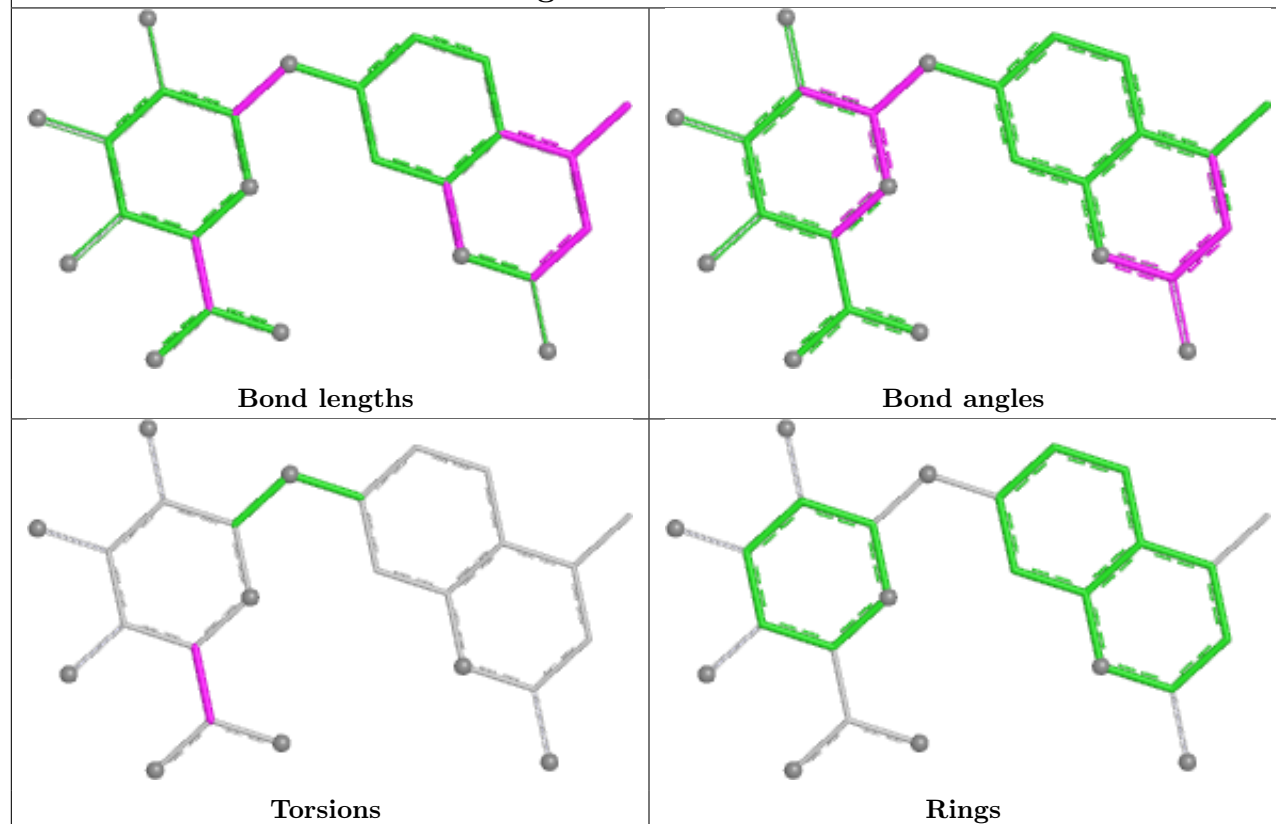
There are no ring outliers.

3 monomers are involved in 7 short contacts:

