

wwPDB X-ray Structure Validation Summary Report (i)

Jan 4, 2021 – 04:20 pm GMT

PDB ID : 7AQ7

Title : Pseudomonas stutzeri nitrous oxide reductase mutant, H583Y

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Deposited on : 2020-10-20

Resolution : 1.61 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 (i) symbol.

The following versions of software and data (see references (1)) 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 : 2.16

buster-report : 1.1.7 (2018)

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)

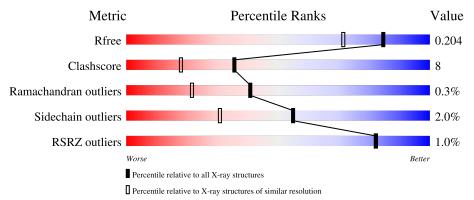
Validation Pipeline (wwPDB-VP) : 2.16

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 1.61 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	$\begin{array}{c} \text{Whole archive} \\ (\#\text{Entries}) \end{array}$	$\begin{array}{c} {\rm Similar \; resolution} \\ (\#{\rm Entries, \; resolution \; range(\AA)}) \end{array}$
R_{free}	130704	3398 (1.60-1.60)
Clashscore	141614	3665 (1.60-1.60)
Ramachandran outliers	138981	3564 (1.60-1.60)
Sidechain outliers	138945	3563 (1.60-1.60)
RSRZ outliers	127900	3321 (1.60-1.60)

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 <=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	646	78%	12%	•	9%
1	В	646	74%	16%	•	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
6	FMT	В	705	_	_	X	-
6	FMT	В	706	-	-	X	-



2 Entry composition (i)

There are 11 unique types of molecules in this entry. The entry contains 10315 atoms, of which 8 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.

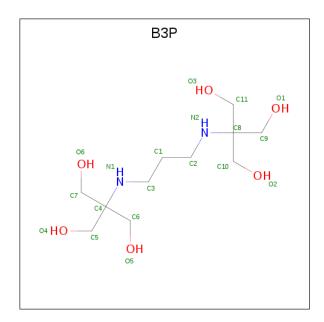
\mathbf{Mol}	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	586	Total 4634	C 2933	N 793	O 875	S 33	0	6	0
1	В	586	Total 4631	C 2934	N 795	O 870	S 32	0	2	0

There are 18 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	583	TYR	HIS	engineered mutation	UNP P19573
A	639	TRP	-	expression tag	UNP P19573
A	640	SER	_	- expression tag	
A	641	HIS	_	- expression tag	
A	642	PRO	_	expression tag	UNP P19573
A	643	GLN	_	expression tag	UNP P19573
A	644	PHE	_	expression tag	UNP P19573
A	645	GLU	_	expression tag	UNP P19573
A	646	LYS	_	expression tag	UNP P19573
В	583	TYR	HIS	engineered mutation	UNP P19573
В	639	TRP	_	expression tag	UNP P19573
В	640	SER	_	expression tag	UNP P19573
В	641	HIS	_	expression tag	UNP P19573
В	642	PRO	_	expression tag	UNP P19573
В	643	GLN	_	expression tag	UNP P19573
В	644	PHE	-	expression tag	UNP P19573
В	645	GLU	-	expression tag	UNP P19573
В	646	LYS	_	expression tag	UNP P19573

• Molecule 2 is 2-[3-(2-HYDROXY-1,1-DIHYDROXYMETHYL-ETHYLAMINO)-PROPYL AMINO]-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: B3P) (formula: $C_{11}H_{26}N_2O_6$).





Mol	Chain	Residues	${f Atoms}$				ZeroOcc	AltConf	
2	Λ	1	Total	С	N	О	0	0	
	Α	1	19	11	2	6	U		
2	D	1	Total	С	N	О	0	0	
	2 B	1	19	11	2	6	0	U	

• Molecule 3 is SODIUM ION (three-letter code: NA) (formula: Na).

