



wwPDB X-ray Structure Validation Summary Report ⓘ

Sep 3, 2023 – 06:33 PM EDT

PDB ID : 3SBR
Title : Pseudomonas stutzeri nitrous oxide reductase, P1 crystal form with substrate
Authors : Pomowski, A.; Zumft, W.G.; Kroneck, P.M.H.; Einsle, O.
Deposited on : 2011-06-06
Resolution : 2.24 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 : 4.02b-467
Mogul : 1.8.5 (274361), CSD as541be (2020)
Xtriage (Phenix) : 1.13
EDS : 2.35
Percentile statistics : 20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac : 5.8.0158
CCP4 : 7.0.044 (Gargrove)
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : 2.35

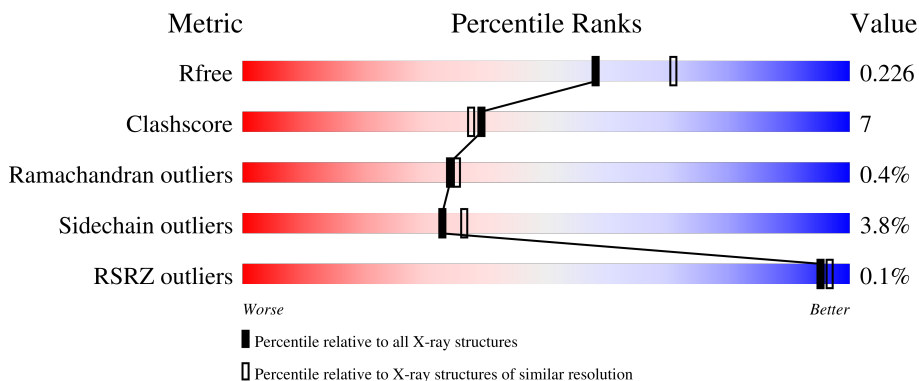
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.24 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}	130704	2391 (2.26-2.22)
Clashscore	141614	2539 (2.26-2.22)
Ramachandran outliers	138981	2489 (2.26-2.22)
Sidechain outliers	138945	2490 (2.26-2.22)
RSRZ outliers	127900	2353 (2.26-2.22)

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	638	 77% 13% • 9%
1	B	638	 75% 15% • 9%
1	C	638	 78% 11% • 9%
1	D	638	 79% 11% • 8%
1	E	638	 76% 13% • 9%

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Mol	Chain	Length	Quality of chain	
1	F	638	79%	11% • 9%
1	G	638	78%	12% • 8%
1	H	638	75%	14% • 9%

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	CL	A	704	-	-	X	-
7	IMD	H	639	-	-	X	-

2 Entry composition

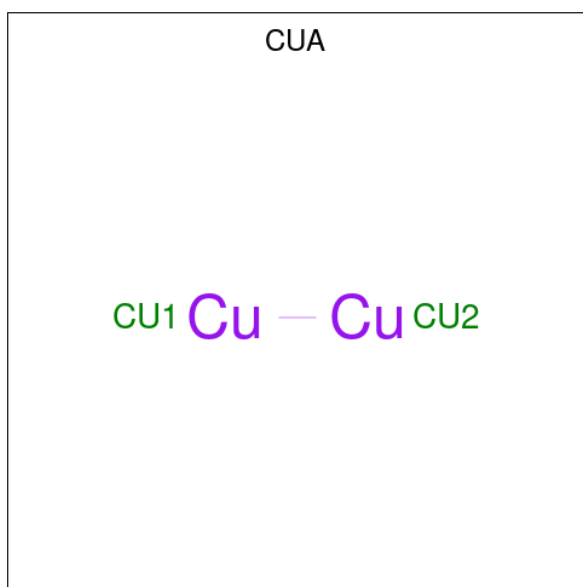
There are 9 unique types of molecules in this entry. The entry contains 39507 atoms, of which 0 are hydrogens and 0 are deuteriums.

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 Nitrous-oxide reductase.

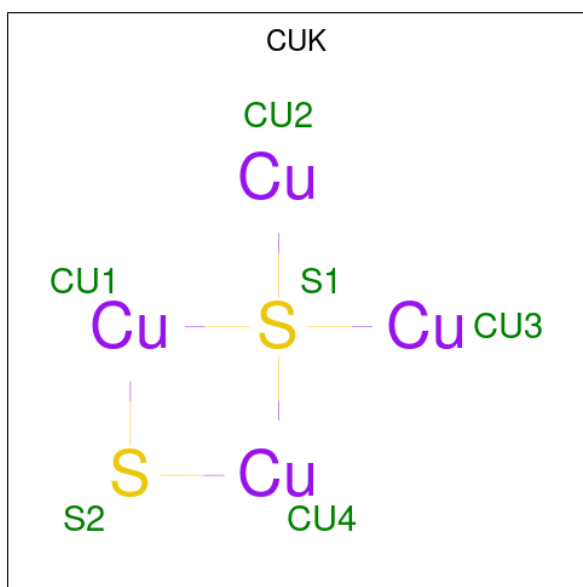
Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	581	4573	2891	788	862	32	0	1	0
1	B	581	4592	2902	792	866	32	0	3	0
1	C	581	4590	2900	790	868	32	0	3	0
1	D	588	4636	2929	799	876	32	0	2	0
1	E	581	4575	2892	788	863	32	0	1	0
1	F	581	4593	2902	790	869	32	0	3	0
1	G	585	4606	2911	794	869	32	0	1	0
1	H	581	4590	2900	790	868	32	0	3	0

