



wwPDB X-ray Structure Validation Summary Report ⓘ

Feb 1, 2016 – 10:40 AM GMT

PDB ID : 3MJZ
Title : The crystal structure of native FG41 MSAD
Authors : Guo, Y.; Serrano, H.; Poelarends, G.J.; Johnson, W.H.Jr.; Hackert, M.L.; Whitman, C.P.
Deposited on : 2010-04-13
Resolution : 2.40 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
<http://wwpdb.org/validation/2016/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 : 1.7 (RC4), CSD as536be (2015)
Xtriage (Phenix) : 1.9-1692
EDS : rb-20026688
Percentile statistics : 20151230.v01 (using entries in the PDB archive December 30th 2015)
Refmac : 5.8.0135
CCP4 : 6.5.0
Ideal geometry (proteins) : Engh & Huber (2001)
Ideal geometry (DNA, RNA) : Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP) : trunk26865

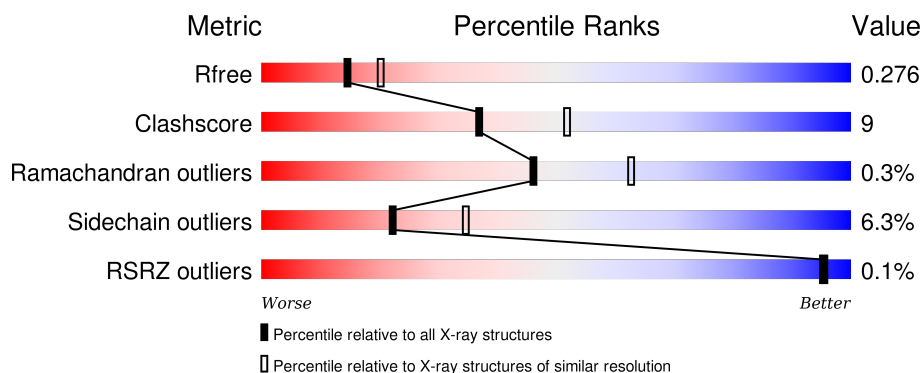
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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}	91344	2919 (2.40-2.40)
Clashscore	102246	3407 (2.40-2.40)
Ramachandran outliers	100387	3351 (2.40-2.40)
Sidechain outliers	100360	3352 (2.40-2.40)
RSRZ outliers	91569	2928 (2.40-2.40)

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. 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	136	<div> <div></div> <div>75%</div> <div>19%</div> <div>• •</div> </div>
1	B	136	<div> <div></div> <div>78%</div> <div>14%</div> <div>• •</div> </div>
1	C	136	<div> <div>%</div> <div>76%</div> <div>16%</div> <div>• •</div> </div>
1	D	136	<div> <div></div> <div>79%</div> <div>15%</div> <div>• •</div> </div>
1	E	136	<div> <div></div> <div>76%</div> <div>19%</div> <div>• •</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	136	<div><div></div><div>82%13%<div><div></div><div></div><div></div></div></div></div>
1	G	136	<div><div></div><div>69%24%<div><div></div><div></div><div></div></div></div></div>
1	H	136	<div><div></div><div>79%15%<div><div></div><div></div><div></div></div></div></div>
1	I	136	<div><div></div><div>71%24%<div><div></div><div></div><div></div></div></div></div>
1	J	136	<div><div></div><div>%70%24%<div><div></div><div></div><div></div></div></div></div>
1	K	136	<div><div></div><div>71%23%<div><div></div><div></div><div></div></div></div></div>
1	L	136	<div><div></div><div>72%21%<div><div></div><div></div><div></div></div></div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 12993 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 FG41 Malonate Semialdehyde Decarboxylase.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
1	A	131	Total	C	N	O	0	0	0
			1002	634	178	190			
1	B	131	Total	C	N	O	0	0	0
			1002	634	178	190			
1	C	131	Total	C	N	O	0	0	0
			1002	634	178	190			
1	D	131	Total	C	N	O	0	0	0
			996	631	175	190			
1	E	131	Total	C	N	O	0	0	0
			996	631	175	190			
1	F	130	Total	C	N	O	0	0	0
			995	629	177	189			
1	G	131	Total	C	N	O	0	0	0
			1002	634	178	190			
1	H	131	Total	C	N	O	0	0	0
			1002	634	178	190			
1	I	131	Total	C	N	O	0	0	0
			1002	634	178	190			
1	J	131	Total	C	N	O	0	0	0
			1002	634	178	190			
1	K	130	Total	C	N	O	0	0	0
			995	629	177	189			
1	L	131	Total	C	N	O	0	0	0
			1002	634	178	190			

- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	80	Total	O	0	0
			80	80		
2	B	86	Total	O	0	0
			86	86		

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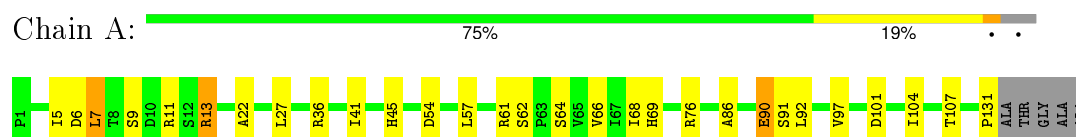
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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	92	Total 92	O 92	0	0
2	D	66	Total 66	O 66	0	0
2	E	98	Total 98	O 98	0	0
2	F	106	Total 106	O 106	0	0
2	G	79	Total 79	O 79	0	0
2	H	72	Total 72	O 72	0	0
2	I	85	Total 85	O 85	0	0
2	J	66	Total 66	O 66	0	0
2	K	74	Total 74	O 74	0	0
2	L	91	Total 91	O 91	0	0

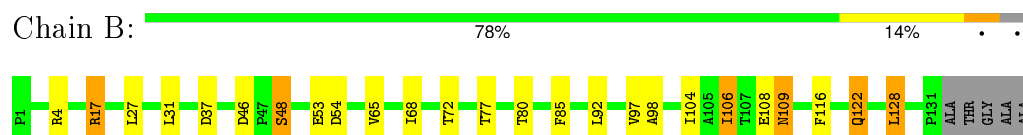
3 Residue-property plots

These plots are drawn for all protein, RNA and DNA chains in the entry. The first graphic for a chain summarises the proportions of errors 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.

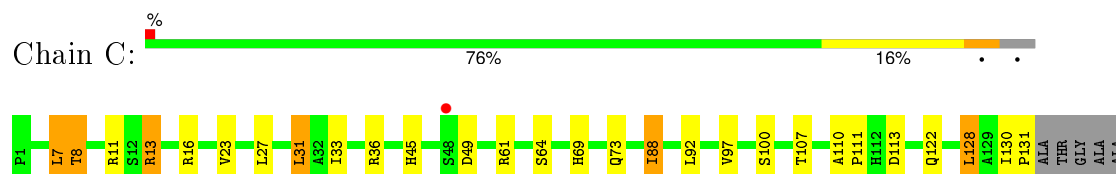
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase



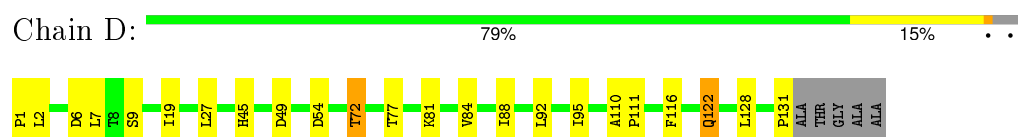
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase



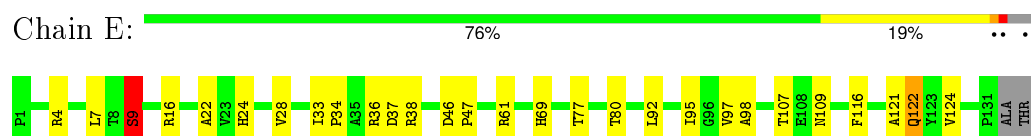
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase



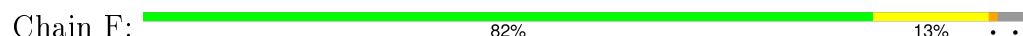
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase

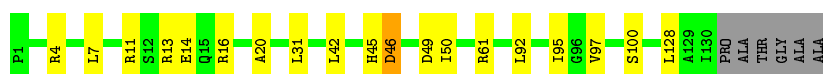


- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase



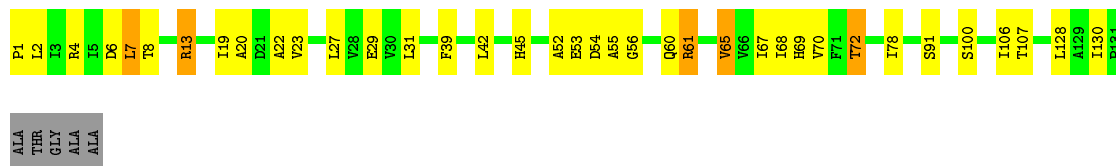
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase





- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase

Chain G: 69% 24%



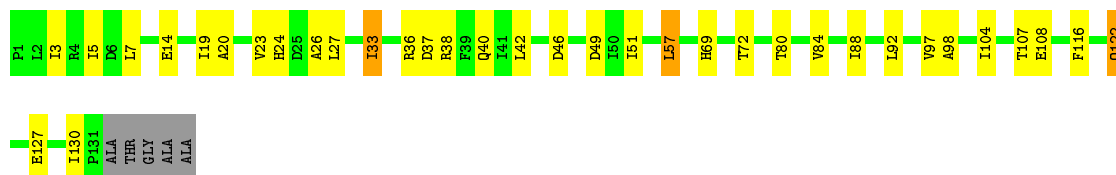
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase

Chain H: 79% 15%



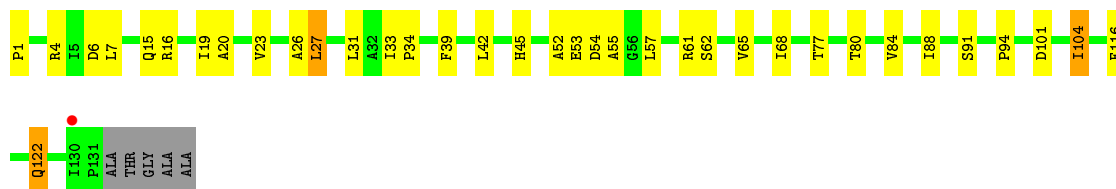
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase

Chain I: 71% 24%



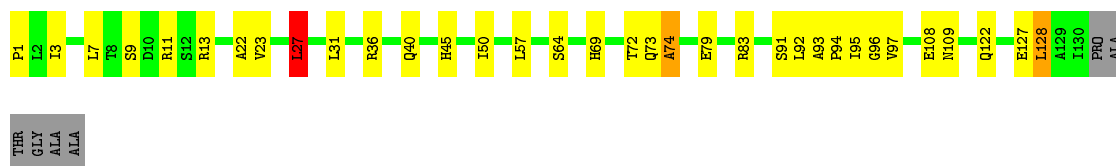
- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase

Chain J: 70% 24%



- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase

Chain K: 71% 23%

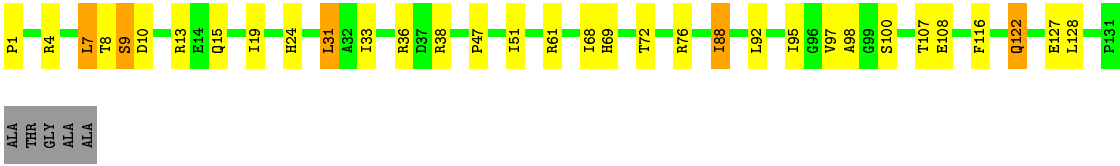


- Molecule 1: FG41 Malonate Semialdehyde Decarboxylase

Chain L:

72%

21%



4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, α , β , γ	88.95Å 94.69Å 190.70Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	42.02 – 2.40 42.02 – 2.02	Depositor EDS
% Data completeness (in resolution range)	84.8 (42.02-2.40) 85.8 (42.02-2.02)	Depositor EDS
R_{merge}	0.15	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.87 (at 2.01Å)	Xtriage
Refinement program	REFMAC 5.2.0019	Depositor
R, R_{free}	0.200 , 0.279 0.201 , 0.276	Depositor DCC
R_{free} test set	2763 reflections (5.38%)	DCC
Wilson B-factor (Å ²)	21.2	Xtriage
Anisotropy	0.192	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.35 , 43.9	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning ²	$\langle L \rangle = 0.44$, $\langle L^2 \rangle = 0.27$	Xtriage
Outliers	2 of 91145 reflections (0.002%)	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	12993	wwPDB-VP
Average B, all atoms (Å ²)	16.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The analyses of the Patterson function reveals a significant off-origin peak that is 53.65 % of the origin peak, indicating pseudo translational symmetry. The chance of finding a peak of this or larger height randomly in a structure without pseudo translational symmetry is equal to 4.0903e-05. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹Intensities estimated from amplitudes.

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

5 Model quality ⓘ

5.1 Standard geometry ⓘ

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	0.56	0/1022	0.73	2/1392 (0.1%)
1	B	0.65	0/1022	0.79	2/1392 (0.1%)
1	C	0.66	0/1022	0.79	1/1392 (0.1%)
1	D	0.55	0/1016	0.71	0/1385
1	E	0.67	0/1016	0.83	3/1385 (0.2%)
1	F	0.66	0/1014	0.78	1/1380 (0.1%)
1	G	0.69	0/1022	0.76	3/1392 (0.2%)
1	H	0.68	0/1022	0.82	3/1392 (0.2%)
1	I	0.69	0/1022	0.79	0/1392
1	J	0.61	0/1022	0.73	0/1392
1	K	0.70	0/1014	0.75	1/1380 (0.1%)
1	L	0.71	0/1022	0.75	1/1392 (0.1%)
All	All	0.65	0/12236	0.77	17/16666 (0.1%)

There are no bond length outliers.

The worst 5 of 17 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	H	61	ARG	NE-CZ-NH1	9.92	125.26	120.30
1	H	61	ARG	NE-CZ-NH2	-7.36	116.62	120.30
1	A	61	ARG	NE-CZ-NH1	6.42	123.51	120.30
1	E	61	ARG	NE-CZ-NH2	-6.00	117.30	120.30
1	H	60	GLN	N-CA-C	5.96	127.10	111.00

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	1002	0	998	18	0
1	B	1002	0	998	19	0
1	C	1002	0	998	21	0
1	D	996	0	987	14	0
1	E	996	0	987	18	0
1	F	995	0	991	12	0
1	G	1002	0	998	26	0
1	H	1002	0	998	19	0
1	I	1002	0	998	27	0
1	J	1002	0	998	26	0
1	K	995	0	991	24	0
1	L	1002	0	998	26	0
2	A	80	0	0	2	0
2	B	86	0	0	1	0
2	C	92	0	0	2	0
2	D	66	0	0	1	0
2	E	98	0	0	1	0
2	F	106	0	0	5	0
2	G	79	0	0	2	0
2	H	72	0	0	0	0
2	I	85	0	0	2	0
2	J	66	0	0	1	0
2	K	74	0	0	1	0
2	L	91	0	0	1	0
All	All	12993	0	11940	224	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.

The worst 5 of 224 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:K:1:PRO:HB3	1:K:72:THR:HG22	1.38	1.05
1:K:1:PRO:HB3	1:K:72:THR:CG2	1.98	0.94
1:K:73:GLN:O	1:K:74:ALA:HB3	1.66	0.92
1:L:116:PHE:H	1:L:122:GLN:NE2	1.77	0.82
1:L:116:PHE:H	1:L:122:GLN:HE22	1.24	0.81

There are no symmetry-related clashes.