Mol	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
3	В	1	Total Na 1 1	0	0
3	A	1	Total Na 1 1	0	0

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

\mathbf{Mol}	Chain	Residues	${f Atoms}$	ZeroOcc	AltConf
4	В	1	Total Ca 1 1	0	0
4	A	1	Total Ca 1 1	0	0

• Molecule 5 is POTASSIUM ION (three-letter code: K) (formula: K).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	В	1	Total K 1 1	0	0

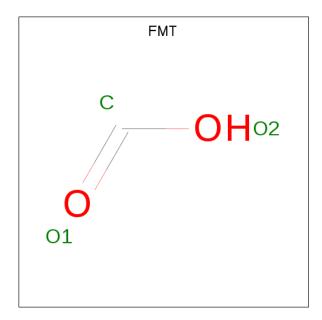
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Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
5	A	1	Total K 1 1	0	0

• Molecule 6 is FORMIC ACID (three-letter code: FMT) (formula: CH₂O₂).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
6	A	1	Total C O 3 1 2	0	0
6	A	1	Total C O 3 1 2	0	0
6	A	1	Total C O 3 1 2	0	0
6	A	1	Total C O 3 1 2	0	0
6	A	1	Total C O 3 1 2	0	0
6	A	1	Total C H O 5 1 2 2	0	0
6	В	1	Total C O 3 1 2	0	0
6	В	1	Total C O 3 1 2	0	0
6	В	1	Total C H O 5 1 2 2	0	0
6	В	1	Total C H O 5 1 2 2	0	0

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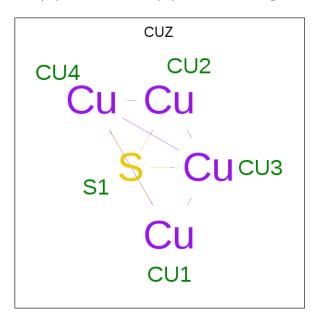
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Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
6	D	1	Total	С	Н	О	0	0
0	Б	1	5	1	2	2	0	0

• Molecule 7 is CHLORIDE ION (three-letter code: CL) (formula: Cl).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
7	В	1	Total Cl 1 1	0	0
7	A	2	Total Cl 2 2	0	0

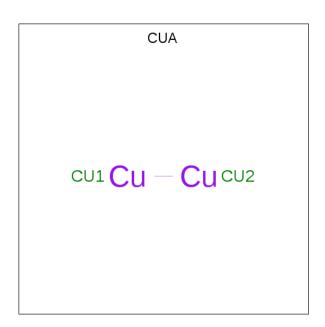
• Molecule 8 is (MU-4-SULFIDO)-TETRA-NUCLEAR COPPER ION (three-letter code: CUZ) (formula: Cu₄S) (labeled as "Ligand of Interest" by depositor).



Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
8	A	1	Total Cu S 5 4 1	0	0
8	В	1	Total Cu S 5 4 1	0	0

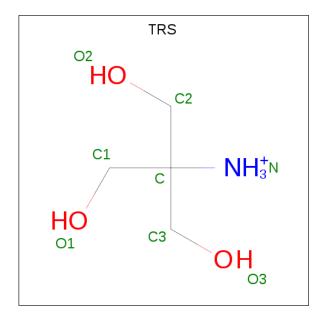
• Molecule 9 is DINUCLEAR COPPER ION (three-letter code: CUA) (formula: Cu₂) (labeled as "Ligand of Interest" by depositor).





Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
9	A	1	Total Cu 2 2	0	0
9	В	1	Total Cu 2 2	0	0

• Molecule 10 is 2-AMINO-2-HYDROXYMETHYL-PROPANE-1,3-DIOL (three-letter code: TRS) (formula: $C_4H_{12}NO_3$).



Mol	Chain	Residues	Atoms		ZeroOcc	AltConf		
10	A	1	Total 8	C 4	N 1	O 3	0	0



• Molecule 11 is water.

