



Full wwPDB X-ray Structure Validation Report ⓘ

Oct 11, 2021 – 06:31 PM EDT

PDB ID : 2O8V
Title : PAPS reductase in a covalent complex with thioredoxin C35A
Authors : Chartron, J.; Shiau, C.; Stout, C.D.; Carroll, K.S.
Deposited on : 2006-12-12
Resolution : 3.00 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 ⓘ symbol.

The following versions of software and data (see [references ⓘ](#)) were used in the production of this report:

MolProbity : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.23.2
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) : 2.23.2

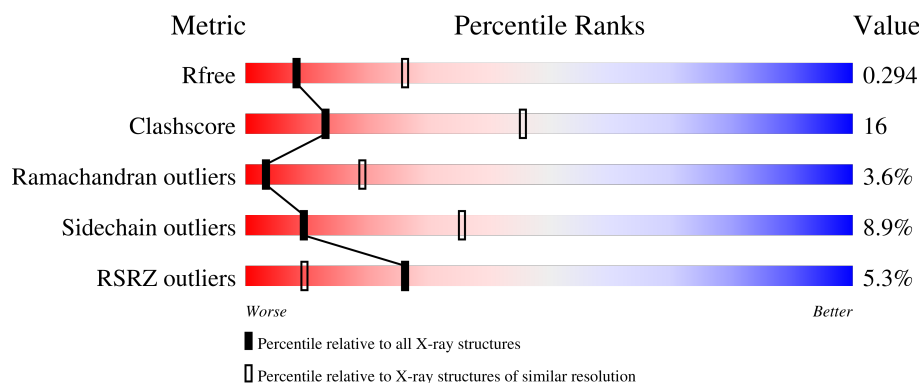
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 3.00 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	2092 (3.00-3.00)
Clashscore	141614	2416 (3.00-3.00)
Ramachandran outliers	138981	2333 (3.00-3.00)
Sidechain outliers	138945	2336 (3.00-3.00)
RSRZ outliers	127900	1990 (3.00-3.00)

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 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 $\leq 5\%$. 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	252	<div> <div>6%</div> <div> <div></div> <div>52%</div> <div>34%</div> <div>• • 9%</div> </div> </div>
2	B	128	<div> <div>2%</div> <div> <div></div> <div>59%</div> <div>23%</div> <div>• 16%</div> </div> </div>

2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 2672 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 Phosphoadenosine phosphosulfate reductase.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	229	Total	C	N	O	S	0	0	0
			1851	1182	323	344	2			

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	245	LEU	-	cloning artifact	UNP P17854
A	246	GLU	-	cloning artifact	UNP P17854
A	247	HIS	-	cloning artifact	UNP P17854
A	248	HIS	-	cloning artifact	UNP P17854
A	249	HIS	-	cloning artifact	UNP P17854
A	250	HIS	-	cloning artifact	UNP P17854
A	251	HIS	-	cloning artifact	UNP P17854
A	252	HIS	-	cloning artifact	UNP P17854

- Molecule 2 is a protein called Thioredoxin 1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	B	108	Total	C	N	O	S	0	0	0
			821	528	132	159	2			

There are 21 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
B	-19	MET	-	cloning artifact	UNP Q1R4F8
B	-18	GLY	-	cloning artifact	UNP Q1R4F8
B	-17	SER	-	cloning artifact	UNP Q1R4F8
B	-16	SER	-	cloning artifact	UNP Q1R4F8
B	-15	HIS	-	cloning artifact	UNP Q1R4F8
B	-14	HIS	-	cloning artifact	UNP Q1R4F8
B	-13	HIS	-	cloning artifact	UNP Q1R4F8
B	-12	HIS	-	cloning artifact	UNP Q1R4F8

