



# Full wwPDB X-ray Structure Validation Report ⓘ

Feb 19, 2016 – 08:55 PM GMT

PDB ID : 4ZHE  
Title : Crystal structure of the SeMet substituted Topless related protein 2 (TPR2)  
N-terminal domain (1-209) from rice  
Authors : Ke, J.; Ma, H.; Gu, X.; Brunzelle, J.S.; Xu, H.E.; Melcher, K.  
Deposited on : 2015-04-24  
Resolution : 2.50 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  
<http://wwpdb.org/validation/2016/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 : unknown  
Xtriage (Phenix) : 1.9-1692  
EDS : rb-20026982  
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) : rb-20026982

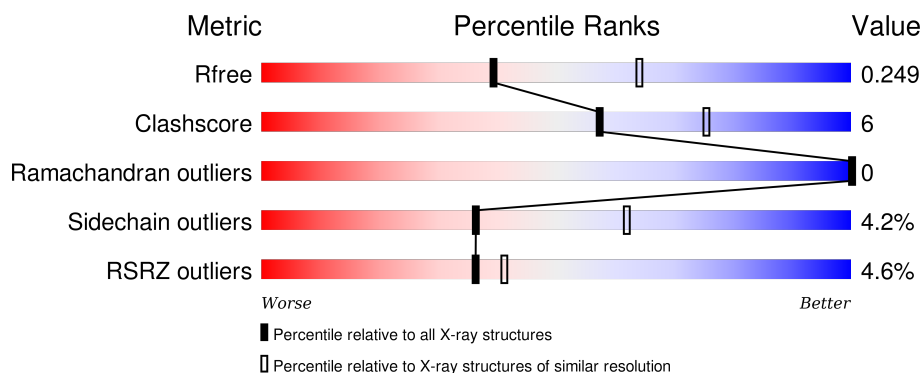
# 1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

## *X-RAY DIFFRACTION*

The reported resolution of this entry is 2.50 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	3553 (2.50-2.50)
Clashscore	102246	4242 (2.50-2.50)
Ramachandran outliers	100387	4156 (2.50-2.50)
Sidechain outliers	100360	4158 (2.50-2.50)
RSRZ outliers	91569	3562 (2.50-2.50)

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. 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	209	<div> <div>4%</div> <div>81% 16% ..</div> </div>
1	B	209	<div> <div>2%</div> <div>83% 12% ..</div> </div>
1	C	209	<div> <div>4%</div> <div>78% 14% • 5%</div> </div>
1	D	209	<div> <div>7%</div> <div>81% 16% ..</div> </div>

## 2 Entry composition

There are 2 unique types of molecules in this entry. The entry contains 7182 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 ASPR2 protein.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
1	A	205	Total	C	N	O	S	Se	0	0	0
			1716	1107	287	316	2	4			
1	B	203	Total	C	N	O	S	Se	0	0	0
			1708	1102	286	314	2	4			
1	C	199	Total	C	N	O	S	Se	0	0	0
			1675	1081	279	309	2	4			
1	D	206	Total	C	N	O	S	Se	0	0	0
			1705	1100	282	318	1	4			

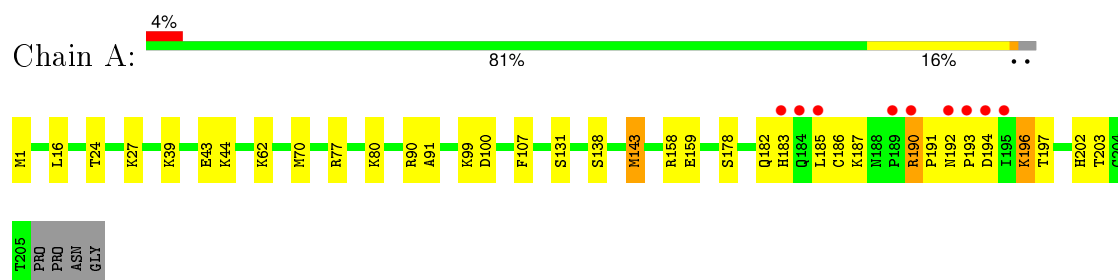
- Molecule 2 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
2	A	126	Total	O	0	0
			126	126		
2	B	134	Total	O	0	0
			134	134		
2	C	44	Total	O	0	0
			44	44		
2	D	74	Total	O	0	0
			74	74		

