



Full wwPDB X-ray Structure Validation Report ⓘ

Mar 17, 2026 – 11:13 PM UTC

PDB ID : 1X0C / pdb_00001x0c
Title : Improved Crystal Structure of Isopullulanase from *Aspergillus niger* ATCC 9642
Authors : Mizuno, M.; TonoZuka, T.; Yamamura, A.; Miyasaka, Y.; Akeboshi, H.; Kami-tori, S.; Nishikawa, A.; Sakano, Y.
Deposited on : 2005-03-17
Resolution : 1.70 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 ⓘ](#)) 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

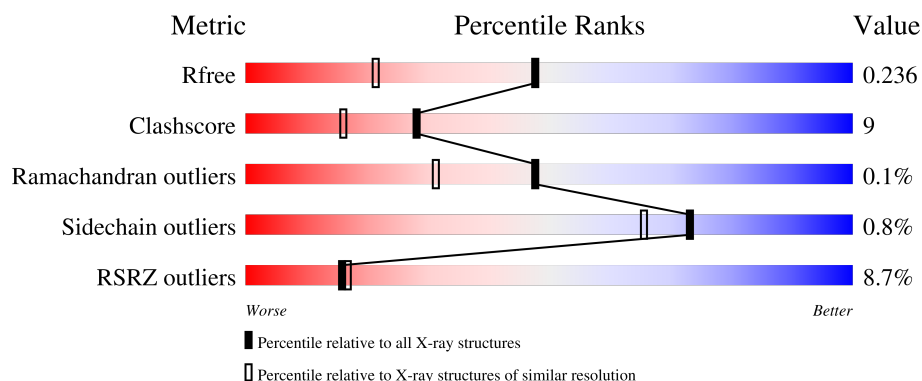
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 1.70 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	5551 (1.70-1.70)
Clashscore	190562	5924 (1.70-1.70)
Ramachandran outliers	187476	5846 (1.70-1.70)
Sidechain outliers	187428	5846 (1.70-1.70)
RSRZ outliers	180081	5554 (1.70-1.70)

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	549	3% 83% 16%
1	B	549	14% 82% 17%

2 Entry composition

There are 3 unique types of molecules in this entry. The entry contains 10079 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.

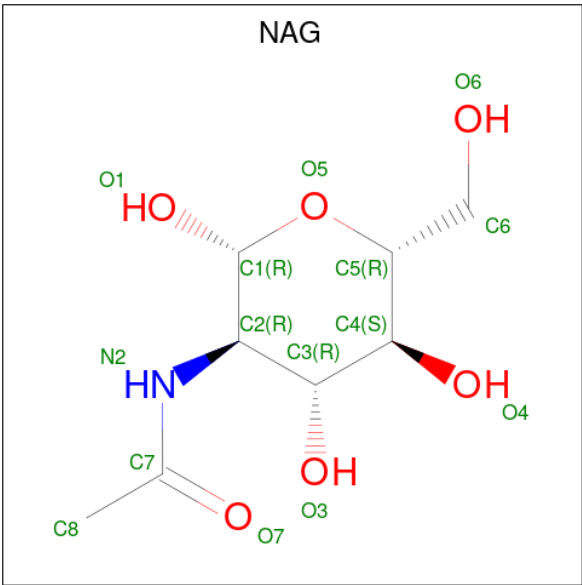
- Molecule 1 is a protein called Isopullulanase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	549	Total	C	N	O	S	0	0	0
			4242	2676	710	845	11			
1	B	549	Total	C	N	O	S	0	0	0
			4242	2676	710	845	11			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	16	ARG	-	expression tag	UNP O00105
A	17	GLU	-	expression tag	UNP O00105
A	18	PHE	-	expression tag	UNP O00105
A	19	MET	-	expression tag	UNP O00105
B	16	ARG	-	expression tag	UNP O00105
B	17	GLU	-	expression tag	UNP O00105
B	18	PHE	-	expression tag	UNP O00105
B	19	MET	-	expression tag	UNP O00105

- Molecule 2 is 2-acetamido-2-deoxy-beta-D-glucopyranose (CCD ID: NAG) (formula: C₈H₁₅NO₆).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	A	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

Continued on next page...

Continued from previous page...

