



# Full wwPDB X-ray Structure Validation Report ⓘ

May 24, 2020 – 06:23 am BST

PDB ID : 5XJM  
Title : Complex structure of angiotensin II type 2 receptor with Fab  
Authors : Asada, H.; Horita, S.; Shimamura, T.; Iwata, S.  
Deposited on : 2017-05-02  
Resolution : 3.20 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](mailto: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.

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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

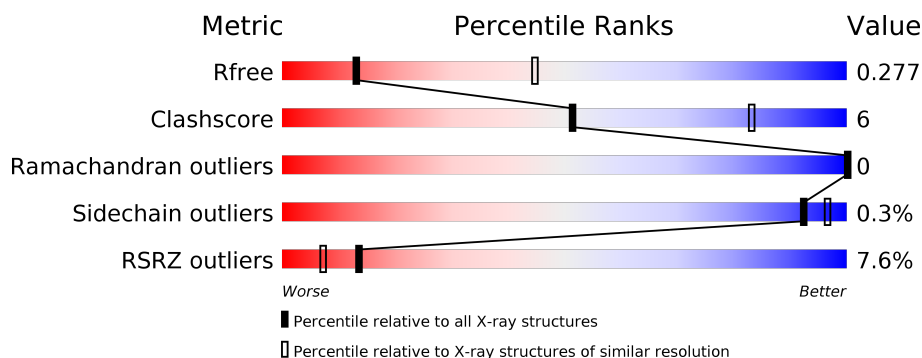
# 1 Overall quality at a glance ⓘ

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 3.20 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))
$R_{free}$	130704	1133 (3.20-3.20)
Clashscore	141614	1253 (3.20-3.20)
Ramachandran outliers	138981	1234 (3.20-3.20)
Sidechain outliers	138945	1233 (3.20-3.20)
RSRZ outliers	127900	1095 (3.20-3.20)

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  $\geq 3$ , 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	422	<div> <div>14%</div> <div> <div></div> <div>77%</div> <div>12%</div> <div>11%</div> </div> </div>
2	H	220	<div> <div>%</div> <div> <div></div> <div>79%</div> <div>20%</div> </div> </div>
3	L	212	<div> <div></div> <div> <div></div> <div>90%</div> <div>10%</div> </div> </div>
4	B	8	<div> <div>13%</div> <div> <div></div> <div>88%</div> <div>13%</div> </div> </div>

The following table lists non-polymeric compounds, carbohydrate monomers and non-standard residues in protein, DNA, RNA chains that are outliers for geometric or electron-density-fit crite-

ria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
4	SAR	B	1	-	-	-	X

## 2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 6335 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 Type-2 angiotensin II receptor,Soluble cytochrome b562,Type-2 angiotensin II receptor.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	375	Total	C	N	O	S	0	0	0
			2992	1980	479	511	22			

There are 10 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	34	GLY	-	expression tag	UNP P50052
A	1007	TRP	MET	engineered mutation	UNP P0ABE7
A	1102	ILE	HIS	engineered mutation	UNP P0ABE7
A	1106	LEU	ARG	engineered mutation	UNP P0ABE7
A	347	GLU	-	expression tag	UNP P50052
A	348	ASN	-	expression tag	UNP P50052
A	349	LEU	-	expression tag	UNP P50052
A	350	TYR	-	expression tag	UNP P50052
A	351	PHE	-	expression tag	UNP P50052
A	352	GLN	-	expression tag	UNP P50052

- Molecule 2 is a protein called FabH.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
2	H	220	Total	C	N	O	S	0	0	0
			1643	1046	265	323	9			

- Molecule 3 is a protein called FabL.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
3	L	212	Total	C	N	O	S	0	0	0
			1631	1017	269	336	9			

