Full wwPDB X-ray Structure Validation Report (i)

Dec 7, 2023 – 10:03 pm GMT

PDB ID	:	2JLP
Title	:	Crystal structure of human extracellular copper-zinc superoxide dismutase.
Authors	:	Antonyuk, S.V.; Strange, R.W.; Marklund, S.L.; Hasnain, S.S.
Deposited on	:	2008-09-14
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 (i) 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 (i)) were used in the production of this report:

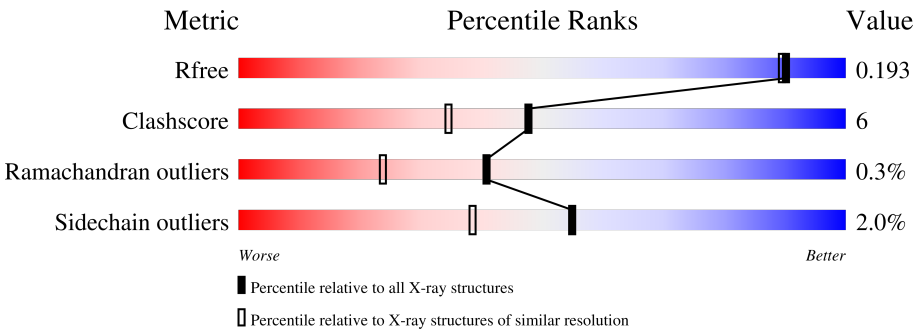
MolProbity	:	4.02b-467
Mogul	:	1.8.4, CSD as541be (2020)
Xtriage (Phenix)	:	1.13
EDS	:	2.36
Percentile statistics	:	20191225.v01 (using entries in the PDB archive December 25th 2019)
Refmac	:	5.8.0158
CCP4	:	7.0.044 (Gargrove)
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.36

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 1.70 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}	130704	4298 (1.70-1.70)
Clashscore	141614	4695 (1.70-1.70)
Ramachandran outliers	138981	4610 (1.70-1.70)
Sidechain outliers	138945	4610 (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 <=5%

Mol	Chain	Length	Quality of chain
1	A	222	71% • 24%
1	B	222	64% 11% 25%
1	C	222	68% 6% • 25%
1	D	222	69% 5% • 24%

2 Entry composition (i)

There are 5 unique types of molecules in this entry. The entry contains 5992 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 EXTRACELLULAR SUPEROXIDE DISMUTASE (CU-ZN).

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	168	1277	791	250	231	5	0	5	0
1	B	166	1264	785	247	227	5	0	6	0
1	C	167	1263	783	242	233	5	0	5	0
1	D	169	1275	790	244	236	5	0	4	0

There are 4 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	40	THR	ALA	conflict	UNP P08294
B	40	THR	ALA	conflict	UNP P08294
C	40	THR	ALA	conflict	UNP P08294
D	40	THR	ALA	conflict	UNP P08294

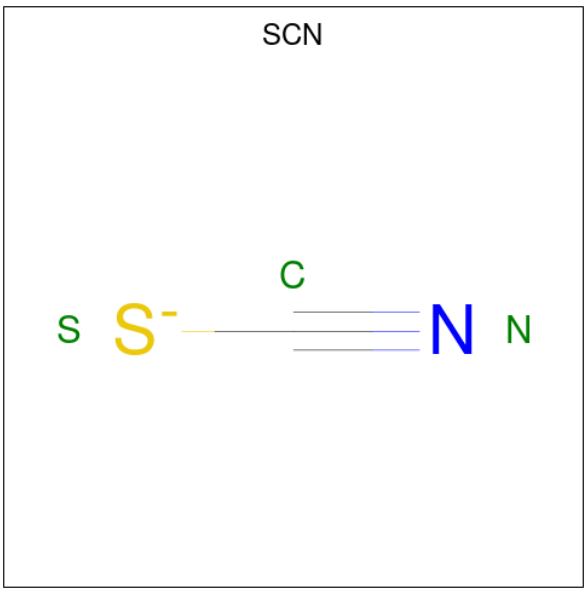
- Molecule 2 is COPPER (II) ION (three-letter code: CU) (formula: Cu).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Cu		
2	A	1	2	2	0	1
2	B	1	2	2	0	1
2	C	1	2	2	0	1
2	D	1	2	2	0	1