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		
2	B	1	Total	C	N	O	0	0
			14	8	1	5		

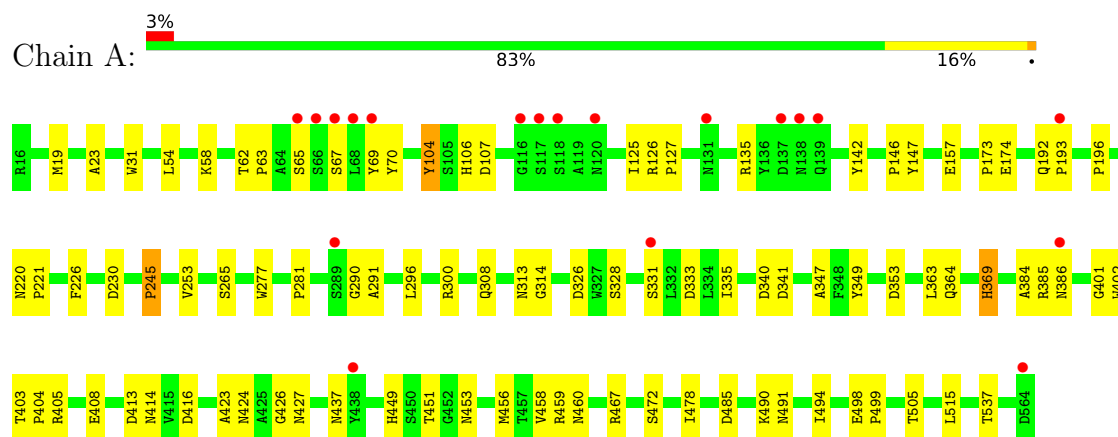
- Molecule 3 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
3	A	731	Total	O	0	0
			731	731		
3	B	542	Total	O	0	0
			542	542		

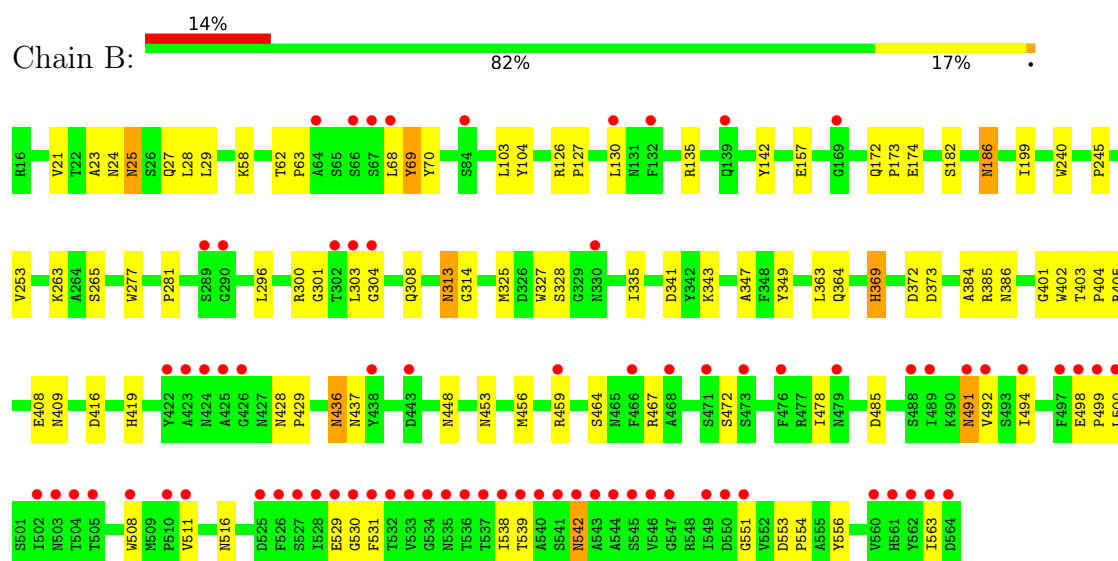
3 Residue-property plots [i](#)

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: Isopullulanase



• Molecule 1: Isopullulanase



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	99.72Å 136.16Å 84.47Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	49.86 – 1.70 49.86 – 1.70	Depositor EDS
% Data completeness (in resolution range)	99.0 (49.86-1.70) 99.1 (49.86-1.70)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.13 (at 1.70Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.195 , 0.229 0.206 , 0.236	Depositor DCC
R_{free} test set	12531 reflections (9.97%)	wwPDB-VP
Wilson B-factor (Å ²)	15.0	Xtriage
Anisotropy	0.486	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 48.5	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	0.95	EDS
Total number of atoms	10079	wwPDB-VP
Average B, all atoms (Å ²)	19.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 19.32% 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: NAG

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	0.34	0/4357	0.91	9/5962 (0.2%)
1	B	0.32	0/4357	0.88	8/5962 (0.1%)
All	All	0.33	0/8714	0.89	17/11924 (0.1%)

There are no bond length outliers.