- Molecule 2 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	1	Total Cu 2 2	0	0
2	B	1	Total Cu 2 2	0	0
2	C	1	Total Cu 2 2	0	0
2	D	1	Total Cu 2 2	0	0
2	E	1	Total Cu 2 2	0	0
2	F	1	Total Cu 2 2	0	0
2	G	1	Total Cu 2 2	0	0
2	H	1	Total Cu 2 2	0	0

- Molecule 3 is [4Cu:2S] cluster (three-letter code: CUK) (formula: Cu₄S₂).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
3	A	1	Total	Cu	S	0	0
			6	4	2		
3	B	1	Total	Cu	S	0	0
			6	4	2		
3	C	1	Total	Cu	S	0	0
			6	4	2		
3	D	1	Total	Cu	S	0	0
			6	4	2		
3	E	1	Total	Cu	S	0	0
			6	4	2		
3	F	1	Total	Cu	S	0	0
			6	4	2		
3	G	1	Total	Cu	S	0	0
			6	4	2		
3	H	1	Total	Cu	S	0	0
			6	4	2		

- Molecule 4 is CALCIUM ION (three-letter code: CA) (formula: Ca).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	A	1	Total	Ca	0	0
			1	1		
4	B	1	Total	Ca	0	0
			1	1		
4	C	1	Total	Ca	0	0
			1	1		
4	D	1	Total	Ca	0	0
			1	1		

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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	E	1	Total Ca 1 1	0	0
4	F	1	Total Ca 1 1	0	0
4	G	1	Total Ca 1 1	0	0
4	H	1	Total Ca 1 1	0	0

- Molecule 5 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total Cl 1 1	0	0
5	B	1	Total Cl 1 1	0	0
5	C	1	Total Cl 1 1	0	0
5	D	1	Total Cl 1 1	0	0
5	E	1	Total Cl 1 1	0	0
5	F	1	Total Cl 1 1	0	0
5	G	1	Total Cl 1 1	0	0
5	H	1	Total Cl 1 1	0	0

- Molecule 6 is POTASSIUM ION (three-letter code: K) (formula: K).

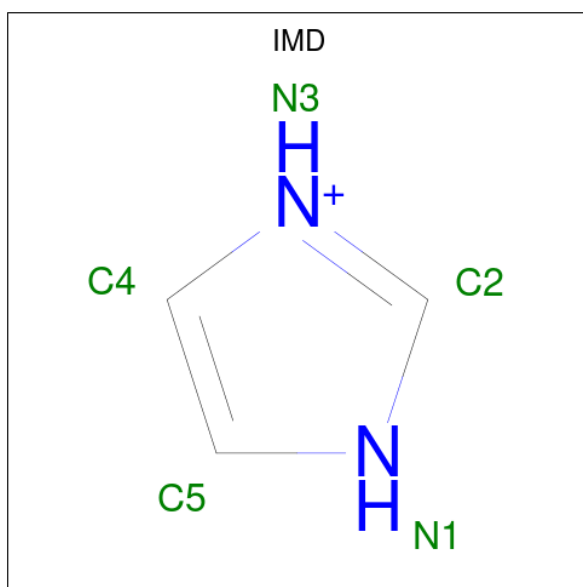
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total K 1 1	0	0
6	B	1	Total K 1 1	0	0
6	C	1	Total K 1 1	0	0
6	D	1	Total K 1 1	0	0
6	E	1	Total K 1 1	0	0

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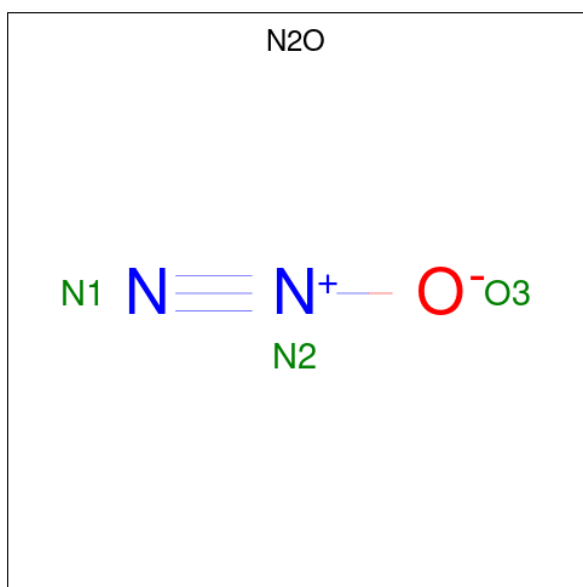
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	F	1	Total K 1 1	0	0
6	G	1	Total K 1 1	0	0
6	H	1	Total K 1 1	0	0

