



wwPDB X-ray Structure Validation Summary Report ⓘ

May 15, 2020 – 03:59 pm BST

PDB ID : 6DTK
Title : Heterodimers of FALS mutant SOD enzyme
Authors : Streltsov, V.A.; Nuttall, S.D.; Ganio, K.E.; Roberts, B.
Deposited on : 2018-06-17
Resolution : 2.00 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 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	:	2.11
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)	:	2.11

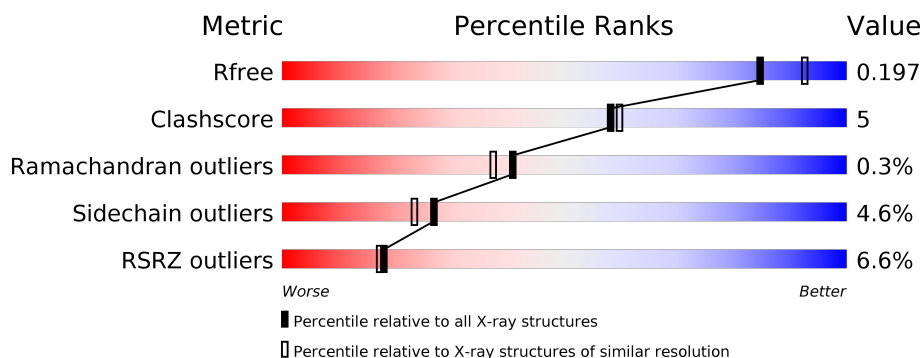
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.00 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	8085 (2.00-2.00)
Clashscore	141614	9178 (2.00-2.00)
Ramachandran outliers	138981	9054 (2.00-2.00)
Sidechain outliers	138945	9053 (2.00-2.00)
RSRZ outliers	127900	7900 (2.00-2.00)

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 on 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	325	<div> <div>9%</div> <div> <div></div> <div>84%</div> <div>11%</div> <div>••</div> </div> </div>
1	C	325	<div> <div>13%</div> <div> <div></div> <div>85%</div> <div>10%</div> <div>••</div> </div> </div>
1	E	325	<div> <div>3%</div> <div> <div></div> <div>89%</div> <div>8%</div> <div>•</div> </div> </div>
1	G	325	<div> <div>2%</div> <div> <div></div> <div>89%</div> <div>7%</div> <div>••</div> </div> </div>
1	I	325	<div> <div>6%</div> <div> <div></div> <div>87%</div> <div>7%</div> <div>••</div> </div> </div>

2 Entry composition

There are 5 unique types of molecules in this entry. The entry contains 12729 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 Superoxide dismutase C111S/D83S-C111S HETERODIMER.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	312	Total	C	N	O	S	0	7	0
			2267	1384	415	462	6			
1	C	311	Total	C	N	O	S	0	2	0
			2252	1375	413	458	6			
1	E	313	Total	C	N	O	S	0	6	0
			2273	1386	417	464	6			
1	G	313	Total	C	N	O	S	0	7	0
			2273	1386	416	465	6			
1	I	313	Total	C	N	O	S	0	6	0
			2272	1386	415	465	6			

There are 100 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	83	SER	ASP	microheterogeneity	UNP P00441
A	111	SER	CYS	engineered mutation	UNP P00441
A	154	GLY	-	linker	UNP P00441
A	155	ALA	-	linker	UNP P00441
A	156	ALA	-	linker	UNP P00441
A	157	ALA	-	linker	UNP P00441
A	158	SER	-	linker	UNP P00441
A	159	GLY	-	linker	UNP P00441
A	160	GLY	-	linker	UNP P00441
A	161	GLY	-	linker	UNP P00441
A	162	GLY	-	linker	UNP P00441
A	163	GLY	-	linker	UNP P00441
A	164	SER	-	linker	UNP P00441
A	165	GLY	-	linker	UNP P00441
A	166	GLY	-	linker	UNP P00441
A	167	GLY	-	linker	UNP P00441
A	168	GLY	-	linker	UNP P00441
A	169	SER	-	linker	UNP P00441
A	252	SER	ASP	microheterogeneity	UNP P00441