All (17) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	369	HIS	N-CA-C	-7.41	96.44	108.52
1	A	478	ILE	N-CA-C	6.52	117.25	107.80
1	A	253	VAL	N-CA-C	6.28	117.34	108.36
1	B	253	VAL	N-CA-C	6.15	117.15	108.36
1	B	478	ILE	N-CA-C	5.74	116.20	108.17
1	A	245	PRO	N-CA-C	-5.72	102.23	111.03
1	A	174	GLU	N-CA-C	-5.71	105.03	112.23
1	B	245	PRO	N-CA-C	-5.55	102.49	111.03
1	B	325	MET	N-CA-C	5.37	117.25	108.55
1	B	369	HIS	N-CA-C	-5.34	98.53	107.99
1	B	174	GLU	N-CA-C	-5.29	105.56	112.23
1	A	505	THR	N-CA-C	5.24	120.68	113.97
1	A	353	ASP	N-CA-C	5.24	117.05	110.24
1	A	458	VAL	N-CA-C	-5.16	100.46	107.99
1	A	196	PRO	N-CA-C	5.13	119.14	111.14
1	B	69	TYR	N-CA-C	-5.09	101.42	109.76
1	B	516	ASN	N-CA-C	5.02	119.40	113.12

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	4242	0	3979	62	0
1	B	4242	0	3978	85	0
2	A	154	0	143	5	0
2	B	168	0	156	10	0
3	A	731	0	0	9	0
3	B	542	0	0	8	0
All	All	10079	0	8256	151	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 9.

All (151) 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:54:LEU:HD11	2:A:1002:NAG:H61	1.53	0.91
1:B:539:THR:H	1:B:542:ASN:HD21	1.16	0.91
1:A:414:ASN:ND2	1:A:467:ARG:HH22	1.72	0.87
1:B:539:THR:H	1:B:542:ASN:ND2	1.76	0.82
1:B:25:ASN:HD22	1:B:27:GLN:H	1.27	0.79
1:B:347:ALA:H	1:B:369:HIS:HD2	1.29	0.79
1:B:157:GLU:OE2	1:B:419:HIS:HE1	1.66	0.78
1:A:347:ALA:H	1:A:369:HIS:HD2	1.29	0.77
1:B:127:PRO:HG2	1:B:130:LEU:CD1	2.17	0.75
1:B:529:GLU:HB2	1:B:563:ILE:HB	1.73	0.70
1:B:127:PRO:HG2	1:B:130:LEU:HD13	1.74	0.69
1:B:25:ASN:ND2	1:B:28:LEU:H	1.91	0.68
1:B:303:LEU:HD23	1:B:304:GLY:O	1.93	0.68
1:A:453:ASN:ND2	1:A:456:MET:HE2	2.11	0.66
1:B:308:GLN:NE2	1:B:327:TRP:HE1	1.93	0.65
1:A:414:ASN:HD21	1:A:467:ARG:HH22	1.42	0.65
1:A:192:GLN:HB3	1:A:193:PRO:HD2	1.79	0.64
1:B:186:ASN:C	1:B:186:ASN:HD22	2.05	0.64
1:A:404:PRO:HB2	1:A:456:MET:HE3	1.78	0.64
1:A:135:ARG:HG2	1:A:142:TYR:HB2	1.78	0.63
1:A:386:ASN:HB3	3:A:1284:HOH:O	1.98	0.63

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:308:GLN:HE21	1:B:327:TRP:HE1	1.47	0.63
1:B:542:ASN:C	1:B:542:ASN:HD22	2.09	0.61
1:B:539:THR:N	1:B:542:ASN:HD21	1.94	0.60
1:B:25:ASN:ND2	1:B:27:GLN:H	1.97	0.60
1:B:157:GLU:HB3	1:B:173:PRO:HG3	1.83	0.60
1:B:436:ASN:ND2	1:B:437:ASN:H	1.99	0.60
1:B:453:ASN:HA	2:B:1008:NAG:H82	1.84	0.60
1:A:146:PRO:HG3	3:A:1498:HOH:O	2.01	0.59
1:B:472:SER:HB3	1:B:494:ILE:HG23	1.84	0.58
1:A:58:LYS:HB3	1:A:69:TYR:HB3	1.85	0.58
1:B:416:ASP:HB2	1:B:467:ARG:NH2	2.18	0.58
1:B:127:PRO:HG2	1:B:130:LEU:HD11	1.86	0.57
1:B:404:PRO:HB2	1:B:456:MET:HE3	1.86	0.57
1:B:135:ARG:HG2	1:B:142:TYR:HB2	1.85	0.57
1:A:54:LEU:HD12	3:A:1364:HOH:O	2.04	0.57
1:B:436:ASN:HD22	1:B:437:ASN:H	1.53	0.57
2:A:1007:NAG:H81	3:A:1362:HOH:O	2.03	0.57
1:B:511:VAL:HA	1:B:556:TYR:CE1	2.40	0.57
2:A:1000:NAG:H81	3:A:1669:HOH:O	2.05	0.56
2:B:1003:NAG:H83	3:B:1392:HOH:O	2.05	0.56
1:A:19:MET:HE2	3:A:1315:HOH:O	2.05	0.56
1:A:127:PRO:HB3	1:A:416:ASP:OD2	2.06	0.56
1:A:423:ALA:H	1:A:427:ASN:ND2	2.03	0.56
1:B:23:ALA:HB2	1:B:70:TYR:CG	2.41	0.56
1:A:404:PRO:HG2	3:A:1398:HOH:O	2.06	0.56
1:A:537:THR:HG23	3:A:1320:HOH:O	2.06	0.56
1:A:424:ASN:H	1:A:427:ASN:ND2	2.04	0.55
1:A:125:ILE:N	1:A:125:ILE:HD12	2.21	0.55
1:B:498:GLU:HB3	1:B:499:PRO:HD2	1.88	0.54
1:B:281:PRO:HG3	1:B:296:LEU:HD13	1.89	0.54
1:B:491:ASN:HD22	2:B:1010:NAG:H82	1.71	0.54
1:A:347:ALA:H	1:A:369:HIS:CD2	2.18	0.54
1:A:331:SER:HB3	1:A:333:ASP:OD1	2.07	0.54
1:B:404:PRO:HG2	3:B:1207:HOH:O	2.07	0.54
1:A:449:HIS:HD2	3:A:1692:HOH:O	1.91	0.53
1:A:157:GLU:HB3	1:A:173:PRO:HG3	1.90	0.53
1:A:23:ALA:HB2	1:A:70:TYR:CG	2.44	0.53
1:B:172:GLN:HG2	1:B:419:HIS:CD2	2.45	0.52
1:B:401:GLY:O	1:B:402:TRP:HB2	2.09	0.52
1:B:437:ASN:HD22	1:B:437:ASN:C	2.16	0.52
1:A:460:ASN:ND2	2:A:1007:NAG:C7	2.72	0.52