- Molecule 3 is ZINC ION (three-letter code: ZN) (formula: Zn).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	Zn		
3	A	1	1	1	0	0
3	B	1	1	1	0	0
3	C	1	1	1	0	0
3	D	1	1	1	0	0

- Molecule 4 is THIOCYANATE ION (three-letter code: SCN) (formula: CNS).



Mol	Chain	Residues	Atoms				ZeroOcc	AltConf
			Total	C	N	S		
4	B	1	6	2	2	2	0	1
4	C	1	6	2	2	2	0	1

- Molecule 5 is water.

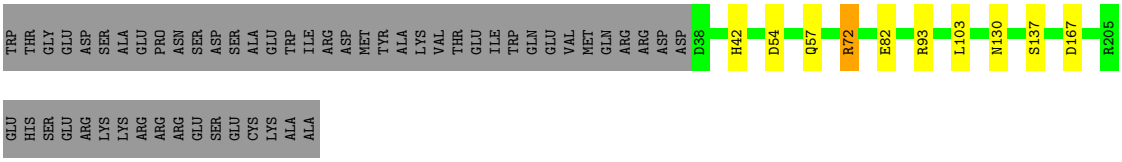
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
			Total	O		
5	A	243	243	243	0	0
5	B	223	223	223	0	0
5	C	215	215	215	0	0
5	D	208	208	208	0	0

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. 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. 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.

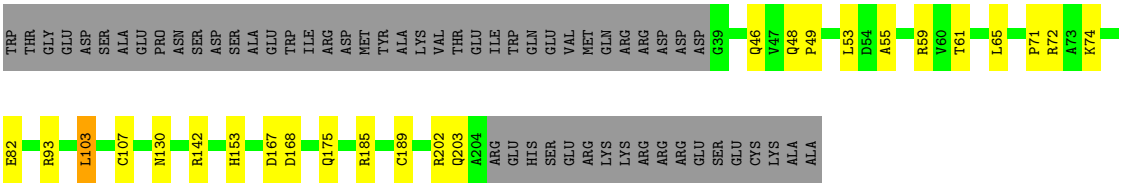
- Molecule 1: EXTRACELLULAR SUPEROXIDE DISMUTASE (CU-ZN)

Chain A:



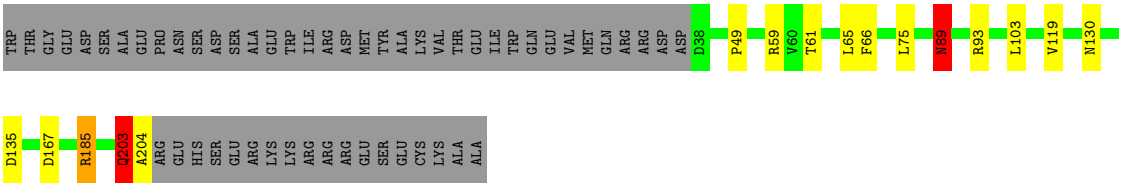
- Molecule 1: EXTRACELLULAR SUPEROXIDE DISMUTASE (CU-ZN)

Chain B:



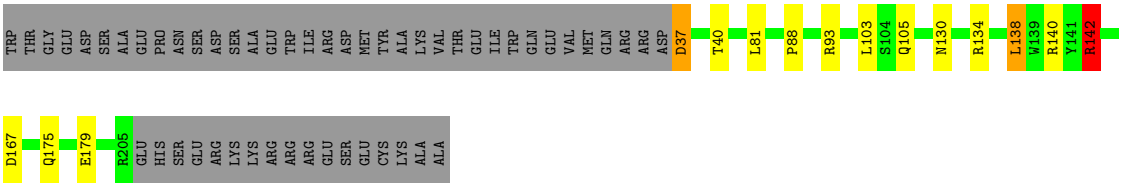
- Molecule 1: EXTRACELLULAR SUPEROXIDE DISMUTASE (CU-ZN)