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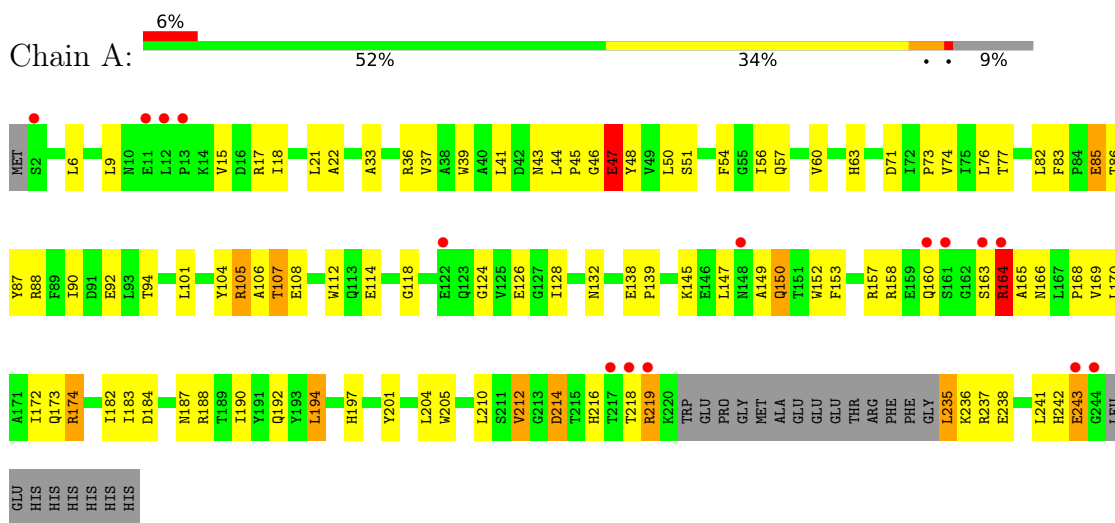
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Chain	Residue	Modelled	Actual	Comment	Reference
B	-11	HIS	-	cloning artifact	UNP Q1R4F8
B	-10	HIS	-	cloning artifact	UNP Q1R4F8
B	-9	SER	-	cloning artifact	UNP Q1R4F8
B	-8	SER	-	cloning artifact	UNP Q1R4F8
B	-7	GLY	-	cloning artifact	UNP Q1R4F8
B	-6	LEU	-	cloning artifact	UNP Q1R4F8
B	-5	VAL	-	cloning artifact	UNP Q1R4F8
B	-4	PRO	-	cloning artifact	UNP Q1R4F8
B	-3	ARG	-	cloning artifact	UNP Q1R4F8
B	-2	GLY	-	cloning artifact	UNP Q1R4F8
B	-1	SER	-	cloning artifact	UNP Q1R4F8
B	0	HIS	-	cloning artifact	UNP Q1R4F8
B	35	ALA	CYS	engineered mutation	UNP Q1R4F8

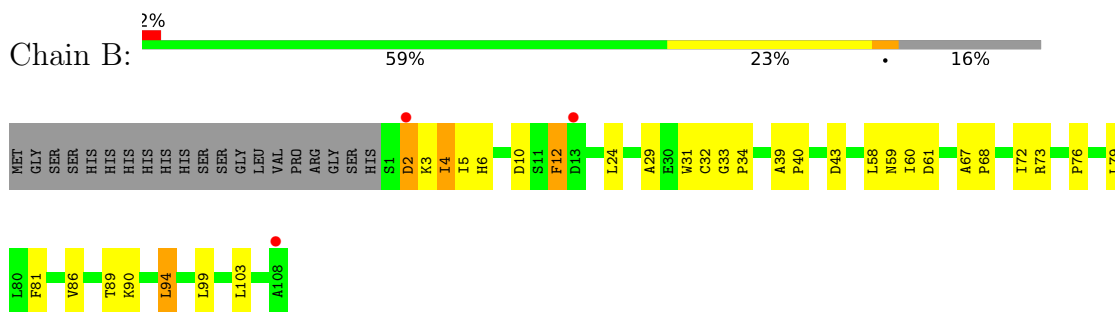
3 Residue-property plots [i](#)

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: Phosphoadenosine phosphosulfate reductase