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Chain	Residue	Modelled	Actual	Comment	Reference
A	280	SER	CYS	engineered mutation	UNP P00441
C	83	SER	ASP	microheterogeneity	UNP P00441
C	111	SER	CYS	engineered mutation	UNP P00441
C	154	GLY	-	linker	UNP P00441
C	155	ALA	-	linker	UNP P00441
C	156	ALA	-	linker	UNP P00441
C	157	ALA	-	linker	UNP P00441
C	158	SER	-	linker	UNP P00441
C	159	GLY	-	linker	UNP P00441
C	160	GLY	-	linker	UNP P00441
C	161	GLY	-	linker	UNP P00441
C	162	GLY	-	linker	UNP P00441
C	163	GLY	-	linker	UNP P00441
C	164	SER	-	linker	UNP P00441
C	165	GLY	-	linker	UNP P00441
C	166	GLY	-	linker	UNP P00441
C	167	GLY	-	linker	UNP P00441
C	168	GLY	-	linker	UNP P00441
C	169	SER	-	linker	UNP P00441
C	252	SER	ASP	microheterogeneity	UNP P00441
C	280	SER	CYS	engineered mutation	UNP P00441
E	83	SER	ASP	microheterogeneity	UNP P00441
E	111	SER	CYS	engineered mutation	UNP P00441
E	154	GLY	-	linker	UNP P00441
E	155	ALA	-	linker	UNP P00441
E	156	ALA	-	linker	UNP P00441
E	157	ALA	-	linker	UNP P00441
E	158	SER	-	linker	UNP P00441
E	159	GLY	-	linker	UNP P00441
E	160	GLY	-	linker	UNP P00441
E	161	GLY	-	linker	UNP P00441
E	162	GLY	-	linker	UNP P00441
E	163	GLY	-	linker	UNP P00441
E	164	SER	-	linker	UNP P00441
E	165	GLY	-	linker	UNP P00441
E	166	GLY	-	linker	UNP P00441
E	167	GLY	-	linker	UNP P00441
E	168	GLY	-	linker	UNP P00441
E	169	SER	-	linker	UNP P00441
E	252	SER	ASP	microheterogeneity	UNP P00441
E	280	SER	CYS	engineered mutation	UNP P00441
G	83	SER	ASP	microheterogeneity	UNP P00441

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Chain	Residue	Modelled	Actual	Comment	Reference
G	111	SER	CYS	engineered mutation	UNP P00441
G	154	GLY	-	linker	UNP P00441
G	155	ALA	-	linker	UNP P00441
G	156	ALA	-	linker	UNP P00441
G	157	ALA	-	linker	UNP P00441
G	158	SER	-	linker	UNP P00441
G	159	GLY	-	linker	UNP P00441
G	160	GLY	-	linker	UNP P00441
G	161	GLY	-	linker	UNP P00441
G	162	GLY	-	linker	UNP P00441
G	163	GLY	-	linker	UNP P00441
G	164	SER	-	linker	UNP P00441
G	165	GLY	-	linker	UNP P00441
G	166	GLY	-	linker	UNP P00441
G	167	GLY	-	linker	UNP P00441
G	168	GLY	-	linker	UNP P00441
G	169	SER	-	linker	UNP P00441
G	252	SER	ASP	microheterogeneity	UNP P00441
G	280	SER	CYS	engineered mutation	UNP P00441
I	83	SER	ASP	microheterogeneity	UNP P00441
I	111	SER	CYS	engineered mutation	UNP P00441
I	154	GLY	-	linker	UNP P00441
I	155	ALA	-	linker	UNP P00441
I	156	ALA	-	linker	UNP P00441
I	157	ALA	-	linker	UNP P00441
I	158	SER	-	linker	UNP P00441
I	159	GLY	-	linker	UNP P00441
I	160	GLY	-	linker	UNP P00441
I	161	GLY	-	linker	UNP P00441
I	162	GLY	-	linker	UNP P00441
I	163	GLY	-	linker	UNP P00441
I	164	SER	-	linker	UNP P00441
I	165	GLY	-	linker	UNP P00441
I	166	GLY	-	linker	UNP P00441
I	167	GLY	-	linker	UNP P00441
I	168	GLY	-	linker	UNP P00441
I	169	SER	-	linker	UNP P00441
I	252	SER	ASP	microheterogeneity	UNP P00441
I	280	SER	CYS	engineered mutation	UNP P00441