Chain C:



- Molecule 1: EXTRACELLULAR SUPEROXIDE DISMUTASE (CU-ZN)

Chain D:



4 Data and refinement statistics (i)

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α, β, γ	56.74Å 93.59Å 75.60Å 90.00° 106.23° 90.00°	Depositor
Resolution (Å)	28.20 – 1.70 28.23 – 1.65	Depositor EDS
% Data completeness (in resolution range)	97.2 (28.20-1.70) 93.7 (28.23-1.65)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$< I/\sigma(I) >$ [1]	2.28 (at 1.65Å)	Xtriage
Refinement program	REFMAC 5.3.0037	Depositor
R, R_{free}	0.150 , 0.185 0.163 , 0.193	Depositor DCC
R_{free} test set	4262 reflections (5.00%)	wwPDB-VP
Wilson B-factor (Å^2)	19.5	Xtriage
Anisotropy	0.414	Xtriage
Bulk solvent k_{sol}(e/Å^3), B_{sol}(Å^2)	0.34 , 51.6	EDS
L-test for twinning[2]	$< \|L\| > = 0.49$, $< L^2 > = 0.33$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o,F_c correlation	0.96	EDS
Total number of atoms	5992	wwPDB-VP
Average B, all atoms (Å^2)	32.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 5.16% of the height of the origin peak. No significant pseudotranslation is detected.*

[1]Intensities estimated from amplitudes.

[2]Theoretical 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.

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: CU, SCN, ZN

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	0.85	0/1324	0.89	1/1799 (0.1%)
1	B	0.83	0/1311	0.93	6/1784 (0.3%)
1	C	0.85	1/1307 (0.1%)	0.88	4/1780 (0.2%)
1	D	0.83	0/1319	0.87	4/1794 (0.2%)
All	All	0.84	1/5261 (0.0%)	0.89	15/7157 (0.2%)

Chiral center outliers are detected by calculating the chiral volume of a chiral center and verifying if the center is modelled as a planar moiety or with the opposite hand.A planarity outlier is detected by checking planarity of atoms in a peptide group, atoms in a mainchain group or atoms of a sidechain that are expected to be planar.

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

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	C	59	ARG	CG-CD	-6.65	1.35	1.51

All (15) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	B	93	ARG	NE-CZ-NH1	9.66	125.13	120.30
1	C	93	ARG	NE-CZ-NH1	7.74	124.17	120.30
1	D	93	ARG	NE-CZ-NH1	6.79	123.69	120.30
1	C	59	ARG	NE-CZ-NH2	-6.42	117.09	120.30
1	A	93	ARG	NE-CZ-NH1	6.33	123.46	120.30
1	B	93	ARG	NE-CZ-NH2	-6.12	117.24	120.30
1	D	142	ARG	NE-CZ-NH2	-6.08	117.26	120.30
1	D	138	LEU	CA-CB-CG	5.92	128.92	115.30

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Mol	Chain	Res	Type	Atoms	Z	Observed(^{o})	Ideal(^{o})
1	C	185[A]	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	C	185[B]	ARG	NE-CZ-NH1	5.57	123.09	120.30
1	B	103	LEU	CB-CG-CD1	5.50	120.36	111.00
1	B	168	ASP	CB-CG-OD1	5.30	123.07	118.30
1	B	185[A]	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	B	185[B]	ARG	NE-CZ-NH1	5.25	122.92	120.30
1	D	142	ARG	NE-CZ-NH1	5.15	122.88	120.30

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	D	37	ASP	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	1277	0	1237	7	0
1	B	1264	0	1231	27	0
1	C	1263	0	1215	12	0
1	D	1275	0	1223	13	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
3	A	1	0	0	0	0
3	B	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	B	6	0	0	0	0
4	C	6	0	0	0	0
5	A	243	0	0	3	0
5	B	223	0	0	15	0
5	C	215	0	0	7	0
5	D	208	0	0	3	0
All	All	5992	0	4906	59	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 6.