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:126:ARG:HA	1:A:127:PRO:C	2.35	0.52
1:B:126:ARG:HA	1:B:127:PRO:C	2.34	0.52
1:A:308:GLN:O	1:A:335:ILE:HD12	2.09	0.52
1:A:472:SER:HB3	1:A:494:ILE:HG23	1.91	0.51
1:B:419:HIS:HD2	3:B:1223:HOH:O	1.93	0.51
2:B:1002:NAG:H81	3:B:1395:HOH:O	2.11	0.51
1:B:21:VAL:HG11	1:B:68:LEU:HD21	1.93	0.50
1:B:542:ASN:ND2	1:B:542:ASN:C	2.70	0.50
1:A:423:ALA:H	1:A:427:ASN:HD22	1.58	0.50
1:A:62:THR:HB	1:A:63:PRO:HA	1.94	0.49
1:B:459:ARG:HA	1:B:485:ASP:O	2.13	0.49
1:A:65:SER:C	1:A:67:SER:H	2.19	0.49
1:B:453:ASN:ND2	1:B:456:MET:HE2	2.28	0.49
1:A:437:ASN:HD22	1:A:437:ASN:C	2.21	0.49
1:B:492:VAL:HG13	1:B:531:PHE:CD1	2.48	0.49
1:B:62:THR:HB	1:B:63:PRO:HA	1.95	0.48
1:B:21:VAL:O	1:B:21:VAL:HG13	2.12	0.48
1:B:186:ASN:C	1:B:186:ASN:ND2	2.70	0.48
1:B:29:LEU:HD23	1:B:103:LEU:HD12	1.96	0.48
1:B:103:LEU:HA	1:B:182:SER:O	2.14	0.48
1:B:347:ALA:N	1:B:369:HIS:HD2	2.03	0.47
1:A:106:HIS:HD2	1:A:107:ASP:O	1.97	0.47
1:A:340:ASP:OD1	1:A:364:GLN:HG3	2.14	0.47
1:B:25:ASN:HD22	1:B:27:GLN:N	2.06	0.47
1:B:58:LYS:HB3	1:B:69:TYR:HB3	1.96	0.47
1:A:490:LYS:O	1:A:491:ASN:HB2	2.15	0.47
1:B:25:ASN:ND2	1:B:28:LEU:N	2.63	0.47
1:B:464:SER:HB2	2:B:1010:NAG:H81	1.95	0.47
1:A:408:GLU:HA	1:A:459:ARG:O	2.15	0.46
1:B:24:ASN:HD22	2:B:1000:NAG:C8	2.29	0.46
1:B:277:TRP:CD1	1:B:349:TYR:HB3	2.50	0.46
1:B:492:VAL:HG13	1:B:492:VAL:O	2.16	0.46
1:A:424:ASN:HD22	1:A:426:GLY:N	2.13	0.45
1:B:265:SER:HA	1:B:313:ASN:O	2.16	0.45
1:A:265:SER:HA	1:A:313:ASN:O	2.17	0.45
1:A:363:LEU:O	1:A:384:ALA:HA	2.16	0.45
1:A:290:GLY:O	1:A:291:ALA:C	2.60	0.45
1:B:467:ARG:HG3	1:B:467:ARG:HH11	1.82	0.45
1:A:401:GLY:O	1:A:402:TRP:HB2	2.17	0.44
1:B:508:TRP:HB3	1:B:551:GLY:HA3	1.99	0.44
1:B:301:GLY:HA3	1:B:327:TRP:CE2	2.53	0.44