- Molecule 2: Thioredoxin 1



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 21	Depositor
Cell constants a, b, c, α , β , γ	40.93Å 111.15Å 153.43Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	27.79 – 3.00 27.79 – 3.00	Depositor EDS
% Data completeness (in resolution range)	99.4 (27.79-3.00) 99.5 (27.79-3.00)	Depositor EDS
R_{merge}	0.14	Depositor
R_{sym}	0.14	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.07 (at 3.00Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.297 , 0.307 0.298 , 0.294	Depositor DCC
R_{free} test set	339 reflections (4.62%)	wwPDB-VP
Wilson B-factor (Å ²)	60.0	Xtriage
Anisotropy	0.631	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.38 , 39.7	EDS
L-test for twinning ²	$\langle L \rangle = 0.42$, $\langle L^2 \rangle = 0.24$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.85	EDS
Total number of atoms	2672	wwPDB-VP
Average B, all atoms (Å ²)	55.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 8.44% 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 [i](#)

5.1 Standard geometry [i](#)

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	0.28	0/1890	0.62	1/2562 (0.0%)
2	B	0.26	0/836	0.52	0/1133
All	All	0.28	0/2726	0.60	1/3695 (0.0%)

There are no bond length outliers.

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	A	243	GLU	N-CA-C	5.08	124.70	111.00

There are no chirality outliers.

There are no planarity outliers.

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	1851	0	1849	70	0
2	B	821	0	832	22	0
All	All	2672	0	2681	87	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 16.

All (87) 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:A:105:ARG:HH21	1:A:105:ARG:HG3	1.29	0.96
1:A:9:LEU:HD23	1:A:172:ILE:HD11	1.63	0.78
1:A:210:LEU:HD21	1:A:235:LEU:HD23	1.67	0.77
1:A:48:TYR:HB3	1:A:153:PHE:HE1	1.58	0.68
1:A:105:ARG:HG3	1:A:105:ARG:NH2	2.02	0.68
1:A:236:LYS:O	1:A:238:GLU:N	2.26	0.68
1:A:47:GLU:HG2	1:A:147:LEU:O	1.96	0.66
2:B:24:LEU:HD22	2:B:103:LEU:HD21	1.78	0.64
1:A:158:ARG:HA	1:A:163:SER:OG	1.99	0.62
1:A:60:VAL:HG21	1:A:190:ILE:HG23	1.80	0.62
1:A:94:THR:HG21	1:A:101:LEU:HD22	1.82	0.62
1:A:47:GLU:HB3	1:A:149:ALA:HA	1.82	0.62
1:A:36:ARG:HD3	1:A:169:VAL:HG11	1.82	0.61
2:B:32:CYS:SG	2:B:34:PRO:HG2	2.40	0.60
1:A:56:ILE:HD12	1:A:205:TRP:HB2	1.83	0.59
2:B:90:LYS:HG2	2:B:94:LEU:HD23	1.85	0.59
1:A:39:TRP:CZ3	1:A:44:LEU:HD11	2.37	0.58
1:A:173:GLN:HG2	1:A:174:ARG:HD3	1.85	0.58
1:A:169:VAL:HG22	1:A:183:ILE:HG21	1.85	0.58
1:A:85:GLU:HG3	1:A:204:LEU:HG	1.86	0.58
1:A:86:THR:O	1:A:90:ILE:HG13	2.04	0.57
1:A:56:ILE:HD11	1:A:212:VAL:HG13	1.86	0.56
2:B:81:PHE:CE1	2:B:86:VAL:HG22	2.41	0.56
1:A:76:LEU:HD21	1:A:90:ILE:HD13	1.88	0.56
1:A:241:LEU:HD21	2:B:60:ILE:HD13	1.87	0.55
1:A:236:LYS:C	1:A:238:GLU:N	2.62	0.53
2:B:67:ALA:HB3	2:B:68:PRO:HD3	1.90	0.53
1:A:6:LEU:HA	1:A:9:LEU:HB2	1.92	0.52
1:A:236:LYS:C	1:A:238:GLU:H	2.13	0.52
1:A:60:VAL:HG22	1:A:194:LEU:HD13	1.92	0.52
1:A:187:ASN:HB3	2:B:31:TRP:HB2	1.92	0.51
1:A:18:ILE:O	1:A:22:ALA:HB2	2.10	0.51
1:A:138:GLU:HB3	1:A:139:PRO:HD3	1.93	0.50
1:A:210:LEU:CD2	1:A:235:LEU:HD23	2.40	0.50
1:A:218:THR:O	1:A:219:ARG:HD2	2.12	0.50
2:B:33:GLY:N	2:B:34:PRO:HD2	2.28	0.49
1:A:17:ARG:O	1:A:21:LEU:HD13	2.11	0.49
1:A:51:SER:HG	1:A:152:TRP:HE1	1.61	0.49
1:A:235:LEU:HD12	2:B:34:PRO:HD3	1.95	0.49
1:A:166:ASN:O	1:A:168:PRO:HD3	2.13	0.49
1:A:57:GLN:OE1	1:A:157:ARG:HD3	2.13	0.48
1:A:157:ARG:HD2	1:A:190:ILE:HD11	1.93	0.48

