



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 5, 2018 – 10:41 AM EST

PDB ID : 5YO5
Title : Crystal Structure of B562RIL with engineered disulfide bond A20C-Q25C
Authors : Pu, M.; Xu, Z.; Song, G.; Liu, Z.J.
Deposited on : 2017-10-26
Resolution : 2.20 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
Xtriage (Phenix)	:	1.9-1692
EDS	:	rb-20030736
Percentile statistics	:	20161228.v01 (using entries in the PDB archive December 28th 2016)
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)	:	rb-20030736

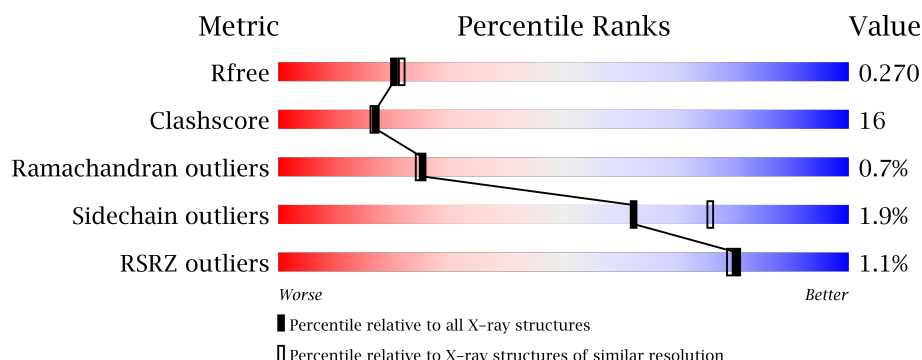
1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.20 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}	100719	4002 (2.20-2.20)
Clashscore	112137	4730 (2.20-2.20)
Ramachandran outliers	110173	4656 (2.20-2.20)
Sidechain outliers	110143	4657 (2.20-2.20)
RSRZ outliers	101464	4033 (2.20-2.20)

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	107	<div> <div>89%</div> <div>11%</div> </div>
1	B	107	<div> <div>81%</div> <div>12%</div> <div>6%</div> <div>•</div> </div>
1	C	107	<div> <div>88%</div> <div>12%</div> </div>
1	D	107	<div> <div>68%</div> <div>30%</div> <div>••</div> </div>
1	E	107	<div> <div>3%</div> <div>64%</div> <div>33%</div> <div>•••</div> </div>

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Mol	Chain	Length	Quality of chain
1	F	107	<div><div>5%</div><div><div></div><div>56%</div><div>40%</div><div></div></div><div>...</div></div>
1	G	107	<div><div>%</div><div><div></div><div>64%</div><div>30%</div><div></div></div><div>..</div></div>
1	H	107	<div><div></div><div><div></div><div>72%</div><div>27%</div><div></div></div><div>.</div></div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 6991 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 Soluble cytochrome b562.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	107	Total	C	N	O	S	0	0	0
			830	515	143	168	4			
1	B	106	Total	C	N	O	S	0	0	0
			819	509	139	167	4			
1	C	107	Total	C	N	O	S	0	0	0
			830	515	143	168	4			
1	D	106	Total	C	N	O	S	0	0	0
			825	512	142	167	4			
1	E	106	Total	C	N	O	S	0	0	0
			825	512	142	167	4			
1	F	106	Total	C	N	O	S	0	0	0
			825	512	142	167	4			
1	G	105	Total	C	N	O	S	0	0	0
			820	509	141	166	4			
1	H	106	Total	C	N	O	S	0	0	0
			825	512	142	167	4			

There are 48 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	0	ALA	-	expression tag	UNP P0ABE7
A	7	TRP	MET	engineered mutation	UNP P0ABE7
A	20	CYS	ALA	engineered mutation	UNP P0ABE7
A	25	CYS	GLN	engineered mutation	UNP P0ABE7
A	102	ILE	HIS	engineered mutation	UNP P0ABE7
A	106	LEU	ARG	engineered mutation	UNP P0ABE7
B	0	ALA	-	expression tag	UNP P0ABE7
B	7	TRP	MET	engineered mutation	UNP P0ABE7
B	20	CYS	ALA	engineered mutation	UNP P0ABE7
B	25	CYS	GLN	engineered mutation	UNP P0ABE7
B	102	ILE	HIS	engineered mutation	UNP P0ABE7
B	106	LEU	ARG	engineered mutation	UNP P0ABE7
C	0	ALA	-	expression tag	UNP P0ABE7