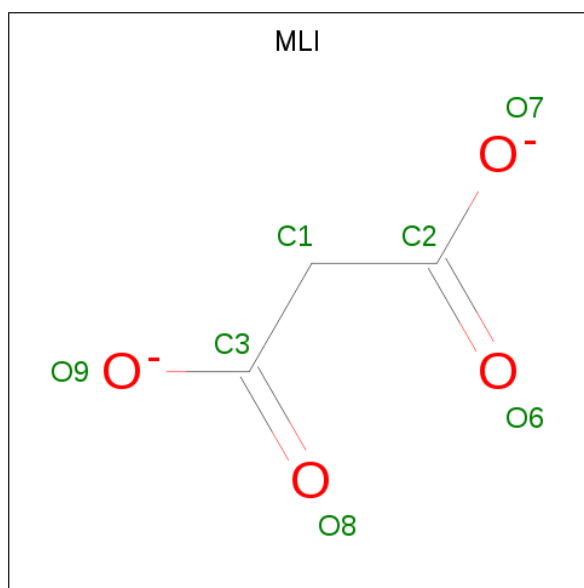
- Molecule 2 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	G	2	Total Zn 2 2	0	0
2	I	2	Total Zn 2 2	0	0
2	A	2	Total Zn 2 2	0	0
2	C	2	Total Zn 2 2	0	0
2	E	2	Total Zn 2 2	0	0

- Molecule 3 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	G	2	Total Cu 4 4	0	2
3	I	2	Total Cu 4 4	0	2
3	A	2	Total Cu 4 4	0	2
3	C	2	Total Cu 3 3	0	1
3	E	2	Total Cu 4 4	0	2

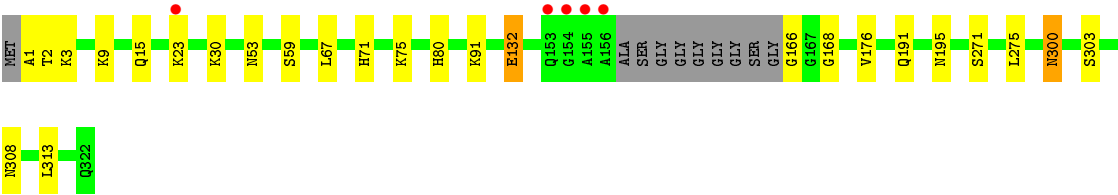
- Molecule 4 is MALONATE ION (three-letter code: MLI) (formula: C₃H₂O₄).



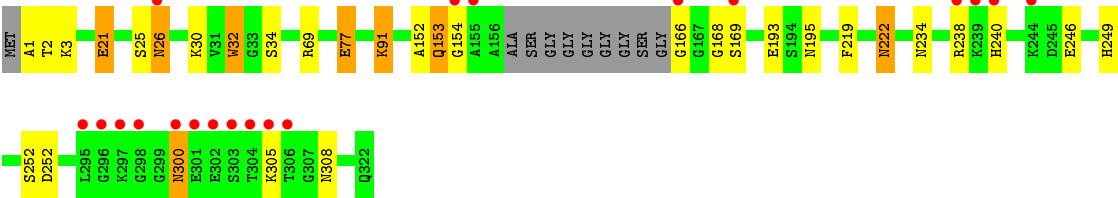
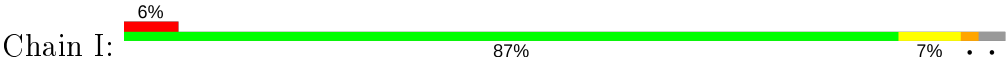
Mol	Chain	Residues	Atoms			ZeroOcc	AltConf
4	E	1	Total	C	O	0	0
			7	3	4		

- Molecule 5 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
5	A	226	Total	O	0	0
			226	226		
5	C	141	Total	O	0	0
			141	141		
5	E	368	Total	O	0	0
			368	368		
5	G	324	Total	O	0	0
			324	324		
5	I	297	Total	O	0	0
			297	297		