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:281:PRO:HG3	1:A:296:LEU:HD13	1.99	0.44
1:B:456:MET:HE1	3:B:1207:HOH:O	2.17	0.44
1:A:300:ARG:NH1	1:A:328:SER:OG	2.49	0.44
1:B:448:ASN:ND2	2:B:1007:NAG:H82	2.33	0.44
1:A:104:TYR:CE2	1:A:147:TYR:HA	2.53	0.44
1:A:300:ARG:NE	1:A:328:SER:OG	2.50	0.44
1:A:424:ASN:HD22	1:A:426:GLY:H	1.65	0.43
1:B:303:LEU:HD13	1:B:335:ILE:HG13	1.98	0.43
1:B:363:LEU:O	1:B:384:ALA:HA	2.18	0.43
1:B:553:ASP:CG	1:B:554:PRO:HD2	2.43	0.43
1:B:24:ASN:HD22	2:B:1000:NAG:H83	1.84	0.43
1:B:408:GLU:HG3	1:B:409:ASN:ND2	2.32	0.43
1:B:403:THR:O	1:B:405:ARG:HG3	2.18	0.43
1:B:343:LYS:N	1:B:343:LYS:HD2	2.34	0.43
1:B:491:ASN:ND2	2:B:1010:NAG:H82	2.33	0.43
1:A:65:SER:C	1:A:67:SER:N	2.77	0.43
1:A:498:GLU:HB3	1:A:499:PRO:HD2	2.01	0.43
1:B:448:ASN:CG	2:B:1007:NAG:H82	2.43	0.43
1:A:300:ARG:HD2	1:A:326:ASP:O	2.19	0.43
1:A:414:ASN:HD21	1:A:467:ARG:NH2	2.14	0.42
1:A:451:THR:HA	1:A:515:LEU:HB2	2.00	0.42
1:A:403:THR:O	1:A:405:ARG:HG3	2.18	0.42
1:A:414:ASN:HD22	1:A:467:ARG:HH22	1.58	0.42
1:A:31:TRP:CZ3	1:A:245:PRO:HB3	2.54	0.42
1:A:226:PHE:O	1:A:230:ASP:HB3	2.20	0.42
1:A:314:GLY:HA2	1:A:341:ASP:O	2.19	0.42
1:A:459:ARG:HA	1:A:485:ASP:O	2.20	0.42
1:B:25:ASN:HD22	1:B:25:ASN:C	2.28	0.42
1:A:220:ASN:HB3	1:A:221:PRO:HD2	2.02	0.42
1:A:467:ARG:HH11	1:A:467:ARG:HG3	1.83	0.42
1:B:281:PRO:CG	1:B:296:LEU:HD13	2.50	0.41
1:B:314:GLY:HA2	1:B:341:ASP:O	2.20	0.41
1:B:240:TRP:CE2	1:B:263:LYS:HE3	2.54	0.41
1:B:364:GLN:HA	1:B:385:ARG:O	2.20	0.41
1:B:428:ASN:N	1:B:429:PRO:CD	2.84	0.41
1:B:500:LEU:HD21	3:B:1303:HOH:O	2.21	0.41
1:A:385:ARG:HA	1:A:413:ASP:O	2.21	0.40
1:B:199:ILE:HD12	3:B:1287:HOH:O	2.20	0.40
1:B:300:ARG:NH2	1:B:328:SER:HB2	2.36	0.40
1:B:511:VAL:HA	1:B:556:TYR:CZ	2.56	0.40
1:B:372:ASP:O	1:B:373:ASP:C	2.64	0.40

Continued on next page...

Continued from previous page...

Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:491:ASN:HA	1:B:530:GLY:O	2.21	0.40
1:A:277:TRP:CD1	1:A:349:TYR:HB3	2.56	0.40
1:B:58:LYS:HA	1:B:70:TYR:O	2.22	0.40
1:B:62:THR:HA	1:B:63:PRO:C	2.47	0.40
1:B:386:ASN:HB3	3:B:1192:HOH:O	2.21	0.40
1:A:221:PRO:HG2	2:A:1000:NAG:H83	2.04	0.40
1:B:538:ILE:HA	1:B:542:ASN:HD21	1.86	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	547/549 (100%)	517 (94%)	30 (6%)	0	100	100
1	B	547/549 (100%)	514 (94%)	32 (6%)	1 (0%)	43	28
All	All	1094/1098 (100%)	1031 (94%)	62 (6%)	1 (0%)	48	31