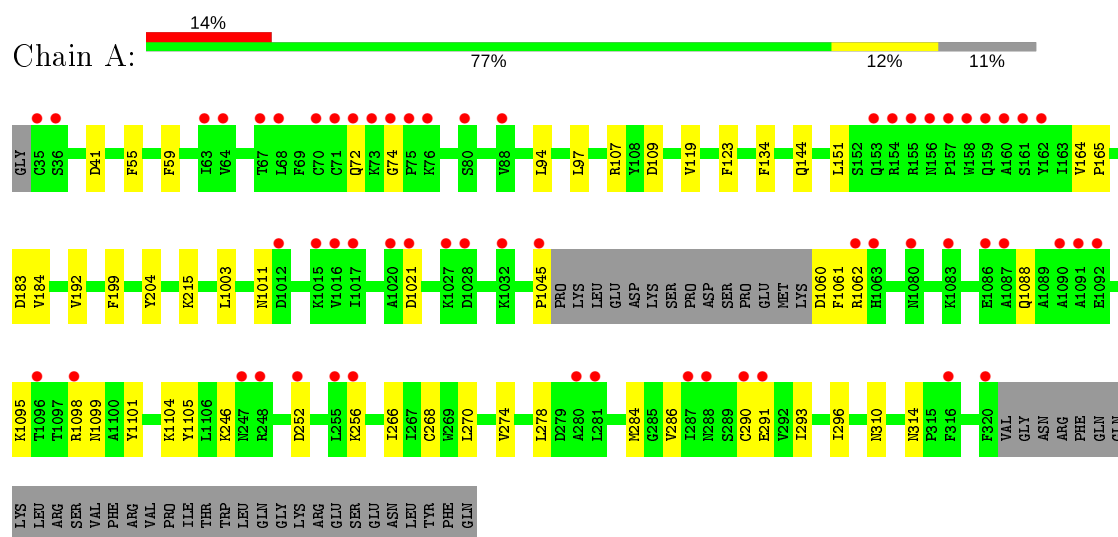
- Molecule 4 is a protein called Sar1, Ile8-angiotensin II.

Mol	Chain	Residues	Atoms				ZeroOcc	AltConf	Trace
4	B	8	Total	C	N	O	0	0	0
			69	46	13	10			

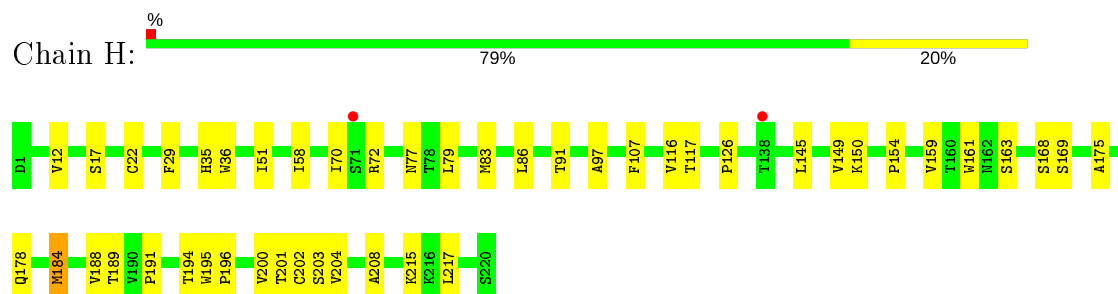
### 3 Residue-property plots [i](#)

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.

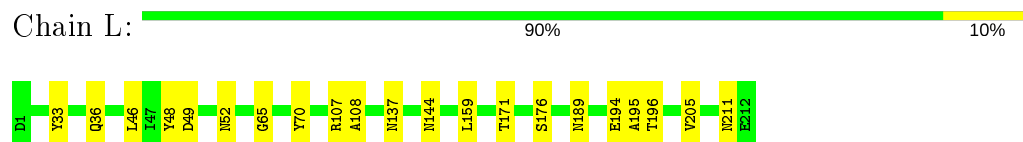
- Molecule 1: Type-2 angiotensin II receptor,Soluble cytochrome b562,Type-2 angiotensin II receptor