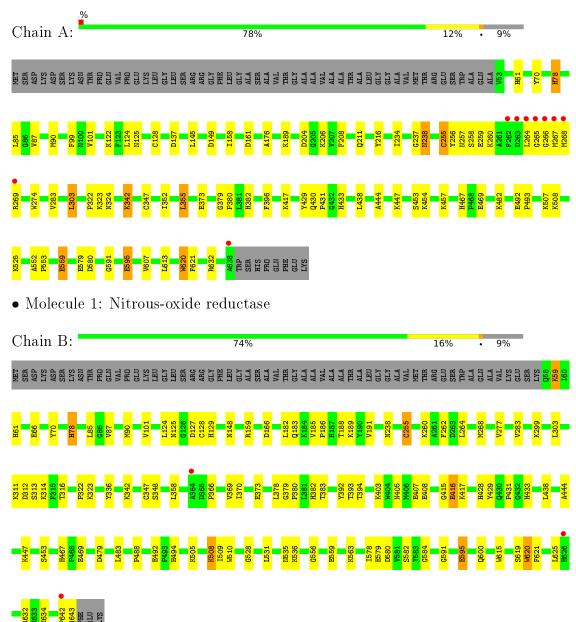
Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
11	A	531	Total O 531 531	0	0
11	В	409	Total O 409 409	0	0



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





4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants	68.73Å 76.07Å 108.47Å	Depositor
a, b, c, α , β , γ	90.00° 93.49° 90.00°	Depositor
Resolution (Å)	68.61 - 1.61	Depositor
Resolution (A)	108.27 - 1.61	EDS
% Data completeness	62.6 (68.61-1.61)	Depositor
(in resolution range)	62.9 (108.27-1.61)	EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) > 1$	1.15 (at 1.61Å)	Xtriage
Refinement program	PHENIX 1.13_2998	Depositor
P. P.	0.152 , 0.204	Depositor
R, R_{free}	0.153 , 0.204	DCC
R_{free} test set	4632 reflections (5.08%)	wwPDB-VP
Wilson B-factor (Å ²)	21.5	Xtriage
Anisotropy	0.061	Xtriage
Bulk solvent $k_{sol}(e/Å^3)$, $B_{sol}(Å^2)$	$0.32\;,50.5$	EDS
L-test for twinning ²	$ < L > = 0.49, < L^2> = 0.32$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	10315	wwPDB-VP
Average B, all atoms $(Å^2)$	31.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: The largest off-origin peak in the Patterson function is 4.17% of the height of the origin peak. No significant pseudotranslation is detected.

²Theoretical values of <|L|>, $< L^2>$ for acentric reflections are 0.5, 0.333 respectively for untwinned datasets, and 0.375, 0.2 for perfectly twinned datasets.



¹Intensities estimated from amplitudes.

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: CL, NA, K, B3P, CUZ, CUA, TRS, CA, FMT

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	Boı	nd lengths	Bond angles		
MIOI	Chain	RMSZ	# Z > 5	RMSZ	# Z > 5	
1	A	0.51	$2/4764 \ (0.0\%)$	0.66	$2/6449 \ (0.0\%)$	
1	В	0.47	0/4755	0.64	0/6444	
All	All	0.49	$2/9519 \ (0.0\%)$	0.65	$2/12893 \ (0.0\%)$	

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 maintain group or atoms of a sidechain that are expected to be planar.

Mol	Chain	#Chirality outliers	#Planarity outliers
1	В	0	1

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$\mathbf{Observed}(\mathbf{\mathring{A}})$	$\operatorname{Ideal}(\text{\AA})$
1	A	128	CYS	CB-SG	-8.09	1.68	1.82
1	A	595	GLU	CB-CG	6.03	1.63	1.52

All (2) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	\mathbf{Z}	$Observed(^o)$	$\operatorname{Ideal}({}^o)$
1	A	303	LEU	CA-CB-CG	-5.96	101.58	115.30
1	A	493	PRO	C-N-CA	-5.16	108.81	121.70

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	В	336	TYR	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	4634	0	4521	71	0
1	В	4631	0	4490	88	0
2	A	19	0	26	1	0
2	В	19	0	26	2	0
3	A	1	0	0	0	0
3	В	1	0	0	0	0
4	A	1	0	0	0	0
4	В	1	0	0	0	0
5	A	1	0	0	0	0
5	В	1	0	0	0	0
6	A	18	2	6	2	0
6	В	15	6	5	4	0
7	A	2	0	0	0	0
7	В	1	0	0	0	0
8	A	5	0	0	0	0
8	В	5	0	0	0	0
9	A	2	0	0	0	0
9	В	2	0	0	0	0
10	A	8	0	12	0	0
11	A	531	0	0	15	2
11	В	409	0	0	17	1
All	All	10307	8	9086	150	3

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 150 close contacts within the same asymmetric unit are listed below, sorted by their clash magnitude.