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Chain	Residue	Modelled	Actual	Comment	Reference
C	7	TRP	MET	engineered mutation	UNP P0ABE7
C	20	CYS	ALA	engineered mutation	UNP P0ABE7
C	25	CYS	GLN	engineered mutation	UNP P0ABE7
C	102	ILE	HIS	engineered mutation	UNP P0ABE7
C	106	LEU	ARG	engineered mutation	UNP P0ABE7
D	0	ALA	-	expression tag	UNP P0ABE7
D	7	TRP	MET	engineered mutation	UNP P0ABE7
D	20	CYS	ALA	engineered mutation	UNP P0ABE7
D	25	CYS	GLN	engineered mutation	UNP P0ABE7
D	102	ILE	HIS	engineered mutation	UNP P0ABE7
D	106	LEU	ARG	engineered mutation	UNP P0ABE7
E	0	ALA	-	expression tag	UNP P0ABE7
E	7	TRP	MET	engineered mutation	UNP P0ABE7
E	20	CYS	ALA	engineered mutation	UNP P0ABE7
E	25	CYS	GLN	engineered mutation	UNP P0ABE7
E	102	ILE	HIS	engineered mutation	UNP P0ABE7
E	106	LEU	ARG	engineered mutation	UNP P0ABE7
F	0	ALA	-	expression tag	UNP P0ABE7
F	7	TRP	MET	engineered mutation	UNP P0ABE7
F	20	CYS	ALA	engineered mutation	UNP P0ABE7
F	25	CYS	GLN	engineered mutation	UNP P0ABE7
F	102	ILE	HIS	engineered mutation	UNP P0ABE7
F	106	LEU	ARG	engineered mutation	UNP P0ABE7
G	0	ALA	-	expression tag	UNP P0ABE7
G	7	TRP	MET	engineered mutation	UNP P0ABE7
G	20	CYS	ALA	engineered mutation	UNP P0ABE7
G	25	CYS	GLN	engineered mutation	UNP P0ABE7
G	102	ILE	HIS	engineered mutation	UNP P0ABE7
G	106	LEU	ARG	engineered mutation	UNP P0ABE7
H	0	ALA	-	expression tag	UNP P0ABE7
H	7	TRP	MET	engineered mutation	UNP P0ABE7
H	20	CYS	ALA	engineered mutation	UNP P0ABE7
H	25	CYS	GLN	engineered mutation	UNP P0ABE7
H	102	ILE	HIS	engineered mutation	UNP P0ABE7
H	106	LEU	ARG	engineered mutation	UNP P0ABE7

- Molecule 2 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	62	Total O 62 62	0	0
2	B	83	Total O 83 83	0	0

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Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	C	69	Total 69	O 69	0	0
2	D	80	Total 80	O 80	0	0
2	E	20	Total 20	O 20	0	0
2	F	14	Total 14	O 14	0	0
2	G	25	Total 25	O 25	0	0
2	H	39	Total 39	O 39	0	0

3 Residue-property plots [i](#)


These plots are drawn for all protein, RNA and DNA 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.