● Molecule 1: Superoxide dismutase C111S/D83S-C111S HETERODIMER



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	162.70Å 201.67Å 143.83Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	47.57 – 2.00 47.52 – 2.00	Depositor EDS
% Data completeness (in resolution range)	99.9 (47.57-2.00) 99.9 (47.52-2.00)	Depositor EDS
R_{merge}	0.09	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.34 (at 2.00Å)	Xtriage
Refinement program	REFMAC 5.8.0230	Depositor
R, R_{free}	0.156 , 0.190 0.167 , 0.197	Depositor DCC
R_{free} test set	7971 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	27.5	Xtriage
Anisotropy	0.010	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.41 , 61.1	EDS
L-test for twinning ²	$\langle L \rangle = 0.50$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.97	EDS
Total number of atoms	12729	wwPDB-VP
Average B, all atoms (Å ²)	40.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.06% 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: ZN, MLI, CU

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	0.51	0/2328	0.66	0/3136
1	C	0.49	1/2286 (0.0%)	0.66	1/3078 (0.0%)
1	E	0.56	0/2328	0.71	0/3135
1	G	0.56	0/2333	0.79	4/3142 (0.1%)
1	I	0.54	0/2327	0.71	2/3133 (0.1%)
All	All	0.53	1/11602 (0.0%)	0.71	7/15624 (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	C	0	2

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	83[A]	SER	C-O	-6.96	1.10	1.23

The worst 5 of 7 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	G	132[A]	GLU	CA-CB-CG	-8.35	95.04	113.40
1	G	132[B]	GLU	CA-CB-CG	-8.35	95.04	113.40
1	G	271[A]	SER	CA-CB-OG	-6.48	93.69	111.20
1	G	271[B]	SER	CA-CB-OG	-6.48	93.69	111.20
1	I	21[A]	GLU	CA-CB-CG	-5.74	100.78	113.40

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	C	195	ASN	Peptide
1	C	83[A]	SER	Mainchain

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	2267	0	2188	24	0
1	C	2252	0	2171	13	0
1	E	2273	0	2190	16	0
1	G	2273	0	2191	20	0
1	I	2272	0	2189	32	0
2	A	2	0	0	0	0
2	C	2	0	0	0	0
2	E	2	0	0	0	0
2	G	2	0	0	0	0
2	I	2	0	0	0	0
3	A	4	0	0	0	0
3	C	3	0	0	0	0
3	E	4	0	0	0	0
3	G	4	0	0	0	0
3	I	4	0	0	0	0
4	E	7	0	2	0	0
5	A	226	0	0	10	0
5	C	141	0	0	1	0
5	E	368	0	0	7	0
5	G	324	0	0	9	1
5	I	297	0	0	10	1
All	All	12729	0	10931	102	1

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.

The worst 5 of 102 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:G:300:ASN:HD21	1:G:308:ASN:HD21	1.26	0.83
1:A:279:HIS:ND1	5:A:502:HOH:O	2.14	0.79
1:A:110:HIS:ND1	5:A:503:HOH:O	2.15	0.79
1:C:39:THR:O	1:C:43:HIS:HE1	1.69	0.75
1:I:300:ASN:HD21	1:I:308:ASN:HD21	1.31	0.75

All (1) 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)
5:G:657:HOH:O	5:I:712:HOH:O[3_455]	2.14	0.06

5.3 Torsion angles ⓘ

5.3.1 Protein backbone ⓘ

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	311/325 (96%)	303 (97%)	6 (2%)	2 (1%)	25	19
1	C	305/325 (94%)	290 (95%)	13 (4%)	2 (1%)	22	16
1	E	311/325 (96%)	308 (99%)	3 (1%)	0	100	100
1	G	312/325 (96%)	308 (99%)	4 (1%)	0	100	100
1	I	311/325 (96%)	303 (97%)	7 (2%)	1 (0%)	41	37
All	All	1550/1625 (95%)	1512 (98%)	33 (2%)	5 (0%)	41	37

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	153	GLN
1	C	195	ASN
1	I	153	GLN
1	A	153	GLN
1	A	74	PRO

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	244/242 (101%)	232 (95%)	12 (5%)	25	21
1	C	239/242 (99%)	222 (93%)	17 (7%)	14	10
1	E	243/242 (100%)	234 (96%)	9 (4%)	34	32
1	G	244/242 (101%)	238 (98%)	6 (2%)	47	49
1	I	243/242 (100%)	231 (95%)	12 (5%)	25	21
All	All	1213/1210 (100%)	1157 (95%)	56 (5%)	27	23

5 of 56 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	C	244	LYS
1	E	91	LYS
1	I	193	GLU
1	C	260	LYS
1	C	322	GLN

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 15 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	184	GLN
1	G	15	GLN
1	I	153	GLN
1	C	322	GLN
1	I	26	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 carbohydrates in this entry.