- Molecule 7 is IMIDAZOLE (three-letter code: IMD) (formula: C₃H₅N₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	D	1	Total C N 5 3 2	0	0
7	E	1	Total C N 5 3 2	0	0
7	E	1	Total C N 5 3 2	0	0
7	F	1	Total C N 5 3 2	0	0
7	G	1	Total C N 5 3 2	0	0
7	H	1	Total C N 5 3 2	0	0

- Molecule 8 is NITROUS OXIDE (three-letter code: N2O) (formula: N₂O).



Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
8	D	1	Total	N	O	0	0
			3	2	1		
8	H	1	Total	N	O	0	0
			3	2	1		

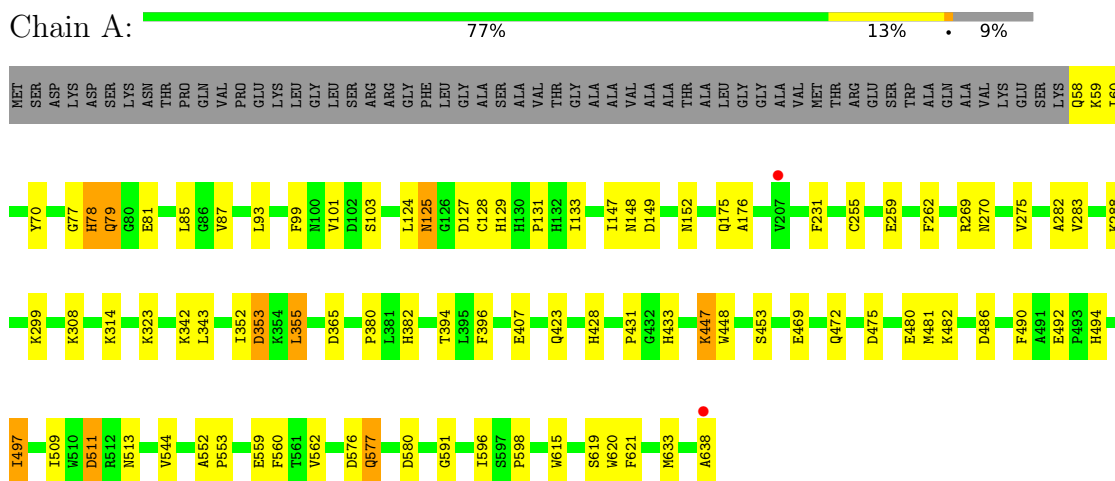
- Molecule 9 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
9	A	207	Total	O	0	0
			207	207		
9	B	183	Total	O	0	0
			183	183		
9	C	367	Total	O	0	0
			367	367		
9	D	365	Total	O	0	0
			365	365		
9	E	393	Total	O	0	0
			393	393		
9	F	411	Total	O	0	0
			411	411		
9	G	349	Total	O	0	0
			349	349		
9	H	353	Total	O	0	0
			353	353		

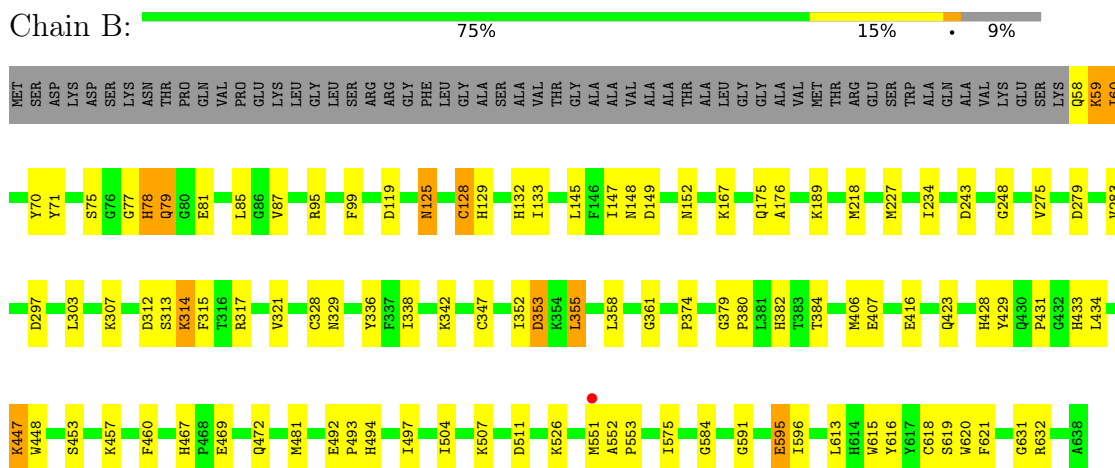
3 Residue-property plots [i](#)

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.