All (1) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	491	ASN

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	466/466 (100%)	465 (100%)	1 (0%)	87	84
1	B	466/466 (100%)	460 (99%)	6 (1%)	61	48
All	All	932/932 (100%)	925 (99%)	7 (1%)	73	65

All (7) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	104	TYR
1	B	25	ASN
1	B	104	TYR
1	B	186	ASN
1	B	313	ASN
1	B	436	ASN
1	B	542	ASN

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (40) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	27	GLN
1	A	41	GLN
1	A	51	GLN
1	A	106	HIS
1	A	120	ASN
1	A	122	ASN
1	A	131	ASN
1	A	139	GLN
1	A	192	GLN
1	A	323	ASN
1	A	369	HIS
1	A	386	ASN
1	A	414	ASN
1	A	424	ASN
1	A	427	ASN
1	A	437	ASN
1	A	449	HIS
1	A	455	ASN
1	A	486	ASN
1	A	516	ASN
1	B	25	ASN
1	B	41	GLN
1	B	60	GLN

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type
1	B	81	ASN
1	B	88	GLN
1	B	186	ASN
1	B	286	GLN
1	B	308	GLN
1	B	323	ASN
1	B	330	ASN
1	B	364	GLN
1	B	369	HIS
1	B	386	ASN
1	B	414	ASN
1	B	419	HIS
1	B	436	ASN
1	B	437	ASN
1	B	486	ASN
1	B	516	ASN
1	B	542	ASN

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](#)

23 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	NAG	A	1008	1	14,14,15	0.44	0	17,19,21	0.66	0
2	NAG	B	1006	1	14,14,15	0.52	0	17,19,21	0.68	1 (5%)
2	NAG	A	1007	1	14,14,15	0.63	0	17,19,21	0.55	0
2	NAG	A	1000	1	14,14,15	0.56	0	17,19,21	0.75	1 (5%)
2	NAG	B	1011	1	14,14,15	0.51	0	17,19,21	0.74	1 (5%)
2	NAG	B	1010	1	14,14,15	0.49	0	17,19,21	0.70	1 (5%)
2	NAG	B	1007	1	14,14,15	0.53	0	17,19,21	0.72	1 (5%)
2	NAG	A	1001	1	14,14,15	0.45	0	17,19,21	0.65	0
2	NAG	B	1003	1	14,14,15	0.50	0	17,19,21	0.73	1 (5%)
2	NAG	A	1009	1	14,14,15	0.55	0	17,19,21	0.77	1 (5%)
2	NAG	B	1001	1	14,14,15	0.52	0	17,19,21	0.69	0
2	NAG	A	1002	1	14,14,15	0.55	0	17,19,21	0.65	0
2	NAG	B	1005	1	14,14,15	0.51	0	17,19,21	0.65	0
2	NAG	A	1010	1	14,14,15	0.53	0	17,19,21	0.66	0
2	NAG	A	1005	1	14,14,15	0.52	0	17,19,21	0.66	1 (5%)
2	NAG	B	1009	1	14,14,15	0.48	0	17,19,21	0.73	1 (5%)
2	NAG	A	1003	1	14,14,15	0.63	0	17,19,21	0.68	0
2	NAG	A	1006	1	14,14,15	0.50	0	17,19,21	0.73	1 (5%)
2	NAG	B	1000	1	14,14,15	0.53	0	17,19,21	0.65	0
2	NAG	A	1004	1	14,14,15	0.52	0	17,19,21	0.59	0
2	NAG	B	1002	1	14,14,15	0.49	0	17,19,21	0.69	1 (5%)
2	NAG	B	1004	1	14,14,15	0.50	0	17,19,21	0.81	1 (5%)
2	NAG	B	1008	1	14,14,15	0.47	0	17,19,21	0.74	1 (5%)

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	A	1008	1	-	1/6/23/26	0/1/1/1
2	NAG	B	1006	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1007	1	-	3/6/23/26	0/1/1/1
2	NAG	A	1000	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1011	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1010	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1007	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1001	1	-	0/6/23/26	0/1/1/1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
2	NAG	B	1003	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1009	1	-	4/6/23/26	0/1/1/1
2	NAG	B	1001	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1002	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1005	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1010	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1005	1	-	1/6/23/26	0/1/1/1
2	NAG	B	1009	1	-	4/6/23/26	0/1/1/1
2	NAG	A	1003	1	-	0/6/23/26	0/1/1/1
2	NAG	A	1006	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1000	1	-	2/6/23/26	0/1/1/1
2	NAG	A	1004	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1002	1	-	2/6/23/26	0/1/1/1
2	NAG	B	1004	1	-	3/6/23/26	0/1/1/1
2	NAG	B	1008	1	-	2/6/23/26	0/1/1/1

There are no bond length outliers.