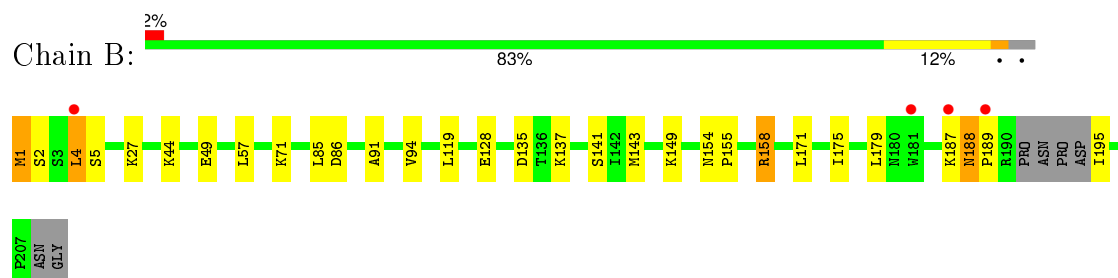
### 3 Residue-property plots [i](#)

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

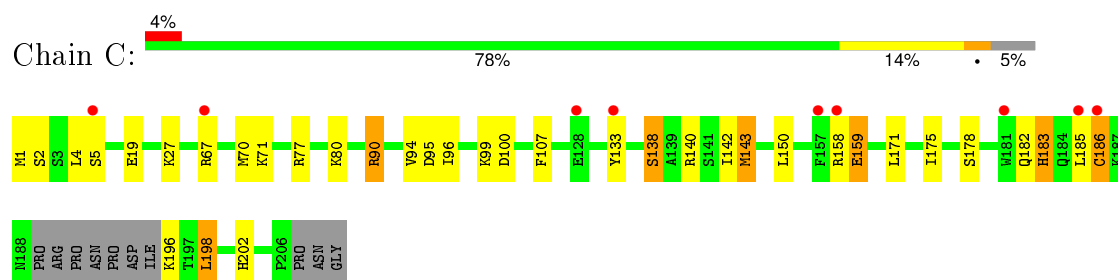
#### • Molecule 1: ASPR2 protein



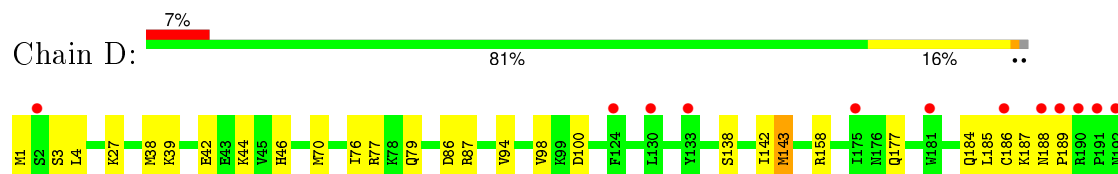
#### • Molecule 1: ASPR2 protein

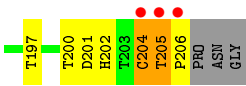


#### • Molecule 1: ASPR2 protein



#### • Molecule 1: ASPR2 protein





## 4 Data and refinement statistics

Property	Value	Source
Space group	P 21 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	70.15Å 111.88Å 144.95Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	44.28 – 2.50 44.36 – 2.50	Depositor EDS
% Data completeness (in resolution range)	100.0 (44.28-2.50) 100.0 (44.36-2.50)	Depositor EDS
$R_{merge}$	0.12	Depositor
$R_{sym}$	0.12	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.98 (at 2.51Å)	Xtriage
Refinement program	PHENIX (phenix.refine: 1.9_1692)	Depositor
R, $R_{free}$	0.199 , 0.242 0.212 , 0.249	Depositor DCC
$R_{free}$ test set	2038 reflections (5.34%)	DCC
Wilson B-factor (Å <sup>2</sup> )	48.8	Xtriage
Anisotropy	0.256	Xtriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.32 , 48.8	EDS
Estimated twinning fraction	No twinning to report.	Xtriage
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.48$ , $\langle L^2 \rangle = 0.32$	Xtriage
Outliers	0 of 40227 reflections	Xtriage
$F_o, F_c$ correlation	0.94	EDS
Total number of atoms	7182	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	59.0	wwPDB-VP

Xtriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 7.52% 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, 0.375 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	0.53	2/1748 (0.1%)	0.68	0/2343
1	B	0.69	4/1739 (0.2%)	0.71	0/2329
1	C	0.60	5/1704 (0.3%)	0.96	8/2279 (0.4%)
1	D	0.59	2/1737 (0.1%)	0.75	2/2333 (0.1%)
All	All	0.61	13/6928 (0.2%)	0.78	10/9284 (0.1%)

All (13) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	B	128	GLU	CG-CD	-13.19	1.32	1.51
1	B	128	GLU	CB-CG	-11.22	1.30	1.52
1	B	128	GLU	CD-OE1	-9.86	1.14	1.25
1	C	159	GLU	CG-CD	-9.15	1.38	1.51
1	C	67	ARG	CZ-NH2	-6.91	1.24	1.33
1	B	149	LYS	CE-NZ	-6.30	1.33	1.49
1	D	185	LEU	CA-CB	6.28	1.68	1.53
1	C	67	ARG	CZ-NH1	-5.96	1.25	1.33
1	C	67	ARG	CD-NE	-5.77	1.36	1.46
1	A	196	LYS	CD-CE	-5.57	1.37	1.51
1	D	186	CYS	CA-CB	5.56	1.66	1.53
1	C	67	ARG	CG-CD	-5.15	1.39	1.51
1	A	196	LYS	CB-CG	-5.10	1.38	1.52

All (10) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	90	ARG	NE-CZ-NH2	22.36	131.48	120.30
1	C	90	ARG	NE-CZ-NH1	-21.36	109.62	120.30
1	D	186	CYS	N-CA-CB	7.13	123.44	110.60
1	C	90	ARG	CD-NE-CZ	-7.09	113.67	123.60
1	C	185	LEU	N-CA-C	-6.00	94.79	111.00
1	D	201	ASP	CB-CG-OD2	-6.00	112.90	118.30
1	C	90	ARG	CG-CD-NE	-5.40	100.47	111.80

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Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	67	ARG	CG-CD-NE	-5.34	100.58	111.80
1	C	159	GLU	OE1-CD-OE2	5.34	129.71	123.30
1	C	186	CYS	CA-CB-SG	5.07	123.13	114.00

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	1716	0	1718	25	1
1	B	1708	0	1720	23	1
1	C	1675	0	1689	23	0
1	D	1705	0	1691	24	0
2	A	126	0	0	2	0
2	B	134	0	0	4	0
2	C	44	0	0	1	0
2	D	74	0	0	2	0
All	All	7182	0	6818	82	1

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 (82) 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:C:90:ARG:HH12	1:D:98:VAL:HG21	1.27	0.98
1:A:27:LYS:HG3	1:D:27:LYS:HG3	1.75	0.69
1:A:186:CYS:SG	1:A:187:LYS:N	2.66	0.69
1:C:90:ARG:NH1	1:D:98:VAL:HG21	2.06	0.66
1:A:190:ARG:HB2	1:A:190:ARG:HH11	1.60	0.66
1:B:44:LYS:NZ	2:B:301:HOH:O	2.28	0.66
1:B:27:LYS:HG3	1:C:27:LYS:HG3	1.79	0.65
1:B:195:ILE:HD11	1:C:4:LEU:HD11	1.80	0.63
1:D:76:ILE:HA	1:D:143:MSE:CE	2.33	0.59