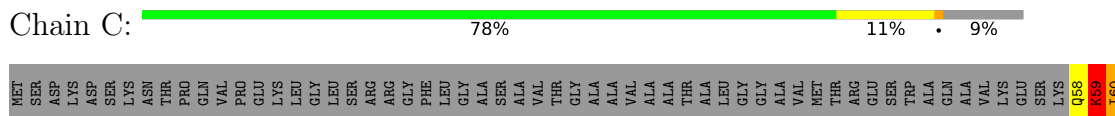
- Molecule 1: Nitrous-oxide reductase

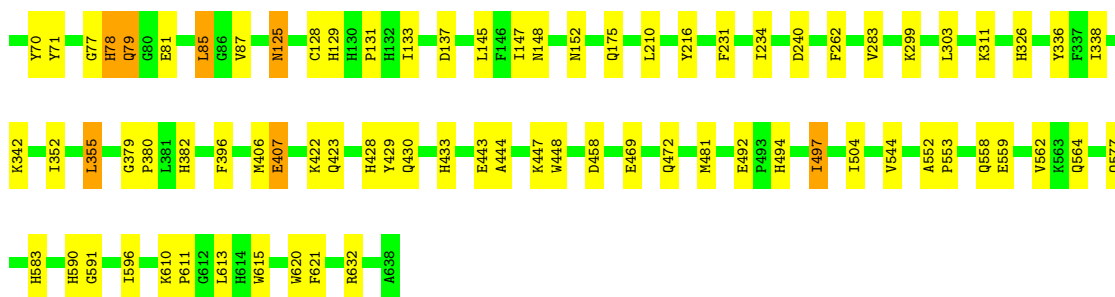


- Molecule 1: Nitrous-oxide reductase



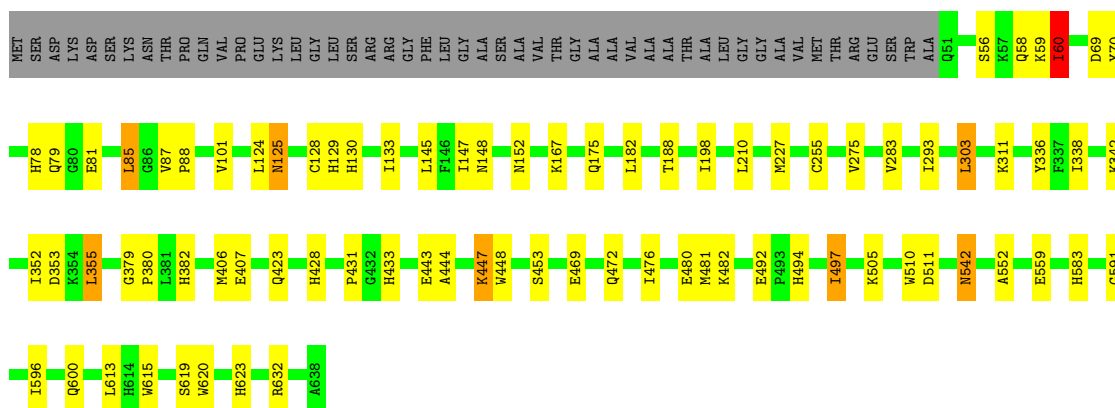
- Molecule 1: Nitrous-oxide reductase





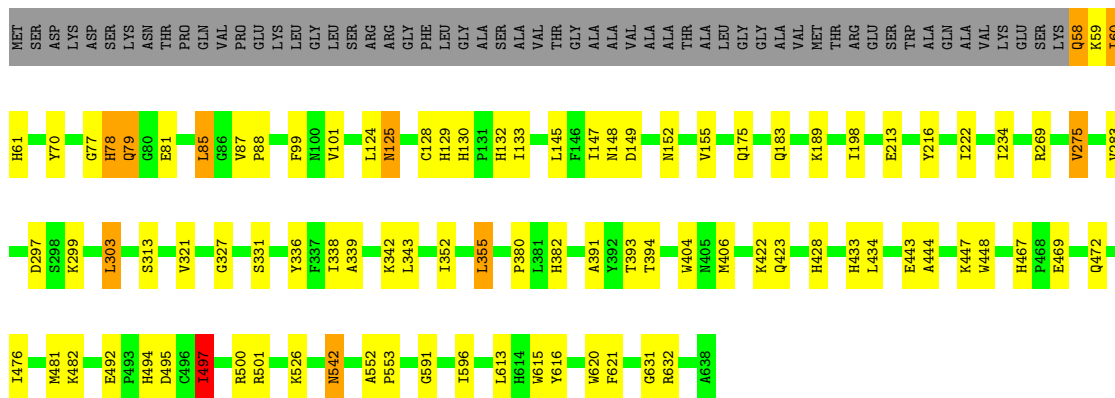
- Molecule 1: Nitrous-oxide reductase

Chain D: 79% 11% 8%



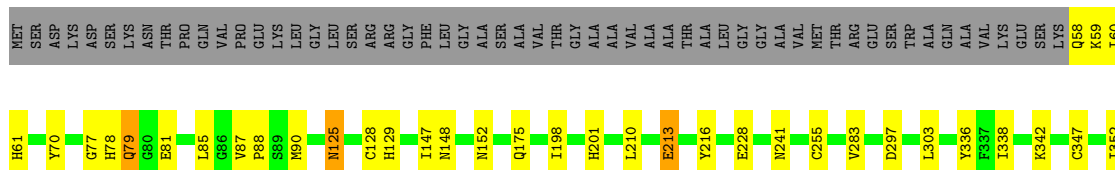
- Molecule 1: Nitrous-oxide reductase

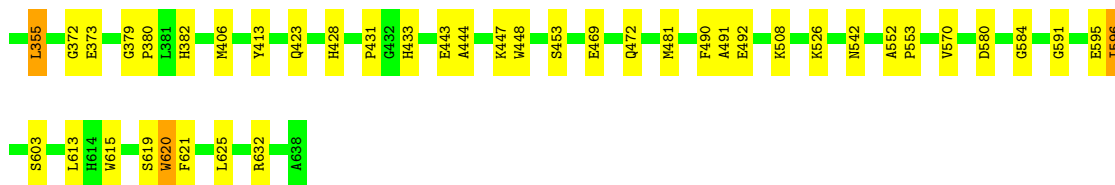
Chain E: 76% 13% 9%



- Molecule 1: Nitrous-oxide reductase

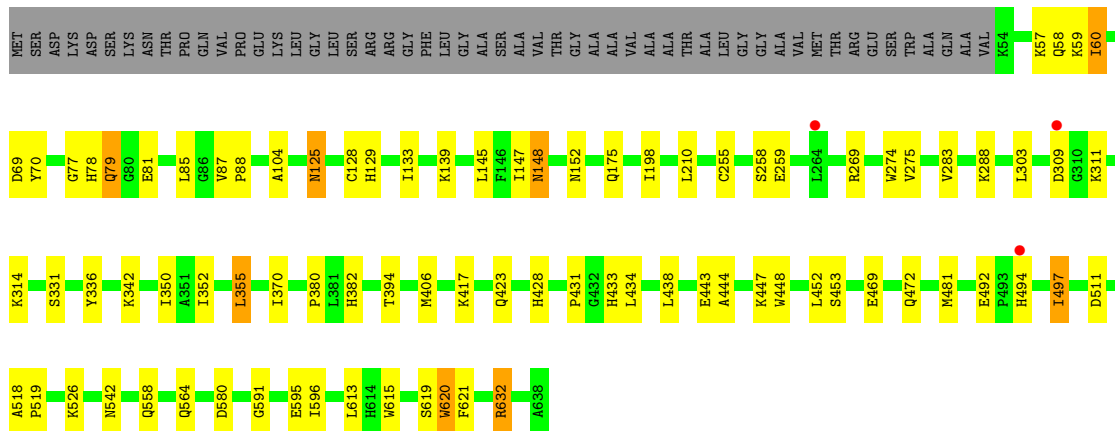
Chain F: 79% 11% 9%





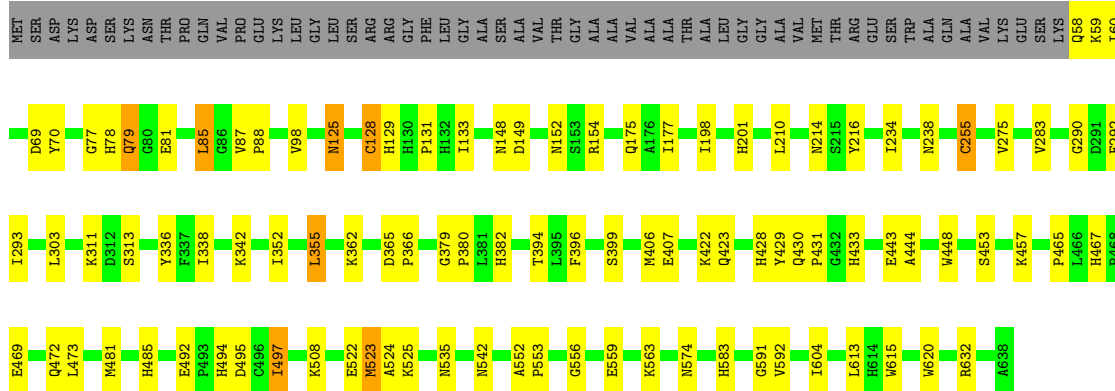
• Molecule 1: Nitrous-oxide reductase

Chain G: 78% 12% 8%



• Molecule 1: Nitrous-oxide reductase

Chain H: 75% 14% 9%



4 Data and refinement statistics i

Property	Value	Source
Space group	P 1	Depositor
Cell constants a, b, c, α , β , γ	96.58Å 106.45Å 130.88Å 111.45° 107.22° 90.72°	Depositor
Resolution (Å)	95.00 – 2.24 95.06 – 2.24	Depositor EDS
% Data completeness (in resolution range)	93.3 (95.00-2.24) 93.3 (95.06-2.24)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	4.89 (at 2.25Å)	Xtrriage
Refinement program	REFMAC 5.5.0109	Depositor
R, R_{free}	0.173 , 0.227 0.174 , 0.226	Depositor DCC
R_{free} test set	10299 reflections (5.02%)	wwPDB-VP
Wilson B-factor (Å ²)	17.8	Xtrriage
Anisotropy	0.103	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 34.6	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	0.012 for -h,k,-k-l	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	39507	wwPDB-VP
Average B, all atoms (Å ²)	20.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.37% 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: CUA, CA, IMD, N2O, CUK, K, CL