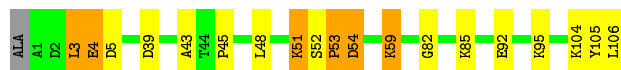
- Molecule 1: Soluble cytochrome b562

Chain A:  89% 11%



- Molecule 1: Soluble cytochrome b562

Chain B:  81% 12% 6%



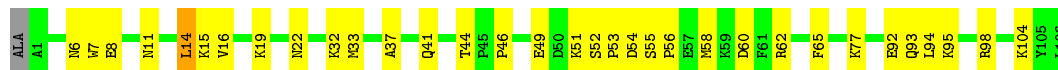
- Molecule 1: Soluble cytochrome b562

Chain C:  88% 12%



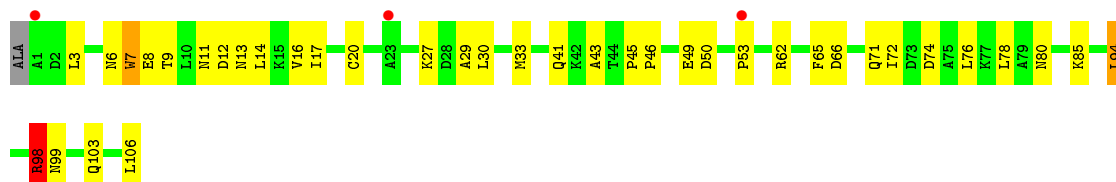
- Molecule 1: Soluble cytochrome b562

Chain D:  68% 30%

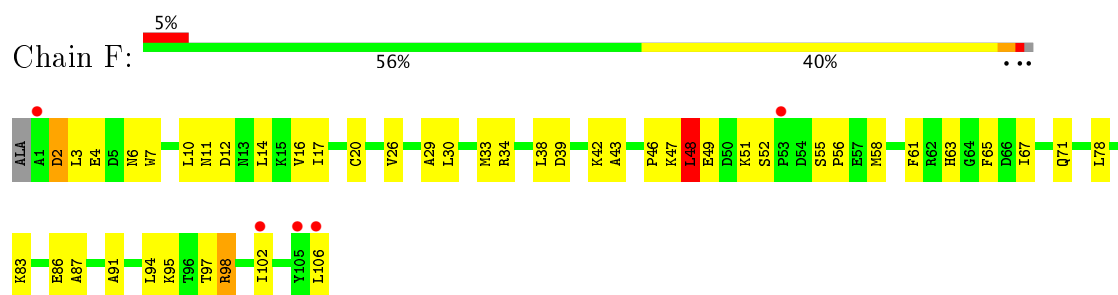


- Molecule 1: Soluble cytochrome b562

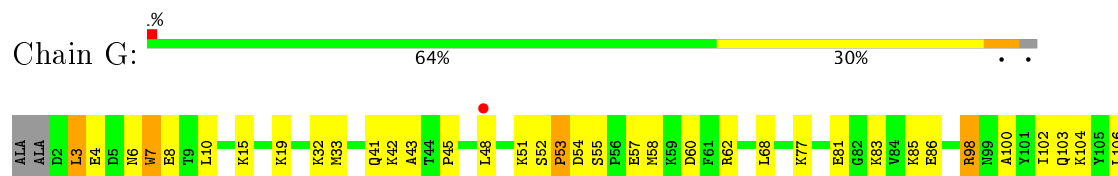
Chain E:  3% 64% 33%



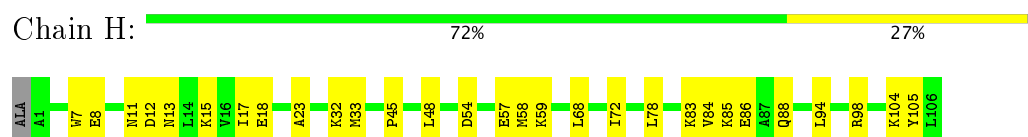
- Molecule 1: Soluble cytochrome b562



- Molecule 1: Soluble cytochrome b562



- Molecule 1: Soluble cytochrome b562



4 Data and refinement statistics

Property	Value	Source
Space group	C 1 2 1	Depositor
Cell constants a, b, c, α , β , γ	71.67Å 120.87Å 95.25Å 90.00° 90.04° 90.00°	Depositor
Resolution (Å)	37.70 – 2.20 37.70 – 1.76	Depositor EDS
% Data completeness (in resolution range)	97.7 (37.70-2.20) 58.2 (37.70-1.76)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.52 (at 1.76Å)	Xtriage
Refinement program	PHENIX 1.10_2155	Depositor
R, R_{free}	0.221 , 0.267 0.221 , 0.270	Depositor DCC
R_{free} test set	1362 reflections (3.52%)	DCC
Wilson B-factor (Å ²)	23.2	Xtriage
Anisotropy	0.229	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 31.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.32$	Xtriage
Estimated twinning fraction	0.014 for -1/2*h+1/2*k,3/2*h+1/2*k,-l 0.013 for -1/2*h-1/2*k,-3/2*h+1/2*k,-l 0.012 for 1/2*h+1/2*k,3/2*h-1/2*k,-l 0.014 for 1/2*h-1/2*k,-3/2*h-1/2*k,-l 0.476 for -h,-k,l	Xtriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	6991	wwPDB-VP
Average B, all atoms (Å ²)	48.0	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 39.27 % 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 3.2539e-04. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

¹ Intensities estimated from amplitudes.

² Theoretical 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

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	0.26	0/840	0.41	0/1131
1	B	0.36	0/829	0.62	2/1117 (0.2%)
1	C	0.27	0/840	0.42	0/1131
1	D	0.29	0/835	0.46	0/1124
1	E	0.63	1/835 (0.1%)	0.69	2/1124 (0.2%)
1	F	0.41	0/835	0.68	2/1124 (0.2%)
1	G	0.46	1/830 (0.1%)	0.51	0/1117
1	H	0.39	0/835	0.53	0/1124
All	All	0.40	2/6679 (0.0%)	0.55	6/8992 (0.1%)

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	B	0	1
1	F	0	1
All	All	0	2

All (2) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	7	TRP	CB-CG	-13.24	1.26	1.50
1	G	7	TRP	CB-CG	-7.29	1.37	1.50

The worst 5 of 6 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	F	48	LEU	CB-CG-CD2	-10.29	93.50	111.00
1	E	7	TRP	CA-CB-CG	-7.69	99.09	113.70
1	B	53	PRO	C-N-CA	6.95	139.08	121.70
1	B	59	LYS	CD-CE-NZ	6.70	127.10	111.70

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	E	98	ARG	NE-CZ-NH1	-6.66	116.97	120.30

There are no chirality outliers.