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:C:140:ARG:HA	1:C:143:MSE:HE2	1.88	0.56
1:A:190:ARG:CB	1:A:190:ARG:HH11	2.18	0.55
1:D:138:SER:O	1:D:142:ILE:HG12	2.07	0.55
1:C:70:MSE:HE1	1:C:107:PHE:CZ	2.40	0.55
1:C:95:ASP:OD1	1:C:99:LYS:HE3	2.08	0.53
1:C:196:LYS:HG2	1:C:202:HIS:CE1	2.43	0.53
1:D:205:THR:O	1:D:205:THR:OG1	2.26	0.52
1:C:133:TYR:HB3	2:C:317:HOH:O	2.10	0.51
1:C:94:VAL:HG21	1:D:94:VAL:HG21	1.92	0.50
1:A:90:ARG:HD3	1:B:94:VAL:HG11	1.93	0.50
1:A:77:ARG:HD3	1:A:100:ASP:HB3	1.93	0.50
1:A:196:LYS:HG2	1:A:197:THR:N	2.26	0.49
1:D:204:CYS:O	1:D:206:PRO:HD3	2.12	0.49
1:B:135:ASP:OD2	1:B:137:LYS:NZ	2.46	0.49
1:D:188:ASN:N	1:D:189:PRO:HD3	2.27	0.49
1:A:39:LYS:O	1:A:43:GLU:HG3	2.13	0.49
1:C:138:SER:O	1:C:142:ILE:HG12	2.13	0.48
1:B:4:LEU:HD11	1:C:198:LEU:HD13	1.94	0.48
1:D:1:MSE:C	1:D:3:SER:H	2.14	0.48
1:C:80:LYS:HE3	1:C:96:ILE:HG12	1.95	0.48
1:B:155:PRO:HA	1:B:158:ARG:HD2	1.95	0.48
1:C:77:ARG:HD3	1:C:100:ASP:HB3	1.96	0.48
1:C:178:SER:O	1:C:182:GLN:HG3	2.14	0.47
1:C:71:LYS:HG2	1:C:150:LEU:HD21	1.96	0.47
1:A:191:PRO:HA	1:A:192:ASN:C	2.34	0.47
1:D:1:MSE:SE	1:D:3:SER:HB3	2.65	0.47
1:A:91:ALA:HB2	1:B:91:ALA:HB2	1.97	0.47
1:A:90:ARG:HD3	1:B:94:VAL:CG1	2.45	0.46
1:D:87:ARG:HD2	2:D:307:HOH:O	2.16	0.46
1:A:143:MSE:HB3	1:A:143:MSE:HE2	1.65	0.46
1:A:44:LYS:HA	1:A:44:LYS:HD3	1.66	0.46
1:D:187:LYS:C	1:D:189:PRO:HD3	2.36	0.46
1:D:1:MSE:HG3	1:D:3:SER:HB3	1.97	0.46
1:B:2:SER:HB3	1:B:5:SER:OG	2.17	0.45
1:B:154:ASN:O	1:B:158:ARG:HG3	2.16	0.45
1:C:158:ARG:HG2	1:C:159:GLU:HG2	1.97	0.45
1:A:99:LYS:HD3	1:A:99:LYS:HA	1.68	0.45
1:D:197:THR:HG23	1:D:200:THR:H	1.80	0.45
1:C:196:LYS:HG2	1:C:202:HIS:ND1	2.32	0.45
1:B:188:ASN:N	1:B:189:PRO:HD3	2.31	0.44
1:A:80:LYS:NZ	2:A:307:HOH:O	2.51	0.44