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	0.46	0/4685	0.61	1/6345 (0.0%)
1	B	0.48	0/4705	0.61	0/6372
1	C	0.57	0/4702	0.65	1/6368 (0.0%)
1	D	0.53	0/4748	0.66	1/6428 (0.0%)
1	E	0.59	0/4687	0.69	3/6348 (0.0%)
1	F	0.57	0/4705	0.66	1/6372 (0.0%)
1	G	0.54	0/4718	0.66	2/6387 (0.0%)
1	H	0.57	0/4702	0.67	1/6368 (0.0%)
All	All	0.54	0/37652	0.65	10/50988 (0.0%)

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	D	0	1
1	E	0	1
1	F	0	1
1	G	0	1
All	All	0	4

There are no bond length outliers.

The worst 5 of 10 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	85	LEU	CA-CB-CG	6.78	130.90	115.30
1	E	85	LEU	CA-CB-CG	6.28	129.74	115.30
1	E	303	LEU	CA-CB-CG	-6.26	100.89	115.30
1	G	632	ARG	NE-CZ-NH2	-6.16	117.22	120.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	497	ILE	CB-CA-C	-5.58	100.44	111.60

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	58	GLN	Peptide
1	E	58	GLN	Peptide
1	F	58	GLN	Peptide
1	G	58	GLN	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	4573	0	4441	59	0
1	B	4592	0	4452	84	0
1	C	4590	0	4449	70	0
1	D	4636	0	4505	64	0
1	E	4575	0	4440	86	0
1	F	4593	0	4450	66	0
1	G	4606	0	4478	71	0
1	H	4590	0	4449	81	0
2	A	2	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	F	2	0	0	0	0
2	G	2	0	0	0	0
2	H	2	0	0	0	0
3	A	6	0	0	0	0
3	B	6	0	0	0	0
3	C	6	0	0	1	0
3	D	6	0	0	0	0
3	E	6	0	0	0	0
3	F	6	0	0	0	0

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Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
3	G	6	0	0	0	0
3	H	6	0	0	1	0
4	A	1	0	0	0	0
4	B	1	0	0	0	0
4	C	1	0	0	0	0
4	D	1	0	0	0	0
4	E	1	0	0	0	0
4	F	1	0	0	0	0
4	G	1	0	0	0	0
4	H	1	0	0	0	0
5	A	1	0	0	2	0
5	B	1	0	0	0	0
5	C	1	0	0	1	0
5	D	1	0	0	0	0
5	E	1	0	0	1	0
5	F	1	0	0	1	0
5	G	1	0	0	0	0
5	H	1	0	0	1	0
6	A	1	0	0	0	0
6	B	1	0	0	0	0
6	C	1	0	0	0	0
6	D	1	0	0	0	0
6	E	1	0	0	0	0
6	F	1	0	0	0	0
6	G	1	0	0	0	0
6	H	1	0	0	0	0
7	D	5	0	5	2	0
7	E	10	0	10	4	0
7	F	5	0	5	2	0
7	G	5	0	5	2	0
7	H	5	0	5	4	0
8	D	3	0	0	1	0
8	H	3	0	0	0	0
9	A	207	0	0	3	0
9	B	183	0	0	5	0
9	C	367	0	0	4	0
9	D	365	0	0	6	0
9	E	393	0	0	9	0
9	F	411	0	0	7	0
9	G	349	0	0	9	0
9	H	353	0	0	5	0
All	All	39507	0	35694	539	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 7.

The worst 5 of 539 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:H:338:ILE:HD11	1:H:406:MET:CE	1.80	1.10
9:D:2328:HOH:O	1:E:542:ASN:HB3	1.58	1.03
1:F:338:ILE:HD11	1:F:406:MET:HE3	1.40	1.01
1:E:336:TYR:HD2	1:E:406:MET:HE1	1.26	0.97
1:F:336:TYR:HD2	1:F:406:MET:HE1	1.31	0.96