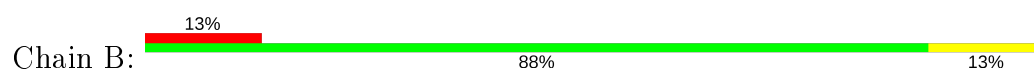
- Molecule 2: FabH



- Molecule 3: FabL



- Molecule 4: Sar1, Ile8-angiotensin II





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 2	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	465.39 Å 48.65 Å 55.70 Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	48.39 – 3.20 48.39 – 3.20	Depositor EDS
% Data completeness (in resolution range)	99.8 (48.39-3.20) 95.2 (48.39-3.20)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	1.40 (at 3.19 Å)	Xtriage
Refinement program	PHENIX 1.11.1 _2575	Depositor
R, $R_{free}$	0.226 , 0.275 0.226 , 0.277	Depositor DCC
$R_{free}$ test set	2000 reflections (9.07%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	44.1	Xtriage
Anisotropy	0.489	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.30 , 57.6	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.45$ , $\langle L^2 \rangle = 0.28$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
$F_o, F_c$ correlation	0.86	EDS
Total number of atoms	6335	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	69.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 4.42% of the height of the origin peak. No significant pseudotranslation is detected.*

<sup>1</sup>Intensities estimated from amplitudes.

<sup>2</sup>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 [i](#)

### 5.1 Standard geometry [i](#)

Bond lengths and bond angles in the following residue types are not validated in this section: SAR

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	0.25	0/3069	0.37	0/4176
2	H	0.25	0/1690	0.47	0/2311
3	L	0.24	0/1669	0.44	0/2269
4	B	0.20	0/66	0.35	0/88
All	All	0.25	0/6494	0.42	0/8844

There are no bond length outliers.

There are no bond angle outliers.

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	2992	0	3053	31	0
2	H	1643	0	1592	27	0
3	L	1631	0	1561	12	0
4	B	69	0	73	1	0
All	All	6335	0	6279	70	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 (70) 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:266:ILE:O	1:A:270:LEU:HB2	1.91	0.69
2:H:22:CYS:HB3	2:H:79:LEU:HB3	1.75	0.69
2:H:29:PHE:O	2:H:72:ARG:NH2	2.32	0.63
3:L:194:GLU:HG2	3:L:205:VAL:HG22	1.82	0.61
3:L:65:GLY:HA3	3:L:70:TYR:HA	1.84	0.60
2:H:168:SER:HA	2:H:189:THR:O	2.01	0.59
2:H:91:THR:HG23	2:H:117:THR:HA	1.84	0.59
1:A:310:ASN:O	1:A:314:ASN:HB2	2.03	0.59
1:A:252:ASP:OD1	1:A:256:LYS:NZ	2.35	0.58
1:A:94:LEU:HA	1:A:97:LEU:HG	1.86	0.57
3:L:189:ASN:ND2	3:L:211:ASN:OD1	2.37	0.57
2:H:159:VAL:HG22	2:H:204:VAL:HG22	1.86	0.56
1:A:1011:ASN:HA	1:A:1098:ARG:HH12	1.71	0.56
3:L:107:ARG:NH1	3:L:108:ALA:O	2.36	0.56
1:A:119:VAL:O	1:A:123:PHE:HB2	2.05	0.56
1:A:55:PHE:O	1:A:59:PHE:HB2	2.05	0.55
2:H:159:VAL:HA	2:H:203:SER:O	2.07	0.55
1:A:1011:ASN:HA	1:A:1098:ARG:NH1	2.23	0.54
2:H:175:ALA:HA	2:H:184:MET:HB3	1.89	0.54
1:A:55:PHE:O	1:A:59:PHE:CB	2.57	0.53
3:L:36:GLN:HB2	3:L:46:LEU:HD11	1.90	0.52
3:L:49:ASP:HB2	3:L:52:ASN:HD22	1.76	0.51
1:A:144:GLN:HB3	1:A:151:LEU:HD12	1.93	0.51
1:A:266:ILE:O	1:A:270:LEU:CB	2.57	0.51
3:L:33:TYR:HD1	3:L:48:TYR:HA	1.76	0.51
1:A:1045:PRO:HD2	1:A:1062:ARG:HH21	1.76	0.50
1:A:1061:PHE:HZ	1:A:246:LYS:HD3	1.77	0.50
3:L:159:LEU:O	3:L:176:SER:HA	2.11	0.50
1:A:41:ASP:OD2	1:A:107:ARG:NH2	2.45	0.49
2:H:150:LYS:NZ	2:H:178:GLN:OE1	2.46	0.49
1:A:268:CYS:HB3	1:A:310:ASN:HB2	1.93	0.49
2:H:51:ILE:HG13	2:H:58:ILE:HG12	1.94	0.49
1:A:284:MET:HG3	1:A:286:VAL:HG23	1.95	0.48
2:H:17:SER:HA	2:H:83:MET:O	2.14	0.48
1:A:1060:ASP:O	1:A:1101:TYR:OH	2.30	0.47
2:H:35:HIS:HB2	2:H:97:ALA:O	2.15	0.47
2:H:29:PHE:HB3	2:H:77:ASN:HD22	1.80	0.46
2:H:145:LEU:HD13	2:H:217:LEU:HD13	1.97	0.46
1:A:183:ASP:OD1	1:A:184:VAL:N	2.48	0.45
1:A:290:CYS:SG	1:A:291:GLU:N	2.90	0.45
1:A:293:ILE:HA	1:A:296:ILE:HD12	1.99	0.45