Atom-1	Atom-2	$egin{aligned} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{aligned}$	$egin{aligned} ext{Clash} \ ext{overlap } (ext{Å}) \end{aligned}$
1:B:531:LEU:H	6:B:705:FMT:H	1.14	1.11
2:B:701:B3P:HN2	6:B:706:FMT:H	1.32	0.95
1:B:90:MET:HE2	11:B:1041:HOH:O	1.68	0.92
1:B:595:GLU:HG3	11:B:803:HOH:O	1.72	0.89
1:A:467:HIS:CE1	1:B:508:LYS:HD2	2.07	0.89



All (3) 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	$egin{array}{c} ext{Interatomic} \ ext{distance} \ (ext{Å}) \end{array}$	Clash overlap (Å)
11:A:1237:HOH:O	11:A:1248:HOH:O[2_556]	1.84	0.36
11:A:802:HOH:O	11:A:1232:HOH:O[2_646]	2.03	0.17
11:B:1186:HOH:O	11:B:1206:HOH:O[2_545]	2.13	0.07

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	590/646 (91%)	564 (96%)	24 (4%)	2 (0%)	41 21	
1	В	586/646 (91%)	560 (96%)	24 (4%)	2 (0%)	41 21	
All	All	1176/1292 (91%)	1124 (96%)	48 (4%)	4 (0%)	41 21	

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	342	LYS
1	В	342	LYS
1	В	416	GLU
1	A	176	ALA

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	Rotameric Outliers	
1	A	507/545~(93%)	497 (98%)	10 (2%)	55 31
1	В	503/545~(92%)	491 (98%)	12 (2%)	49 24
All	All	1010/1090 (93%)	988 (98%)	22 (2%)	55 27

5 of 22 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type	
1	A	621	PHE	
1	В	85	LEU	
1	В	620[A]	TRP	
1	В	59	LYS	
1	В	78	HIS	

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

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 27 ligands modelled in this entry, 9 are monoatomic - leaving 18 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

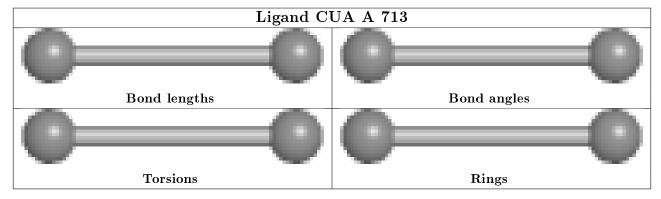
There are no torsion outliers.

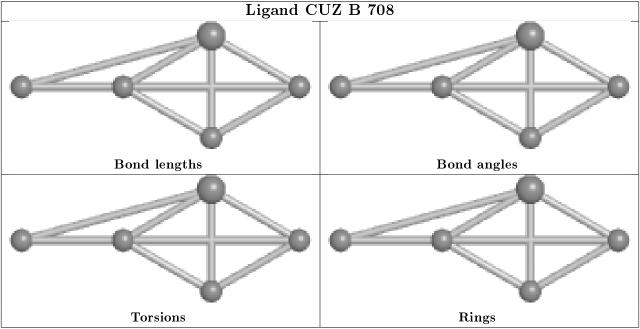
There are no ring outliers.

No monomer is involved in short contacts.