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	580/638 (91%)	544 (94%)	32 (6%)	4 (1%)	22	20
1	B	582/638 (91%)	554 (95%)	24 (4%)	4 (1%)	22	20
1	C	582/638 (91%)	560 (96%)	19 (3%)	3 (0%)	29	28
1	D	588/638 (92%)	561 (95%)	25 (4%)	2 (0%)	41	44
1	E	580/638 (91%)	555 (96%)	24 (4%)	1 (0%)	47	53
1	F	582/638 (91%)	552 (95%)	27 (5%)	3 (0%)	29	28
1	G	584/638 (92%)	556 (95%)	27 (5%)	1 (0%)	47	53
1	H	582/638 (91%)	557 (96%)	23 (4%)	2 (0%)	41	44
All	All	4660/5104 (91%)	4439 (95%)	201 (4%)	20 (0%)	34	35

5 of 20 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	60	ILE

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Mol	Chain	Res	Type
1	B	342	LYS
1	C	59	LYS
1	A	342	LYS
1	E	342	LYS

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	497/537 (93%)	475 (96%)	22 (4%)	28	30
1	B	499/537 (93%)	479 (96%)	20 (4%)	31	34
1	C	499/537 (93%)	480 (96%)	19 (4%)	33	36
1	D	504/537 (94%)	485 (96%)	19 (4%)	33	36
1	E	497/537 (93%)	480 (97%)	17 (3%)	37	42
1	F	499/537 (93%)	485 (97%)	14 (3%)	43	49
1	G	501/537 (93%)	481 (96%)	20 (4%)	31	34
1	H	499/537 (93%)	480 (96%)	19 (4%)	33	36
All	All	3995/4296 (93%)	3845 (96%)	150 (4%)	33	36

5 of 150 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	G	85	LEU
1	H	407	GLU
1	G	255	CYS
1	G	621	PHE
1	C	210	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 111 such sidechains are listed below:

Mol	Chain	Res	Type
1	D	558	GLN

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Mol	Chain	Res	Type
1	H	583	HIS
1	E	542	ASN
1	H	577	GLN
1	H	79	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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 48 ligands modelled in this entry, 24 are monoatomic - leaving 24 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	CUK	C	702	1	0,6,6	-	-	-		
3	CUK	H	702	1	0,6,6	-	-	-		
2	CUA	C	701	1	0,1,1	-	-	-		
7	IMD	E	640	-	3,5,5	0.43	0	4,5,5	0.36	0
7	IMD	G	639	-	3,5,5	0.34	0	4,5,5	0.49	0
8	N2O	D	640	-	0,2,2	-	-	0,1,1	-	-
2	CUA	D	701	1	0,1,1	-	-	-		
2	CUA	E	701	1	0,1,1	-	-	-		
2	CUA	A	701	1	0,1,1	-	-	-		
7	IMD	H	639	-	3,5,5	0.43	0	4,5,5	0.37	0

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	# Z > 2	Counts	RMSZ	# Z > 2
3	CUK	D	702	1	0,6,6	-	-	-		
2	CUA	H	701	1	0,1,1	-	-	-		
7	IMD	E	639	-	3,5,5	0.47	0	4,5,5	0.46	0
3	CUK	E	702	1	0,6,6	-	-	-		
7	IMD	F	639	-	3,5,5	0.34	0	4,5,5	0.69	0
2	CUA	B	701	1	0,1,1	-	-	-		
2	CUA	F	701	1	0,1,1	-	-	-		
3	CUK	A	702	1	0,6,6	-	-	-		
3	CUK	B	702	1	0,6,6	-	-	-		
3	CUK	F	702	1	0,6,6	-	-	-		
2	CUA	G	701	1	0,1,1	-	-	-		
3	CUK	G	702	1	0,6,6	-	-	-		
8	N2O	H	640	-	0,2,2	-	-	0,1,1	-	-
7	IMD	D	639	-	3,5,5	0.45	0	4,5,5	0.50	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
7	IMD	F	639	-	-	-	0/1/1/1
7	IMD	H	639	-	-	-	0/1/1/1
3	CUK	C	702	1	-	-	0/1/1/1
3	CUK	A	702	1	-	-	0/1/1/1
3	CUK	B	702	1	-	-	0/1/1/1
3	CUK	F	702	1	-	-	0/1/1/1
3	CUK	H	702	1	-	-	0/1/1/1
3	CUK	D	702	1	-	-	0/1/1/1
7	IMD	E	640	-	-	-	0/1/1/1
7	IMD	G	639	-	-	-	0/1/1/1
7	IMD	E	639	-	-	-	0/1/1/1
3	CUK	G	702	1	-	-	0/1/1/1
3	CUK	E	702	1	-	-	0/1/1/1
7	IMD	D	639	-	-	-	0/1/1/1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

9 monomers are involved in 16 short contacts:

Mol	Chain	Res	Type	Clashes	Symm-Clashes
3	C	702	CUK	1	0
3	H	702	CUK	1	0
7	E	640	IMD	3	0
7	G	639	IMD	2	0
8	D	640	N2O	1	0
7	H	639	IMD	4	0
7	E	639	IMD	1	0
7	F	639	IMD	2	0
7	D	639	IMD	2	0

5.7 Other polymers [i](#)

There are no such residues in this entry.

5.8 Polymer linkage issues [i](#)

There are no chain breaks in this entry.