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:199:PHE:HB2	1:A:204:TYR:CD2	2.52	0.45
2:H:97:ALA:HB1	2:H:107:PHE:HB3	1.99	0.45
3:L:144:ASN:O	3:L:195:ALA:HA	2.17	0.45
2:H:163:SER:HB3	2:H:200:VAL:HG13	1.98	0.45
2:H:12:VAL:HG11	2:H:86:LEU:HD12	1.98	0.44
2:H:36:TRP:HD1	2:H:70:ILE:HD12	1.82	0.44
1:A:215:LYS:NZ	4:B:8:ILE:O	2.41	0.44
1:A:109:ASP:HA	1:A:192:VAL:HG13	1.99	0.44
1:A:1021:ASP:OD1	1:A:1088:GLN:NE2	2.38	0.43
1:A:72:GLN:O	1:A:74:GLY:N	2.44	0.43
1:A:1095:LYS:O	1:A:1099:ASN:HB2	2.18	0.43
1:A:1098:ARG:HG3	1:A:1099:ASN:N	2.33	0.43
2:H:191:PRO:HG2	2:H:194:THR:HG23	2.01	0.42
3:L:144:ASN:HB3	3:L:196:THR:OG1	2.19	0.42
2:H:154:PRO:HD2	2:H:208:ALA:HB1	2.02	0.42
2:H:126:PRO:HB2	2:H:149:VAL:HG13	2.01	0.42
3:L:107:ARG:HG2	3:L:108:ALA:N	2.35	0.42
2:H:51:ILE:HD13	2:H:72:ARG:HB2	2.02	0.41
1:A:274:VAL:O	1:A:278:LEU:HG	2.20	0.41
2:H:195:TRP:HA	2:H:196:PRO:HA	1.88	0.41
1:A:164:VAL:HB	1:A:165:PRO:HD3	2.04	0.40
2:H:161:TRP:CZ3	2:H:202:CYS:HB3	2.56	0.40
2:H:83:MET:HB3	2:H:86:LEU:HD21	2.03	0.40
2:H:201:THR:HA	2:H:215:LYS:O	2.21	0.40
2:H:83:MET:HE1	2:H:116:VAL:HG11	2.04	0.40
3:L:137:ASN:HD22	3:L:171:THR:HG21	1.85	0.40
2:H:169:SER:O	2:H:188:VAL:HA	2.20	0.40
1:A:1061:PHE:CE2	1:A:1104:LYS:HB3	2.56	0.40
1:A:1003:LEU:HG	1:A:1105:TYR:HE1	1.86	0.40

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	371/422 (88%)	354 (95%)	17 (5%)	0	100	100
2	H	218/220 (99%)	204 (94%)	14 (6%)	0	100	100
3	L	210/212 (99%)	201 (96%)	9 (4%)	0	100	100
4	B	6/8 (75%)	6 (100%)	0	0	100	100
All	All	805/862 (93%)	765 (95%)	40 (5%)	0	100	100

There are no Ramachandran outliers to report.