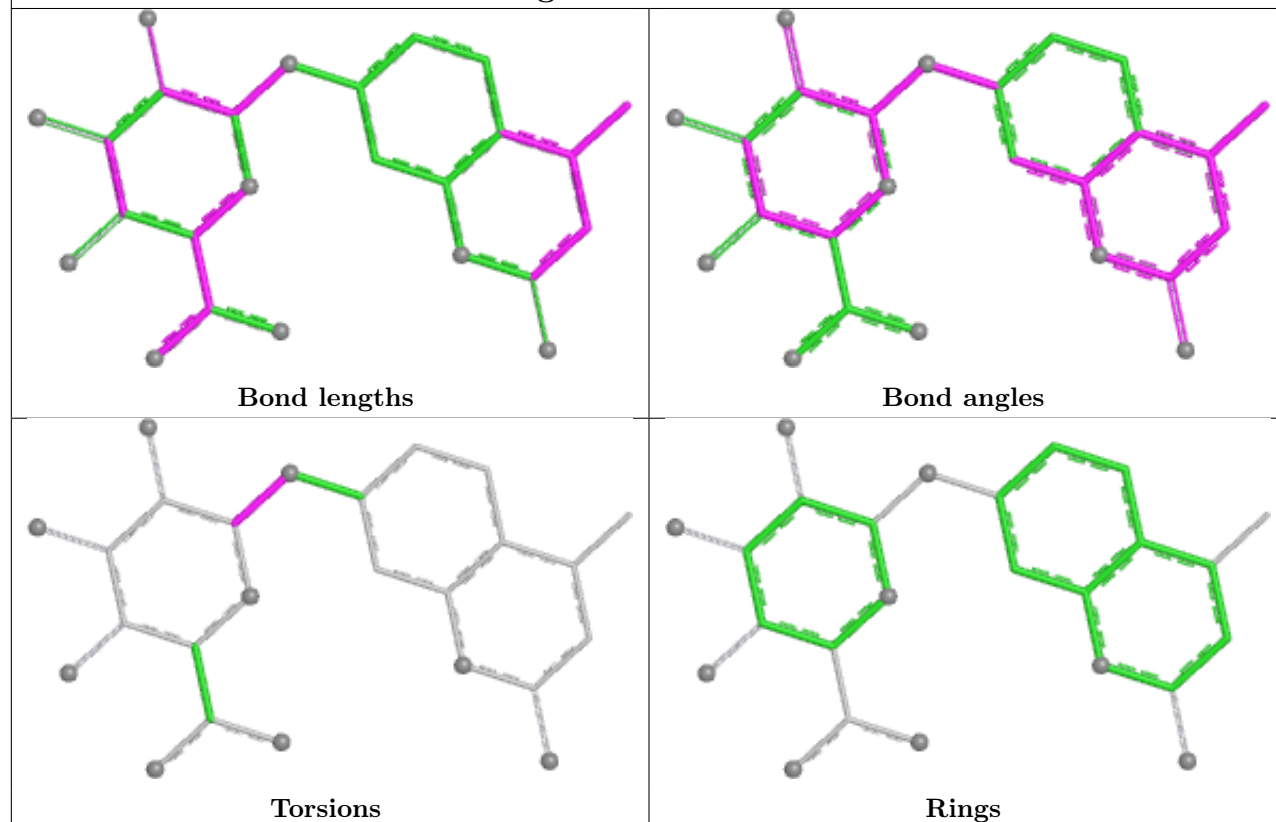
Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	702	SO4	0	5
3	A	712	8U8	1	0
2	A	710	SO4	1	0

The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less than 5% of the Mogul distribution of torsion angles is within 10 degrees of the torsion angle in question, then that torsion angle is considered an outlier. Any bond that is central to one or more torsion angles identified as an outlier by Mogul will be highlighted in the graph. For rings, the root-mean-square deviation (RMSD) between the ring in question and similar rings identified by Mogul is calculated over all ring torsion angles. If the average RMSD is greater than 60 degrees and the minimal RMSD between the ring in question and any Mogul-identified rings is also greater than 60 degrees, then that ring is considered an outlier. The outliers are highlighted in purple. The color gray indicates Mogul did not find sufficient equivalents in the CSD to analyse the geometry.

Ligand 8U8 A 713



Ligand 8U8 A 712



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	606/621 (97%)	-0.14	32 (5%) 32 29	21, 42, 78, 130	5 (0%)

All (32) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	1	MET	6.4
1	A	152	TRP	5.5
1	A	147	ALA	5.4
1	A	145	ASN	4.8
1	A	146	GLN	4.7
1	A	153	THR	4.5
1	A	71	ALA	4.5
1	A	150	GLY	3.8
1	A	69	GLY	3.7
1	A	561[A]	ILE	3.6
1	A	605	CYS	3.4
1	A	573	THR	3.4
1	A	503	CYS	3.3
1	A	68	LYS	3.1
1	A	352	VAL	3.0
1	A	335	THR	2.9
1	A	149	SER	2.9
1	A	621	SER	2.8
1	A	617	CYS	2.7
1	A	3	GLU	2.7
1	A	616	LEU	2.7
1	A	620	ARG	2.6
1	A	203	THR	2.6
1	A	2	ARG	2.6
1	A	615	GLU	2.5
1	A	144	THR	2.5
1	A	151	TRP	2.4

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Mol	Chain	Res	Type	RSRZ
1	A	574	ASP	2.3
1	A	575	GLY	2.2
1	A	354	ARG	2.2
1	A	148	ASP	2.2
1	A	154	TYR	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 oligosaccharides in this entry.