All (13) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	1004	NAG	C2-N2-C7	-2.49	119.56	122.90
2	A	1000	NAG	C2-N2-C7	-2.42	119.65	122.90
2	A	1009	NAG	C2-N2-C7	-2.33	119.78	122.90
2	A	1006	NAG	C2-N2-C7	-2.29	119.83	122.90
2	B	1008	NAG	C2-N2-C7	-2.25	119.88	122.90
2	B	1009	NAG	C2-N2-C7	-2.24	119.90	122.90
2	B	1010	NAG	C2-N2-C7	-2.20	119.94	122.90
2	B	1007	NAG	C2-N2-C7	-2.19	119.97	122.90
2	B	1011	NAG	C2-N2-C7	-2.18	119.97	122.90
2	B	1003	NAG	C2-N2-C7	-2.18	119.98	122.90
2	B	1002	NAG	C2-N2-C7	-2.17	119.99	122.90
2	B	1006	NAG	C2-N2-C7	-2.11	120.07	122.90
2	A	1005	NAG	C2-N2-C7	-2.05	120.16	122.90

There are no chirality outliers.

All (44) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
2	A	1000	NAG	O7-C7-N2-C2

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	A	1002	NAG	C8-C7-N2-C2
2	A	1002	NAG	O7-C7-N2-C2
2	A	1007	NAG	C1-C2-N2-C7
2	A	1007	NAG	C8-C7-N2-C2
2	A	1007	NAG	O7-C7-N2-C2
2	A	1009	NAG	C8-C7-N2-C2
2	A	1009	NAG	O7-C7-N2-C2
2	B	1000	NAG	C8-C7-N2-C2
2	B	1000	NAG	O7-C7-N2-C2
2	B	1004	NAG	C8-C7-N2-C2
2	B	1004	NAG	O7-C7-N2-C2
2	B	1005	NAG	C8-C7-N2-C2
2	B	1005	NAG	O7-C7-N2-C2
2	B	1007	NAG	C8-C7-N2-C2
2	B	1007	NAG	O7-C7-N2-C2
2	B	1009	NAG	C8-C7-N2-C2
2	B	1009	NAG	O7-C7-N2-C2
2	B	1010	NAG	C8-C7-N2-C2
2	B	1010	NAG	O7-C7-N2-C2
2	B	1011	NAG	C8-C7-N2-C2
2	B	1011	NAG	O7-C7-N2-C2
2	A	1000	NAG	C8-C7-N2-C2
2	A	1006	NAG	C8-C7-N2-C2
2	B	1002	NAG	C8-C7-N2-C2
2	B	1002	NAG	O7-C7-N2-C2
2	A	1006	NAG	O7-C7-N2-C2
2	B	1006	NAG	C4-C5-C6-O6
2	B	1006	NAG	O5-C5-C6-O6
2	A	1008	NAG	O5-C5-C6-O6
2	B	1003	NAG	C8-C7-N2-C2
2	B	1006	NAG	C8-C7-N2-C2
2	B	1009	NAG	C4-C5-C6-O6
2	B	1003	NAG	O7-C7-N2-C2
2	B	1006	NAG	O7-C7-N2-C2
2	A	1009	NAG	C4-C5-C6-O6
2	B	1009	NAG	O5-C5-C6-O6
2	A	1009	NAG	O5-C5-C6-O6
2	A	1004	NAG	C8-C7-N2-C2
2	B	1008	NAG	C8-C7-N2-C2
2	A	1004	NAG	O7-C7-N2-C2
2	A	1005	NAG	C4-C5-C6-O6
2	B	1004	NAG	C4-C5-C6-O6

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	Atoms
2	B	1008	NAG	O7-C7-N2-C2

There are no ring outliers.

9 monomers are involved in 15 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
2	A	1007	NAG	2	0
2	A	1000	NAG	2	0
2	B	1010	NAG	3	0
2	B	1007	NAG	2	0
2	B	1003	NAG	1	0
2	A	1002	NAG	1	0
2	B	1000	NAG	2	0
2	B	1002	NAG	1	0
2	B	1008	NAG	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	549/549 (100%)	-0.00	19 (3%) 47 52	7, 13, 27, 48	0
1	B	549/549 (100%)	0.81	76 (13%) 6 6	9, 20, 34, 62	0
All	All	1098/1098 (100%)	0.41	95 (8%) 16 17	7, 16, 32, 62	0