### 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	322/366 (88%)	321 (100%)	1 (0%)	92	96
2	H	185/185 (100%)	184 (100%)	1 (0%)	88	95
3	L	187/187 (100%)	187 (100%)	0	100	100
4	B	7/7 (100%)	7 (100%)	0	100	100
All	All	701/745 (94%)	699 (100%)	2 (0%)	92	96

All (2) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	134	PHE
2	H	184	MET

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. All (4) such sidechains are listed below:

Mol	Chain	Res	Type
1	A	1013	ASN
1	A	1103	GLN
1	A	310	ASN
2	H	77	ASN

### 5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains ⓘ

1 non-standard protein/DNA/RNA residue is modelled in this entry.

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	SAR	B	1	4	4,4,5	1.22	0	1,3,5	1.93	0

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	SAR	B	1	4	-	1/1/2/3	-

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
4	B	1	SAR	C-CA-N-CN

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates ⓘ

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, 95<sup>th</sup> 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 <sup>2</sup> )	Q<0.9
1	A	375/422 (88%)	0.72	59 (15%) 2 1	61, 101, 143, 176	0
2	H	220/220 (100%)	-0.08	2 (0%) 84 75	18, 42, 69, 98	0
3	L	212/212 (100%)	-0.26	0 100 100	14, 28, 49, 87	0
4	B	7/8 (87%)	0.85	1 (14%) 2 1	84, 86, 94, 98	0
All	All	814/862 (94%)	0.25	62 (7%) 13 7	14, 61, 137, 176	0

All (62) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	35	CYS	7.1
1	A	158	TRP	7.1
1	A	72	GLN	4.9
1	A	153	GLN	4.6
1	A	156	ASN	4.3
1	A	1091	ALA	4.3
1	A	157	PRO	4.0
1	A	162	TYR	3.9
1	A	74	GLY	3.8
1	A	154	ARG	3.6
1	A	1028	ASP	3.6
1	A	71	CYS	3.6
1	A	256	LYS	3.6
1	A	1090	ALA	3.6
1	A	288	ASN	3.5
1	A	252	ASP	3.5
1	A	1086	GLU	3.5
1	A	36	SER	3.5
1	A	1017	ILE	3.3
1	A	1027	LYS	3.2
1	A	64	VAL	3.2

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Mol	Chain	Res	Type	RSRZ
1	A	80	SER	3.2
1	A	316	PHE	3.2
1	A	287	ILE	3.1
1	A	1021	ASP	3.1
1	A	68	LEU	3.1
1	A	1015	LYS	3.0
1	A	1012	ASP	3.0
1	A	1063	HIS	3.0
1	A	1045	PRO	3.0
1	A	1062	ARG	3.0
1	A	160	ALA	2.9
1	A	247	ASN	2.9
1	A	290	CYS	2.9
1	A	1083	LYS	2.8
2	H	138	THR	2.8
1	A	70	CYS	2.8
1	A	73	LYS	2.8
1	A	159	GLN	2.7
1	A	1020	ALA	2.6
1	A	1092	GLU	2.6
1	A	281	LEU	2.6
1	A	63	ILE	2.5
1	A	88	VAL	2.5
1	A	1080	ASN	2.5
1	A	1032	LYS	2.4
1	A	291	GLU	2.4
1	A	1087	ALA	2.4
1	A	1016	VAL	2.3
1	A	155	ARG	2.3
1	A	75	PRO	2.3
1	A	280	ALA	2.2
1	A	76	LYS	2.2
1	A	1098	ARG	2.2
1	A	1096	THR	2.2
2	H	71	SER	2.1
1	A	255	LEU	2.1
1	A	248	ARG	2.1
1	A	161	SER	2.1
1	A	320	PHE	2.0
1	A	67	THR	2.0
4	B	2	ARG	2.0



## 6.2 Non-standard residues in protein, DNA, RNA chains [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, 95<sup>th</sup> 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( $\text{\AA}^2$ )	Q<0.9
4	SAR	B	1	5/6	0.43	0.58	72,73,82,83	0

## 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.