6.4 Ligands [i](#)

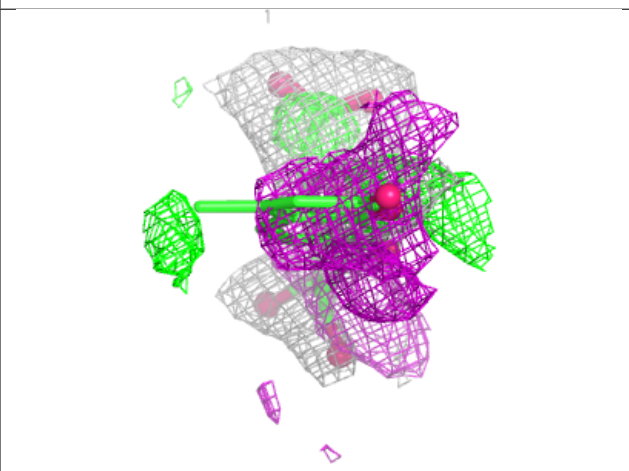
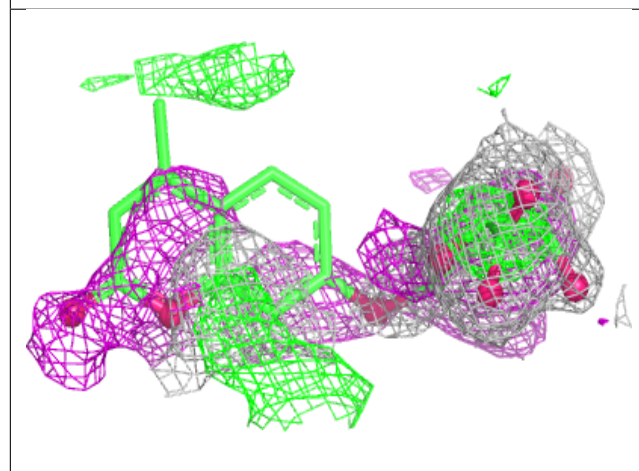
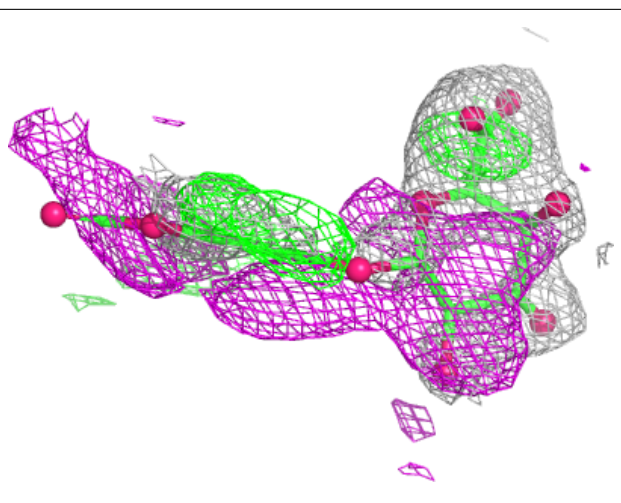
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95th percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9' lists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