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:4:ILE:HG23	2:B:5:ILE:N	2.28	0.48
2:B:39:ALA:N	2:B:40:PRO:HD2	2.29	0.47
1:A:164:ARG:O	1:A:166:ASN:N	2.40	0.47
2:B:94:LEU:HD13	2:B:99:LEU:HB2	1.97	0.47
2:B:4:ILE:HG13	2:B:5:ILE:H	1.79	0.47
1:A:54:PHE:CD1	1:A:76:LEU:HD13	2.50	0.46
2:B:59:ASN:OD1	2:B:61:ASP:HB2	2.14	0.46
1:A:124:GLY:O	1:A:128:ILE:HG13	2.16	0.46
1:A:236:LYS:HA	1:A:236:LYS:HD2	1.75	0.46
1:A:82:LEU:HB2	1:A:87:TYR:CZ	2.52	0.45
1:A:106:ALA:HB3	1:A:108:GLU:O	2.16	0.45
1:A:158:ARG:HG2	1:A:183:ILE:HG13	1.98	0.45
1:A:108:GLU:HB2	1:A:112:TRP:HB3	1.98	0.45
1:A:168:PRO:HB2	1:A:170:LEU:O	2.16	0.45
1:A:50:LEU:O	1:A:74:VAL:HA	2.17	0.45
1:A:210:LEU:HD11	1:A:235:LEU:HG	2.00	0.44
1:A:214:ASP:O	1:A:219:ARG:HB2	2.17	0.44
1:A:183:ILE:HG23	1:A:184:ASP:N	2.32	0.44
2:B:2:ASP:HB3	2:B:6:HIS:HE1	1.82	0.43
2:B:12:PHE:CE1	2:B:58:LEU:HD13	2.53	0.43
1:A:235:LEU:CG	2:B:34:PRO:HD3	2.47	0.43
1:A:158:ARG:CG	1:A:183:ILE:HG13	2.49	0.43
1:A:85:GLU:CD	1:A:85:GLU:H	2.21	0.42
1:A:45:PRO:HG2	1:A:150:GLN:HB3	2.02	0.42
1:A:157:ARG:HD2	1:A:190:ILE:CD1	2.49	0.42
1:A:33:ALA:O	1:A:37:VAL:HG23	2.19	0.42
1:A:15:VAL:HA	1:A:18:ILE:HG22	2.02	0.42
1:A:107:THR:HB	1:A:108:GLU:OE2	2.19	0.42
2:B:29:ALA:HA	2:B:59:ASN:ND2	2.35	0.42
2:B:32:CYS:SG	2:B:76:PRO:HD3	2.61	0.41
1:A:76:LEU:CD2	1:A:90:ILE:HD13	2.50	0.41
1:A:114:GLU:O	1:A:118:GLY:HA2	2.19	0.41
1:A:88:ARG:O	1:A:92:GLU:HB2	2.21	0.41
1:A:235:LEU:HD13	1:A:235:LEU:HA	1.83	0.41
1:A:235:LEU:HG	2:B:34:PRO:HD3	2.03	0.41
2:B:79:LEU:HD13	2:B:89:THR:HB	2.03	0.41
1:A:87:TYR:HA	1:A:90:ILE:HD12	2.01	0.41
1:A:194:LEU:HD12	1:A:194:LEU:HA	1.90	0.41
1:A:214:ASP:HB2	1:A:218:THR:HG21	2.03	0.41
1:A:43:ASN:C	1:A:44:LEU:HD12	2.42	0.40
1:A:63:HIS:HE1	1:A:197:HIS:ND1	2.18	0.40