All (59) 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:B:65:LEU:HD11	1:B:203:GLN:OE1	1.42	1.18
1:D:37:ASP:CB	1:D:40:THR:HB	1.83	1.08
1:B:55:ALA:CB	5:B:2030:HOH:O	2.07	1.01
1:A:130:ASN:HD21	1:A:167:ASP:H	1.09	0.98
1:B:130:ASN:HD21	1:B:167:ASP:H	1.09	0.98
1:D:130:ASN:HD21	1:D:167:ASP:H	1.05	0.95
1:D:37:ASP:HB3	1:D:40:THR:HB	1.53	0.89
1:C:130:ASN:HD21	1:C:167:ASP:H	1.17	0.88
1:B:55:ALA:HB2	5:B:2030:HOH:O	1.73	0.84
5:A:2114:HOH:O	1:B:46:GLN:HG2	1.75	0.84
1:C:119:VAL:HG11	5:C:2077:HOH:O	1.82	0.80
1:B:48[A]:GLN:NE2	5:B:2009:HOH:O	2.14	0.79
1:B:153:HIS:HD2	5:B:2164:HOH:O	1.66	0.78
1:D:37:ASP:HB2	1:D:40:THR:HB	1.64	0.78
1:A:54:ASP:H	1:A:57:GLN:HE21	1.35	0.73
1:B:48[A]:GLN:OE1	5:B:2008:HOH:O	2.06	0.72
1:C:203:GLN:O	1:C:204:ALA:CB	2.38	0.71
1:C:203:GLN:O	1:C:204:ALA:HB2	1.91	0.70
1:C:135:ASP:HB2	5:C:2141:HOH:O	1.90	0.70
1:B:65:LEU:CD1	1:B:203:GLN:OE1	2.33	0.67
1:B:55:ALA:HB3	5:B:2030:HOH:O	1.85	0.67
1:B:175:GLN:NE2	5:B:2190:HOH:O	2.22	0.67
1:B:59[B]:ARG:NH2	5:B:2049:HOH:O	2.32	0.63
1:B:49:PRO:HD3	1:B:61[A]:THR:HG22	1.82	0.62
1:B:130:ASN:ND2	1:B:167:ASP:H	1.90	0.62
1:D:130:ASN:HD21	1:D:167:ASP:N	1.89	0.61
1:B:59[A]:ARG:NH2	5:B:2047:HOH:O	2.34	0.60
1:C:49:PRO:HD3	1:C:61:THR:HG22	1.85	0.59
1:D:140:ARG:NH1	1:D:142:ARG:HE	2.01	0.57
1:B:55:ALA:HB3	5:C:2009:HOH:O	2.05	0.57
1:C:89:ASN:HB3	5:C:2088:HOH:O	2.04	0.57
1:C:185[B]:ARG:NH1	5:C:2199:HOH:O	2.38	0.57
1:D:130:ASN:ND2	1:D:167:ASP:H	1.89	0.57
1:A:42:HIS:HD2	5:A:2004:HOH:O	1.86	0.57
1:C:203:GLN:HE21	1:C:203:GLN:HA	1.70	0.56
1:A:72[B]:ARG:HG3	5:A:2061:HOH:O	2.05	0.56
1:B:74:LYS:NZ	5:B:2068:HOH:O	2.38	0.55