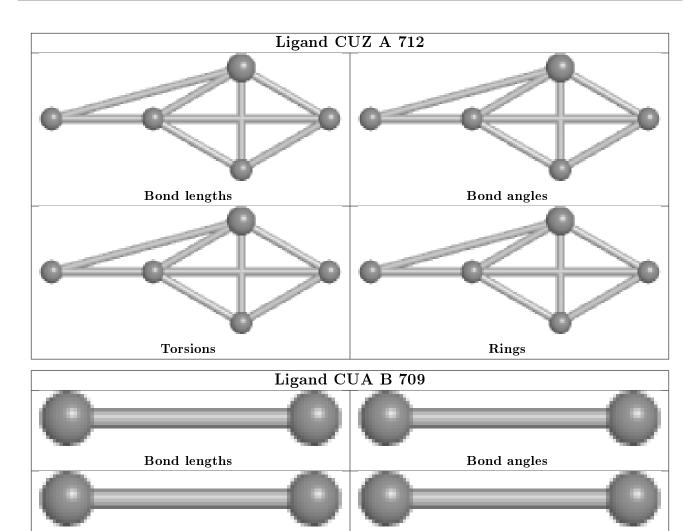


The following is a two-dimensional graphical depiction of Mogul quality analysis of bond lengths, bond angles, torsion angles, and ring geometry for all instances of the Ligand of Interest. In addition, ligands with molecular weight > 250 and outliers as shown on the validation Tables will also be included. For torsion angles, if less then 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.









Rings

5.7 Other polymers (i)

There are no such residues in this entry.

Torsions

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, 95^{th} 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 $>$	$\#\mathrm{RSRZ}{>}2$	$OWAB(A^2)$	Q<0.9
1	A	586/646 (90%)	-0.65	9 (1%) 73 73	13, 25, 52, 89	0
1	В	586/646 (90%)	-0.58	3 (0%) 91 90	15, 31, 55, 88	0
All	All	1172/1292 (90%)	-0.61	12 (1%) 82 82	13, 28, 54, 89	0

The worst 5 of 12 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	266	GLY	4.3
1	A	264	LEU	4.3
1	A	638	ALA	3.6
1	A	269	ARG	3.5
1	A	265	GLY	3.4

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)

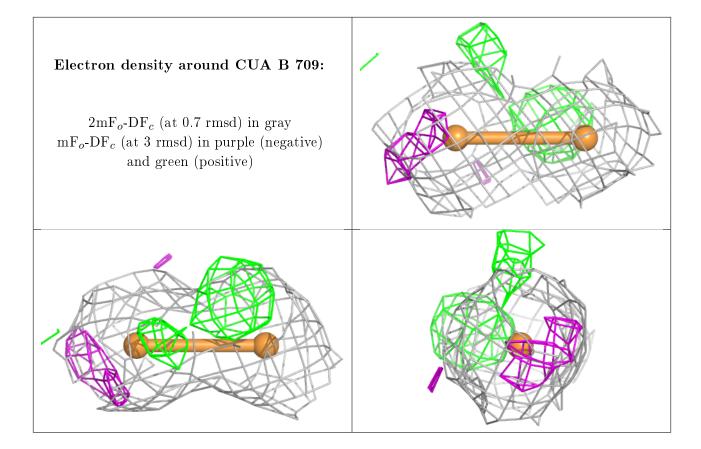
In the following table, the Atoms column lists the number of modelled atoms in the group and the number defined in the chemical component dictionary. The B-factors column lists the minimum, median, 95^{th} percentile and maximum values of B factors of atoms in the group. The column labelled 'Q< 0.9'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