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
2:B:72:ILE:HD11	2:B:79:LEU:HD21	2.02	0.40
1:A:83:PHE:HB2	1:A:86:THR:OG1	2.22	0.40
1:A:188:ARG:O	1:A:192:GLN:HG3	2.22	0.40
1:A:77:THR:HA	1:A:104:TYR:O	2.22	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	225/252 (89%)	190 (84%)	24 (11%)	11 (5%)	2	13
2	B	106/128 (83%)	96 (91%)	9 (8%)	1 (1%)	17	55
All	All	331/380 (87%)	286 (86%)	33 (10%)	12 (4%)	3	19

All (12) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	47	GLU
1	A	160	GLN
1	A	165	ALA
1	A	216	HIS
1	A	237	ARG
1	A	243	GLU
1	A	46	GLY
1	A	242	HIS
1	A	164	ARG
2	B	4	ILE
1	A	182	ILE
1	A	73	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	196/216 (91%)	178 (91%)	18 (9%)	9	34
2	B	86/103 (84%)	79 (92%)	7 (8%)	11	40
All	All	282/319 (88%)	257 (91%)	25 (9%)	9	35

All (25) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	41	LEU
1	A	47	GLU
1	A	71	ASP
1	A	85	GLU
1	A	105	ARG
1	A	107	THR
1	A	126	GLU
1	A	132	ASN
1	A	145	LYS
1	A	150	GLN
1	A	164	ARG
1	A	174	ARG
1	A	194	LEU
1	A	201	TYR
1	A	212	VAL
1	A	214	ASP
1	A	219	ARG
1	A	235	LEU
2	B	2	ASP
2	B	3	LYS
2	B	10	ASP
2	B	12	PHE
2	B	43	ASP
2	B	73	ARG
2	B	94	LEU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (7) such

sidechains are listed below:

Mol	Chain	Res	Type
1	A	10	ASN
1	A	63	HIS
1	A	150	GLN
1	A	166	ASN
2	B	6	HIS
2	B	98	GLN
2	B	106	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](#)

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 [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	229/252 (90%)	0.46	15 (6%)	18 5	34, 54, 85, 94	0
2	B	108/128 (84%)	0.34	3 (2%)	53 25	34, 52, 71, 79	0
All	All	337/380 (88%)	0.42	18 (5%)	26 10	34, 54, 83, 94	0

All (18) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	161	SER	6.3
1	A	217	THR	6.1
1	A	11	GLU	5.6
1	A	2	SER	5.3
1	A	218	THR	3.5
1	A	219	ARG	3.4
2	B	13	ASP	3.3
1	A	163	SER	3.2
2	B	108	ALA	2.9
1	A	160	GLN	2.8
1	A	12	LEU	2.6
2	B	2	ASP	2.4
1	A	148	ASN	2.3
1	A	244	GLY	2.2
1	A	13	PRO	2.1
1	A	164	ARG	2.1
1	A	243	GLU	2.1
1	A	122	GLU	2.0

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](#)

There are no ligands in this entry.

6.5 Other polymers [i](#)

There are no such residues in this entry.