All (95) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	538	ILE	6.1
1	B	500	LEU	5.5
1	B	544	ALA	5.4
1	B	540	ALA	5.3
1	B	424	ASN	4.7
1	B	533	VAL	4.7
1	B	539	THR	4.7
1	B	423	ALA	4.7
1	B	550	ASP	4.5
1	B	505	THR	4.3
1	A	116	GLY	4.2
1	B	542	ASN	4.1
1	B	561	HIS	3.9
1	B	549	ILE	3.9
1	B	543	ALA	3.8
1	B	564	ASP	3.8
1	B	534	GLY	3.7
1	B	508	TRP	3.7
1	B	68	LEU	3.7
1	B	546	VAL	3.6
1	B	425	ALA	3.6
1	B	290	GLY	3.6
1	B	536	THR	3.5
1	B	551	GLY	3.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	B	530	GLY	3.5
1	B	562	TYR	3.4
1	B	545	SER	3.4
1	B	504	THR	3.4
1	B	492	VAL	3.4
1	B	528	ILE	3.3
1	B	531	PHE	3.3
1	B	426	GLY	3.3
1	B	303	LEU	3.3
1	B	459	ARG	3.2
1	B	503	ASN	3.2
1	B	489	ILE	3.2
1	A	138	ASN	3.1
1	B	535	ASN	3.1
1	B	541	SER	3.1
1	A	120	ASN	3.1
1	B	497	PHE	3.1
1	A	118	SER	3.1
1	B	563	ILE	3.1
1	B	473	SER	3.1
1	A	564	ASP	3.1
1	B	499	PRO	3.0
1	A	68	LEU	3.0
1	B	537	THR	2.9
1	B	67	SER	2.9
1	B	502	ILE	2.8
1	B	468	ALA	2.8
1	A	139	GLN	2.8
1	B	560	VAL	2.8
1	A	65	SER	2.8
1	B	422	TYR	2.7
1	A	67	SER	2.7
1	A	289	SER	2.7
1	B	527	SER	2.7
1	B	302	THR	2.7
1	A	117	SER	2.6
1	B	169	GLY	2.5
1	B	532	THR	2.5
1	B	488	SER	2.5
1	B	471	SER	2.5
1	B	476	PHE	2.5
1	B	525	ASP	2.5

Continued on next page...

Continued from previous page...

Mol	Chain	Res	Type	RSRZ
1	A	131	ASN	2.5
1	B	511	VAL	2.5
1	B	547	GLY	2.5
1	B	130	LEU	2.4
1	B	84	SER	2.4
1	B	510	PRO	2.3
1	B	494	ILE	2.3
1	B	66	SER	2.3
1	B	443	ASP	2.3
1	B	466	PHE	2.3
1	B	330	ASN	2.3
1	B	289	SER	2.3
1	B	132	PHE	2.3
1	A	66	SER	2.2
1	B	498	GLU	2.2
1	B	438	TYR	2.2
1	A	386	ASN	2.2
1	A	331	SER	2.1
1	B	526	PHE	2.1
1	A	69	TYR	2.1
1	B	64	ALA	2.1
1	B	304	GLY	2.1
1	B	529	GLU	2.1
1	A	193	PRO	2.1
1	B	139	GLN	2.1
1	A	438	TYR	2.1
1	A	137	ASP	2.0
1	B	479	ASN	2.0
1	B	491	ASN	2.0

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

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

6.3 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

6.4 Ligands

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

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(Å ²)	Q<0.9
2	NAG	B	1004	14/15	0.74	0.15	32,35,40,41	0
2	NAG	A	1000	14/15	0.75	0.14	32,34,39,42	0
2	NAG	B	1006	14/15	0.75	0.14	33,38,43,47	0
2	NAG	B	1009	14/15	0.75	0.15	37,41,47,49	0
2	NAG	A	1009	14/15	0.76	0.15	21,36,40,40	0
2	NAG	A	1007	14/15	0.76	0.14	30,36,41,43	0
2	NAG	B	1010	14/15	0.77	0.12	42,46,48,48	0
2	NAG	B	1011	14/15	0.77	0.15	34,38,49,51	0
2	NAG	B	1000	14/15	0.79	0.14	29,33,37,39	0
2	NAG	B	1008	14/15	0.81	0.13	38,41,43,45	0
2	NAG	B	1002	14/15	0.81	0.13	31,40,47,47	0
2	NAG	B	1005	14/15	0.83	0.12	27,34,44,45	0
2	NAG	A	1004	14/15	0.84	0.12	24,29,34,34	0
2	NAG	A	1008	14/15	0.86	0.11	17,22,28,39	0
2	NAG	B	1007	14/15	0.86	0.13	33,35,42,43	0
2	NAG	A	1005	14/15	0.86	0.12	22,28,33,37	0
2	NAG	A	1002	14/15	0.87	0.10	27,29,32,36	0
2	NAG	A	1006	14/15	0.88	0.11	22,29,33,35	0
2	NAG	B	1003	14/15	0.88	0.11	31,33,40,40	0
2	NAG	B	1001	14/15	0.89	0.10	22,26,31,33	0
2	NAG	A	1010	14/15	0.90	0.09	24,27,31,34	0
2	NAG	A	1003	14/15	0.96	0.06	16,18,21,22	0
2	NAG	A	1001	14/15	0.96	0.05	13,15,17,17	0

6.5 Other polymers

There are no such residues in this entry.