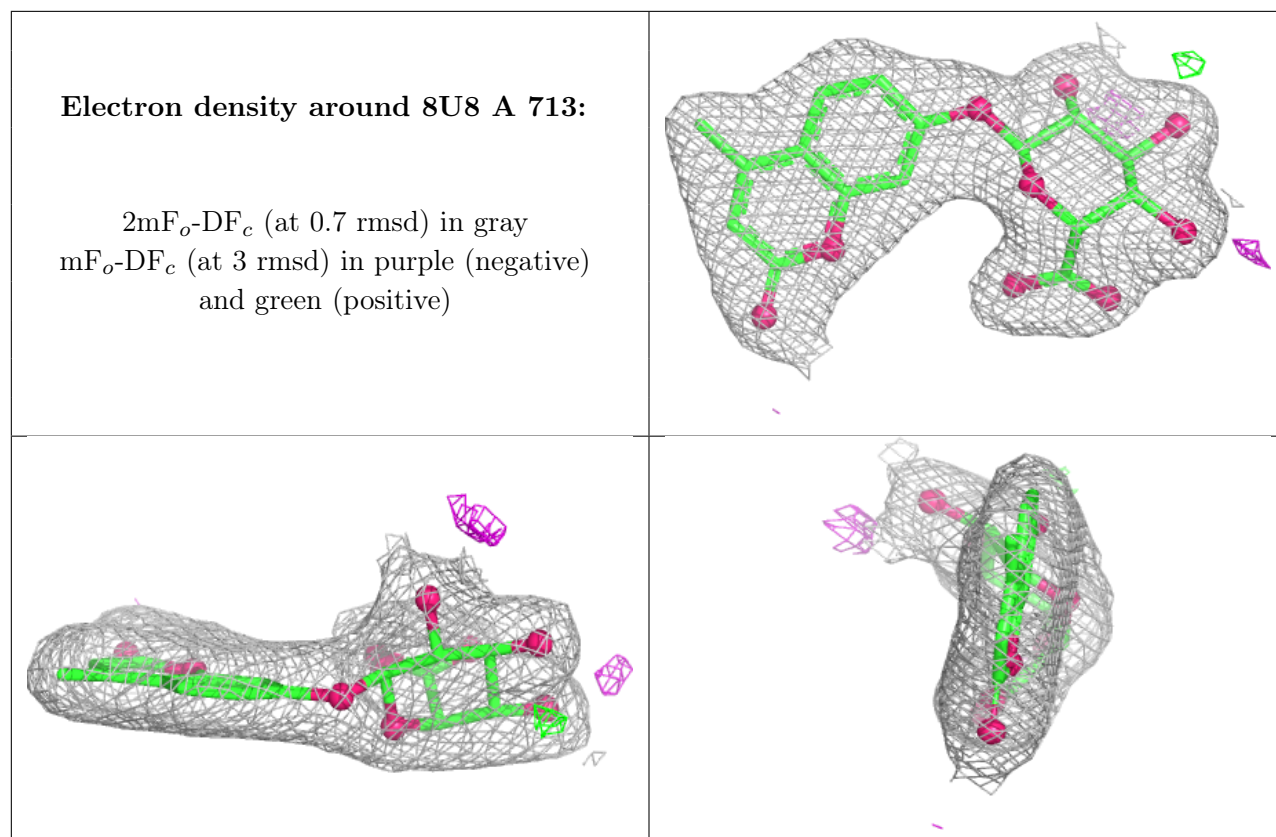
Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	SO4	A	711	5/5	0.54	0.14	81,87,91,92	0
2	SO4	A	708	5/5	0.58	0.16	97,98,111,114	0
2	SO4	A	709	5/5	0.72	0.12	102,102,110,116	0
2	SO4	A	706	5/5	0.77	0.10	117,117,120,122	0
2	SO4	A	703	5/5	0.77	0.11	80,88,92,103	0
2	SO4	A	704	5/5	0.78	0.14	120,125,126,140	0
3	8U8	A	712	25/25	0.80	0.28	35,68,131,132	0
2	SO4	A	710	5/5	0.82	0.15	84,93,95,102	0
2	SO4	A	707	5/5	0.84	0.14	102,105,113,121	0
2	SO4	A	702	5/5	0.85	0.15	59,64,139,140	3
2	SO4	A	705	5/5	0.88	0.14	132,134,141,144	0
3	8U8	A	713	25/25	0.96	0.06	34,39,43,51	0
2	SO4	A	701	5/5	0.98	0.10	47,50,58,59	0

The following is a graphical depiction of the model fit to experimental electron density of all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the geometry validation Tables will also be included. Each fit is shown from different orientation to approximate a three-dimensional view.

Electron density around 8U8 A 712:

$2mF_o-DF_c$ (at 0.7 rmsd) in gray
 mF_o-DF_c (at 3 rmsd) in purple (negative)
and green (positive)





6.5 Other polymers [i](#)

There are no such residues in this entry.