6 Fit of model and data [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	581/638 (91%)	-0.17	2 (0%) 94 94	18, 30, 52, 61	0
1	B	581/638 (91%)	-0.21	1 (0%) 95 96	15, 27, 46, 57	0
1	C	581/638 (91%)	-0.62	0 100 100	7, 14, 28, 39	0
1	D	588/638 (92%)	-0.53	0 100 100	7, 18, 32, 43	0
1	E	581/638 (91%)	-0.68	0 100 100	7, 11, 23, 31	0
1	F	581/638 (91%)	-0.67	0 100 100	7, 12, 26, 35	0
1	G	585/638 (91%)	-0.48	3 (0%) 91 91	8, 17, 39, 53	0
1	H	581/638 (91%)	-0.58	0 100 100	7, 15, 30, 38	0
All	All	4659/5104 (91%)	-0.49	6 (0%) 95 97	7, 18, 40, 61	0

The worst 5 of 6 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	B	551	MET	3.2
1	G	264	LEU	2.7
1	A	638	ALA	2.6
1	G	309	ASP	2.3
1	A	207	VAL	2.2

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 monosaccharides 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
6	K	H	705	1/1	0.65	0.14	56,56,56,56	0
6	K	G	705	1/1	0.69	0.17	57,57,57,57	0
6	K	A	705	1/1	0.69	0.12	56,56,56,56	0
6	K	E	705	1/1	0.76	0.11	55,55,55,55	0
3	CUK	B	702	6/6	0.83	0.15	51,53,55,57	6
6	K	C	705	1/1	0.85	0.09	40,40,40,40	0
6	K	D	705	1/1	0.89	0.07	42,42,42,42	0
6	K	F	705	1/1	0.90	0.07	30,30,30,30	0
7	IMD	G	639	5/5	0.91	0.24	27,28,28,28	0
6	K	B	705	1/1	0.92	0.14	62,62,62,62	0
7	IMD	F	639	5/5	0.92	0.22	32,33,33,34	0
3	CUK	H	702	6/6	0.92	0.13	32,36,39,41	6
8	N2O	H	640	3/3	0.93	0.37	51,51,51,52	0
7	IMD	D	639	5/5	0.95	0.26	27,27,28,28	0
4	CA	A	703	1/1	0.95	0.08	37,37,37,37	0
3	CUK	G	702	6/6	0.95	0.10	33,38,40,42	6
3	CUK	A	702	6/6	0.95	0.10	42,45,47,47	6
3	CUK	E	702	6/6	0.96	0.08	27,32,35,36	6
3	CUK	D	702	6/6	0.96	0.06	27,32,32,35	6
7	IMD	H	639	5/5	0.96	0.13	11,13,14,14	0
5	CL	B	704	1/1	0.96	0.18	45,45,45,45	0
5	CL	A	704	1/1	0.97	0.16	39,39,39,39	0
7	IMD	E	639	5/5	0.97	0.10	26,27,28,28	0
3	CUK	C	702	6/6	0.97	0.11	27,31,34,34	6
2	CUA	A	701	2/2	0.97	0.06	30,30,30,33	0
2	CUA	C	701	2/2	0.97	0.06	21,21,21,25	0
4	CA	H	703	1/1	0.97	0.09	9,9,9,9	0
2	CUA	B	701	2/2	0.98	0.04	37,37,37,38	0
7	IMD	E	640	5/5	0.98	0.14	12,12,14,14	0
2	CUA	F	701	2/2	0.98	0.07	18,18,18,21	0
4	CA	G	703	1/1	0.98	0.05	31,31,31,31	0
3	CUK	F	702	6/6	0.98	0.07	22,27,28,29	5
8	N2O	D	640	3/3	0.98	0.36	43,43,44,45	0
2	CUA	H	701	2/2	0.98	0.06	29,29,29,31	0
4	CA	B	703	1/1	0.99	0.07	23,23,23,23	0
4	CA	C	703	1/1	0.99	0.05	11,11,11,11	0
5	CL	C	704	1/1	0.99	0.07	24,24,24,24	0

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Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors(\AA^2)	Q<0.9
5	CL	E	704	1/1	0.99	0.06	20,20,20,20	0
5	CL	F	704	1/1	0.99	0.05	17,17,17,17	0
5	CL	H	704	1/1	0.99	0.07	27,27,27,27	0
4	CA	D	703	1/1	0.99	0.06	19,19,19,19	0
4	CA	E	703	1/1	0.99	0.08	10,10,10,10	0
4	CA	F	703	1/1	0.99	0.05	13,13,13,13	0
2	CUA	D	701	2/2	0.99	0.06	17,17,17,18	0
2	CUA	G	701	2/2	0.99	0.07	15,15,15,18	0
5	CL	G	704	1/1	1.00	0.05	26,26,26,26	0
2	CUA	E	701	2/2	1.00	0.06	14,14,14,17	0
5	CL	D	704	1/1	1.00	0.10	25,25,25,25	0

6.5 Other polymers [\(i\)](#)

There are no such residues in this entry.