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	129/136 (95%)	126 (98%)	3 (2%)	0	100	100
1	B	129/136 (95%)	125 (97%)	4 (3%)	0	100	100
1	C	129/136 (95%)	126 (98%)	3 (2%)	0	100	100
1	D	129/136 (95%)	124 (96%)	5 (4%)	0	100	100
1	E	129/136 (95%)	126 (98%)	2 (2%)	1 (1%)	24	35
1	F	128/136 (94%)	126 (98%)	2 (2%)	0	100	100
1	G	129/136 (95%)	125 (97%)	4 (3%)	0	100	100
1	H	129/136 (95%)	124 (96%)	4 (3%)	1 (1%)	24	35
1	I	129/136 (95%)	126 (98%)	3 (2%)	0	100	100
1	J	129/136 (95%)	126 (98%)	3 (2%)	0	100	100
1	K	128/136 (94%)	122 (95%)	4 (3%)	2 (2%)	12	16
1	L	129/136 (95%)	125 (97%)	3 (2%)	1 (1%)	24	35
All	All	1546/1632 (95%)	1501 (97%)	40 (3%)	5 (0%)	46	63

All (5) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	9	SER
1	L	9	SER
1	H	61	ARG
1	K	74	ALA
1	K	128	LEU

5.3.2 Protein sidechains

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	105/106 (99%)	97 (92%)	8 (8%)	16	25
1	B	105/106 (99%)	98 (93%)	7 (7%)	20	31
1	C	105/106 (99%)	98 (93%)	7 (7%)	20	31
1	D	104/106 (98%)	97 (93%)	7 (7%)	20	31
1	E	104/106 (98%)	99 (95%)	5 (5%)	31	49
1	F	104/106 (98%)	100 (96%)	4 (4%)	40	60
1	G	105/106 (99%)	97 (92%)	8 (8%)	16	25
1	H	105/106 (99%)	98 (93%)	7 (7%)	20	31
1	I	105/106 (99%)	97 (92%)	8 (8%)	16	25
1	J	105/106 (99%)	100 (95%)	5 (5%)	31	49
1	K	104/106 (98%)	99 (95%)	5 (5%)	31	49
1	L	105/106 (99%)	97 (92%)	8 (8%)	16	25
All	All	1256/1272 (99%)	1177 (94%)	79 (6%)	22	35

5 of 79 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	F	31	LEU
1	G	72	THR
1	L	31	LEU
1	F	46	ASP
1	G	29	GLU

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 37 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	109	ASN
1	G	69	HIS
1	L	60	GLN
1	E	122	GLN
1	G	45	HIS

5.3.3 RNA ⓘ

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](#)

There are no ligands in this entry.

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	131/136 (96%)	-0.51	0 100 100	8, 18, 28, 37	0
1	B	131/136 (96%)	-0.55	0 100 100	5, 12, 24, 35	0
1	C	131/136 (96%)	-0.55	1 (0%) 87 87	5, 11, 19, 27	0
1	D	131/136 (96%)	-0.55	0 100 100	6, 17, 25, 35	0
1	E	131/136 (96%)	-0.56	0 100 100	5, 12, 21, 36	0
1	F	130/136 (95%)	-0.63	0 100 100	5, 12, 19, 30	0
1	G	131/136 (96%)	-0.38	0 100 100	6, 15, 28, 36	0
1	H	131/136 (96%)	-0.45	0 100 100	6, 17, 28, 38	0
1	I	131/136 (96%)	-0.49	0 100 100	5, 13, 23, 36	0
1	J	131/136 (96%)	-0.31	1 (0%) 87 87	8, 17, 29, 37	0
1	K	130/136 (95%)	-0.36	0 100 100	10, 18, 28, 37	0
1	L	131/136 (96%)	-0.54	0 100 100	5, 14, 24, 37	0
All	All	1570/1632 (96%)	-0.49	2 (0%) 95 95	5, 15, 27, 38	0

All (2) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	130	ILE	3.6
1	C	48	SER	2.1

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 [i](#)

There are no carbohydrates in this entry.

6.4 Ligands [i](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.