All (2) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	B	54	ASP	Peptide
1	F	48	LEU	Peptide

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	830	0	829	9	0
1	B	819	0	813	18	0
1	C	830	0	829	8	0
1	D	825	0	824	29	0
1	E	825	0	824	40	0
1	F	825	0	824	46	0
1	G	820	0	816	35	0
1	H	825	0	824	25	0
2	A	62	0	0	3	2
2	B	83	0	0	5	1
2	C	69	0	0	3	2
2	D	80	0	0	10	2
2	E	20	0	0	7	1
2	F	14	0	0	1	0
2	G	25	0	0	4	0
2	H	39	0	0	5	0
All	All	6991	0	6583	205	4

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 16.

The worst 5 of 205 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:E:7:TRP:CH2	1:E:98:ARG:NH2	2.13	1.15
1:G:4:GLU:HA	1:G:7:TRP:HB3	1.34	1.07
1:F:78:LEU:HD22	1:F:87:ALA:HB2	1.35	1.04
1:E:8:GLU:OE2	2:E:301:HOH:O	1.86	0.92
1:E:7:TRP:HH2	1:E:98:ARG:NH2	1.59	0.92

All (4) 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)
2:B:306:HOH:O	2:C:313:HOH:O[3_445]	1.95	0.25
2:A:318:HOH:O	2:E:320:HOH:O[1_455]	2.00	0.20
2:C:369:HOH:O	2:D:280:HOH:O[3_555]	2.14	0.06
2:A:355:HOH:O	2:D:272:HOH:O[3_455]	2.19	0.01

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	105/107 (98%)	104 (99%)	1 (1%)	0	100	100
1	B	104/107 (97%)	100 (96%)	2 (2%)	2 (2%)	9	6
1	C	105/107 (98%)	104 (99%)	0	1 (1%)	18	16
1	D	104/107 (97%)	103 (99%)	0	1 (1%)	18	16
1	E	104/107 (97%)	99 (95%)	5 (5%)	0	100	100
1	F	104/107 (97%)	99 (95%)	4 (4%)	1 (1%)	18	16
1	G	103/107 (96%)	100 (97%)	2 (2%)	1 (1%)	18	16
1	H	104/107 (97%)	104 (100%)	0	0	100	100
All	All	833/856 (97%)	813 (98%)	14 (2%)	6 (1%)	25	24

5 of 6 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	B	4	GLU
1	F	49	GLU
1	B	3	LEU
1	G	53	PRO
1	D	53	PRO

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	87/87 (100%)	87 (100%)	0	100	100
1	B	86/87 (99%)	84 (98%)	2 (2%)	56	69
1	C	87/87 (100%)	86 (99%)	1 (1%)	78	88
1	D	87/87 (100%)	84 (97%)	3 (3%)	42	53
1	E	87/87 (100%)	85 (98%)	2 (2%)	56	69
1	F	87/87 (100%)	85 (98%)	2 (2%)	56	69
1	G	87/87 (100%)	85 (98%)	2 (2%)	56	69
1	H	87/87 (100%)	86 (99%)	1 (1%)	78	88
All	All	695/696 (100%)	682 (98%)	13 (2%)	62	76

5 of 13 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	D	62	ARG
1	E	94	LEU
1	G	3	LEU
1	D	16	VAL
1	F	98	ARG

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (3) such sidechains are listed below:

Mol	Chain	Res	Type
1	E	11	ASN

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Mol	Chain	Res	Type
1	E	41	GLN
1	F	88	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 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	107/107 (100%)	-0.92	0 100 100	22, 34, 50, 59	0
1	B	106/107 (99%)	-0.86	0 100 100	19, 32, 65, 73	0
1	C	107/107 (100%)	-0.96	0 100 100	22, 34, 54, 71	0
1	D	106/107 (99%)	-0.85	0 100 100	19, 32, 67, 91	0
1	E	106/107 (99%)	0.04	3 (2%) 53 51	33, 66, 84, 89	0
1	F	106/107 (99%)	0.12	5 (4%) 32 31	36, 67, 84, 93	0
1	G	105/107 (98%)	-0.54	1 (0%) 82 81	24, 52, 73, 88	0
1	H	106/107 (99%)	-0.45	0 100 100	27, 57, 86, 100	0
All	All	849/856 (99%)	-0.55	9 (1%) 80 79	19, 45, 79, 100	0

The worst 5 of 9 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	E	1	ALA	4.5
1	E	53	PRO	3.8
1	F	1	ALA	3.5
1	F	53	PRO	3.3
1	F	105	TYR	2.9

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 ⓘ

There are no carbohydrates in this entry.

6.4 Ligands

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.