5.6 Ligand geometry [i](#)

Of 30 ligands modelled in this entry, 29 are monoatomic - leaving 1 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	$\# Z > 2$
4	MLI	E	405	-	0,6,6	0.00	-	0,7,7	0.00	-

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

Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
4	MLI	E	405	-	-	0/0/4/4	-

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.

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	314/325 (96%)	0.16	28 (8%) 9 8	24, 36, 86, 105	4 (1%)
1	C	313/325 (96%)	0.62	41 (13%) 3 3	29, 47, 83, 103	4 (1%)
1	E	315/325 (96%)	-0.20	9 (2%) 51 50	18, 27, 57, 83	4 (1%)
1	G	315/325 (96%)	-0.21	5 (1%) 72 70	19, 28, 51, 74	4 (1%)
1	I	315/325 (96%)	-0.04	20 (6%) 20 19	19, 31, 71, 102	4 (1%)
All	All	1572/1625 (96%)	0.06	103 (6%) 18 17	18, 34, 74, 105	20 (1%)

The worst 5 of 103 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	C	70	LYS	6.1
1	A	75	LYS	5.3
1	C	77	GLU	5.1
1	C	26	ASN	5.1
1	C	154	GLY	5.1

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 carbohydrates 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
4	MLI	E	405	7/7	0.89	0.17	49,50,52,54	7
2	ZN	C	401	1/1	0.96	0.07	54,54,54,54	1
3	CU	C	402	1/1	0.96	0.06	49,49,49,49	1
2	ZN	C	403	1/1	0.98	0.06	33,33,33,33	1
2	ZN	A	401	1/1	0.98	0.09	49,49,49,49	1
2	ZN	G	403	1/1	0.99	0.05	34,34,34,34	1
3	CU	A	402[B]	1/1	0.99	0.10	39,39,39,39	1
3	CU	A	402[A]	1/1	0.99	0.10	37,37,37,37	1
3	CU	C	404[B]	1/1	0.99	0.08	30,30,30,30	1
3	CU	I	404[B]	1/1	0.99	0.10	33,33,33,33	1
3	CU	C	404[A]	1/1	0.99	0.08	32,32,32,32	1
3	CU	A	404[A]	1/1	0.99	0.12	31,31,31,31	1
3	CU	G	402[B]	1/1	0.99	0.11	21,21,21,21	1
3	CU	A	404[B]	1/1	0.99	0.12	31,31,31,31	1
3	CU	G	402[A]	1/1	0.99	0.11	23,23,23,23	1
2	ZN	I	403	1/1	0.99	0.05	43,43,43,43	1
3	CU	G	404[B]	1/1	0.99	0.12	28,28,28,28	1
3	CU	G	404[A]	1/1	0.99	0.12	27,27,27,27	1
3	CU	I	404[A]	1/1	0.99	0.10	35,35,35,35	1
2	ZN	A	403	1/1	0.99	0.08	30,30,30,30	1
3	CU	E	404[A]	1/1	1.00	0.08	23,23,23,23	1
3	CU	E	404[B]	1/1	1.00	0.08	21,21,21,21	1
2	ZN	E	403	1/1	1.00	0.06	25,25,25,25	1
3	CU	E	402[A]	1/1	1.00	0.09	28,28,28,28	1
2	ZN	I	401	1/1	1.00	0.09	23,23,23,23	1
3	CU	I	402[B]	1/1	1.00	0.09	23,23,23,23	1
3	CU	I	402[A]	1/1	1.00	0.09	24,24,24,24	1
2	ZN	E	401	1/1	1.00	0.07	29,29,29,29	1
3	CU	E	402[B]	1/1	1.00	0.09	25,25,25,25	1
2	ZN	G	401	1/1	1.00	0.09	26,26,26,26	1

6.5 Other polymers

There are no such residues in this entry.