Mol	Type	Chain	Res	Atoms	RSCC	RSR	$\mathbf{B} ext{-}\mathbf{factors}(\mathbf{\mathring{A}}^2)$	Q < 0.9
6	FMT	A	706	3/3	0.60	0.20	86,86,88,89	0
6	FMT	В	712	3/3	0.63	0.19	65,68,82,84	0
6	FMT	A	708	3/3	0.66	0.13	75,75,77,79	0
6	FMT	В	710	3/3	0.73	0.26	76,76,91,94	0
6	FMT	В	711	3/3	0.74	0.14	88,89,107,107	0
6	FMT	A	705	3/3	0.76	0.16	62,62,65,65	0
10	TRS	A	714	8/8	0.78	0.18	44,51,55,56	0
6	FMT	A	709	3/3	0.81	0.11	70,70,72,74	0
6	FMT	A	715	3/3	0.85	0.14	62,67,81,81	0
6	FMT	A	707	3/3	0.89	0.12	35,35,47,50	0
6	FMT	В	705	3/3	0.91	0.15	72,72,74,74	0
2	ВЗР	A	701	19/19	0.95	0.07	20,24,27,31	0
2	ВЗР	В	701	19/19	0.96	0.06	20,23,29,30	0
9	CUA	В	709	2/2	0.96	0.06	30,30,30,56	1
9	CUA	A	713	2/2	0.96	0.07	27,27,27,44	2
8	CUZ	A	712	5/5	0.97	0.08	21,29,39,39	5
5	K	A	704	1/1	0.97	0.07	33,33,33,33	1
8	CUZ	В	708	5/5	0.98	0.06	25,27,42,43	5
7	CL	A	711	1/1	0.98	0.05	39,39,39,39	1
4	CA	A	703	1/1	0.98	0.06	20,20,20,20	1
5	K	В	704	1/1	0.99	0.05	21,21,21,21	1
3	NA	В	702	1/1	0.99	0.04	24,24,24,24	1
7	CL	A	710	1/1	0.99	0.07	21,21,21,21	1
4	CA	В	703	1/1	0.99	0.06	26,26,26,26	1
6	FMT	В	706	3/3	0.99	0.07	24,24,27,39	0
7	CL	В	707	1/1	0.99	0.08	25,25,25,25	1
3	NA	A	702	1/1	1.00	0.06	17,17,17,17	1

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.

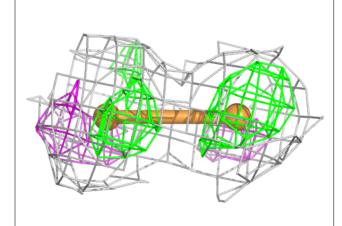


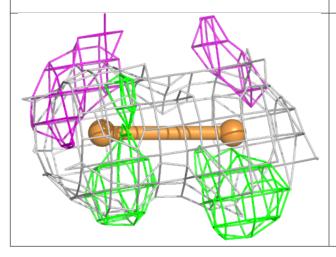


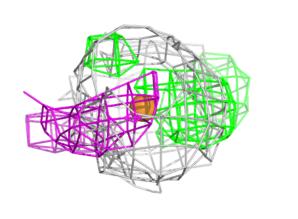


Electron density around CUA A 713:

 $2 \text{mF}_o\text{-DF}_c$ (at 0.7 rmsd) in gray $\text{mF}_o\text{-DF}_c$ (at 3 rmsd) in purple (negative) and green (positive)



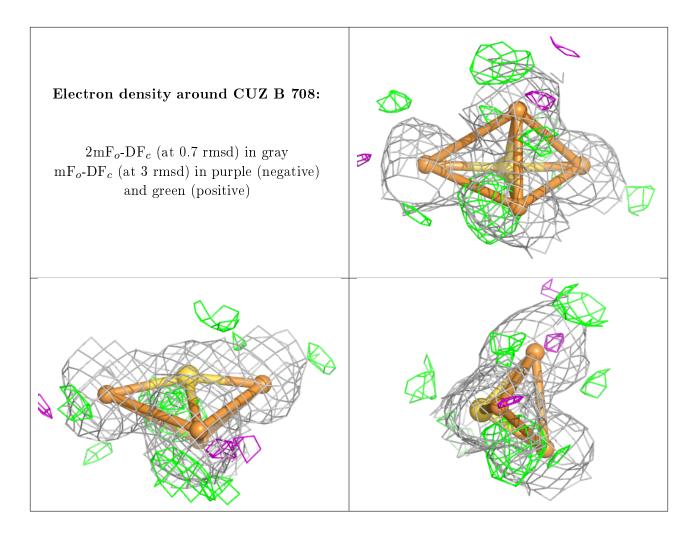






Electron density around CUZ A 712: 2mF_o-DF_c (at 0.7 rmsd) in gray mF_o-DF_c (at 3 rmsd) in purple (negative) and green (positive)





6.5 Other polymers (i)

There are no such residues in this entry.