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:54:ASP:H	1:A:57:GLN:NE2	2.04	0.55
1:B:130:ASN:HD21	1:B:167:ASP:N	1.91	0.54
1:A:82[B]:GLU:OE1	1:A:137[B]:SER:HB3	2.08	0.54
1:B:55:ALA:HB1	5:C:2015:HOH:O	2.08	0.53
1:A:130:ASN:ND2	1:A:167:ASP:H	1.92	0.53
1:D:105[A]:GLN:HG2	5:D:2100:HOH:O	2.09	0.52
1:D:81:LEU:HD12	1:D:138:LEU:HD13	1.91	0.51
1:B:202:ARG:HD3	5:B:2215:HOH:O	2.10	0.50
1:B:53:LEU:HD12	1:B:59[A]:ARG:NH1	2.26	0.50
1:D:37:ASP:CA	1:D:40:THR:HB	2.39	0.48
1:B:59[A]:ARG:CZ	5:B:2047:HOH:O	2.60	0.48
1:C:65:LEU:HD11	1:C:204:ALA:HA	1.96	0.48
1:B:153:HIS:CD2	5:B:2164:HOH:O	2.52	0.46
1:D:175:GLN:NE2	1:D:179:GLU:OE2	2.48	0.45
1:B:107:CYS:HG	1:B:189:CYS:HG	0.47	0.44
1:D:37:ASP:N	5:D:2004:HOH:O	2.51	0.43
1:D:88:PRO:HD2	5:D:2080:HOH:O	2.18	0.43
1:C:135:ASP:CB	5:C:2141:HOH:O	2.56	0.42
1:C:66:PHE:HB3	1:C:75:LEU:HD11	2.02	0.41
1:B:82:GLU:HB3	5:B:2148:HOH:O	2.20	0.41
1:B:55:ALA:N	5:B:2030:HOH:O	2.38	0.41
1:B:71:PRO:HD2	1:B:72[B]:ARG:CZ	2.52	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	171/222 (77%)	169 (99%)	2 (1%)	0	100 100
1	B	170/222 (77%)	167 (98%)	3 (2%)	0	100 100
1	C	170/222 (77%)	165 (97%)	3 (2%)	2 (1%)	13 3

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
1	D	171/222 (77%)	167 (98%)	4 (2%)	0	100	100
All	All	682/888 (77%)	668 (98%)	12 (2%)	2 (0%)	41	24

All (2) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	C	89	ASN
1	C	203	GLN

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	130/173 (75%)	127 (98%)	3 (2%)	50	33
1	B	128/173 (74%)	126 (98%)	2 (2%)	62	48
1	C	129/173 (75%)	126 (98%)	3 (2%)	50	33
1	D	130/173 (75%)	127 (98%)	3 (2%)	50	33
All	All	517/692 (75%)	506 (98%)	11 (2%)	55	36

All (11) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	72[A]	ARG
1	A	72[B]	ARG
1	A	103	LEU
1	B	103	LEU
1	B	142	ARG
1	C	89	ASN
1	C	103	LEU
1	C	203	GLN
1	D	103	LEU
1	D	134	ARG
1	D	142	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (12) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	42	HIS
1	A	57	GLN
1	A	130	ASN
1	B	89	ASN
1	B	130	ASN
1	B	153	HIS
1	B	175	GLN
1	C	130	ASN
1	C	153	HIS
1	C	203	GLN
1	D	46	GLN
1	D	130	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 monosaccharides in this entry.

5.6 Ligand geometry (i)

Of 16 ligands modelled in this entry, 12 are monoatomic - leaving 4 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	SCN	B	227[A]	-	1,2,2	0.96	0	0,1,1	-	-

Mol	Type	Chain	Res	Link	Bond lengths			Bond angles		
					Counts	RMSZ	$\#\|Z\| > 2$	Counts	RMSZ	$\#\|Z\| > 2$
4	SCN	B	227[B]	-	1,2,2	2.88	1 (100%)	0,1,1	-	-
4	SCN	C	227[B]	-	1,2,2	2.58	1 (100%)	0,1,1	-	-
4	SCN	C	227[A]	-	1,2,2	1.14	0	0,1,1	-	-

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
4	B	227[B]	SCN	C-N	2.88	1.25	1.15
4	C	227[B]	SCN	C-N	2.58	1.24	1.15

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)

Unable to reproduce the depositors R factor - this section is therefore empty.

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

Unable to reproduce the depositors R factor - this section is therefore empty.

6.3 Carbohydrates (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.4 Ligands (i)

Unable to reproduce the depositors R factor - this section is therefore empty.

6.5 Other polymers (i)

Unable to reproduce the depositors R factor - this section is therefore empty.