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:D:79:GLN:HB3	1:D:143:MSE:HE3	1.99	0.44
1:B:85:LEU:HD21	1:B:119:LEU:HD23	2.00	0.44
1:B:49:GLU:HG3	2:B:301:HOH:O	2.17	0.44
1:A:16:LEU:HD13	1:A:24:THR:HG22	1.99	0.44
1:D:46:HIS:HD2	2:D:339:HOH:O	2.01	0.44
1:A:178:SER:O	1:A:182:GLN:HG3	2.17	0.44
1:D:76:ILE:HA	1:D:143:MSE:HE2	1.99	0.43
1:A:178:SER:HB2	1:D:177:GLN:HB2	2.00	0.43
1:D:77:ARG:HD3	1:D:100:ASP:HB3	1.99	0.43
1:A:62:LYS:HA	1:A:62:LYS:HD3	1.76	0.43
1:B:171:LEU:O	1:B:175:ILE:HG12	2.19	0.43
1:A:70:MSE:HE1	1:A:107:PHE:CZ	2.54	0.43
1:A:183:HIS:O	1:A:186:CYS:HB3	2.19	0.42
1:B:4:LEU:HA	1:B:4:LEU:HD13	1.85	0.42
1:A:158:ARG:O	1:A:159:GLU:HB2	2.19	0.42
1:D:38:MSE:HE3	1:D:42:GLU:HG3	2.01	0.42
1:D:79:GLN:CB	1:D:143:MSE:HE3	2.49	0.42
1:C:183:HIS:O	1:C:186:CYS:HB2	2.20	0.42
1:A:80:LYS:NZ	2:A:305:HOH:O	2.52	0.42
1:A:192:ASN:N	1:A:193:PRO:HA	2.35	0.42
1:B:188:ASN:ND2	2:B:309:HOH:O	2.52	0.41
1:B:1:MSE:HB3	1:B:2:SER:H	1.34	0.41
1:B:1:MSE:HE2	1:C:19:GLU:OE1	2.20	0.41
1:D:44:LYS:HA	1:D:44:LYS:HD3	1.67	0.41
1:B:143:MSE:HE2	1:B:143:MSE:HB3	1.81	0.41
1:B:158:ARG:NH1	2:B:311:HOH:O	2.54	0.41
1:A:70:MSE:HE1	1:A:107:PHE:CE1	2.56	0.41
1:C:90:ARG:O	1:C:94:VAL:HG23	2.21	0.41
1:B:4:LEU:HD12	1:C:198:LEU:HD22	2.04	0.40
1:C:171:LEU:O	1:C:175:ILE:HG12	2.20	0.40
1:D:4:LEU:HD23	1:D:4:LEU:HA	1.74	0.40
1:B:179:LEU:HA	1:B:179:LEU:HD23	1.92	0.40

All (1) 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)
1:A:131:SER:O	1:B:141:SER:OG[4_566]	2.18	0.02

## 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	203/209 (97%)	198 (98%)	5 (2%)	0	100	100
1	B	199/209 (95%)	198 (100%)	1 (0%)	0	100	100
1	C	195/209 (93%)	194 (100%)	1 (0%)	0	100	100
1	D	204/209 (98%)	196 (96%)	8 (4%)	0	100	100
All	All	801/836 (96%)	786 (98%)	15 (2%)	0	100	100

There are no Ramachandran outliers to report.

### 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	190/193 (98%)	182 (96%)	8 (4%)	36	62
1	B	191/193 (99%)	183 (96%)	8 (4%)	36	62
1	C	187/193 (97%)	180 (96%)	7 (4%)	41	68
1	D	187/193 (97%)	178 (95%)	9 (5%)	31	55
All	All	755/772 (98%)	723 (96%)	32 (4%)	36	62

All (32) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	1	MSE
1	A	138	SER

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Mol	Chain	Res	Type
1	A	143	MSE
1	A	185	LEU
1	A	190	ARG
1	A	194	ASP
1	A	202	HIS
1	A	203	THR
1	B	1	MSE
1	B	4	LEU
1	B	57	LEU
1	B	71	LYS
1	B	86	ASP
1	B	158	ARG
1	B	187	LYS
1	B	188	ASN
1	C	1	MSE
1	C	2	SER
1	C	5	SER
1	C	138	SER
1	C	143	MSE
1	C	183	HIS
1	C	198	LEU
1	D	39	LYS
1	D	70	MSE
1	D	86	ASP
1	D	143	MSE
1	D	158	ARG
1	D	184	GLN
1	D	202	HIS
1	D	204	CYS
1	D	205	THR

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

Mol	Chain	Res	Type
1	C	202	HIS
1	D	117	GLN
1	D	202	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, 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	201/209 (96%)	0.17	9 (4%)	37 42	26, 42, 143, 166	0
1	B	199/209 (95%)	0.07	4 (2%)	68 72	25, 45, 90, 127	0
1	C	195/209 (93%)	0.38	9 (4%)	36 41	43, 67, 107, 142	0
1	D	202/209 (96%)	0.42	15 (7%)	17 19	34, 57, 135, 182	0
All	All	797/836 (95%)	0.26	37 (4%)	36 41	25, 55, 119, 182	0

All (37) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	D	190	ARG	7.0
1	A	183	HIS	5.4
1	D	191	PRO	4.6
1	D	206	PRO	4.6
1	D	188	ASN	4.0
1	A	184	GLN	4.0
1	D	189	PRO	3.8
1	A	185	LEU	3.6
1	D	192	ASN	3.6
1	D	2	SER	3.5
1	D	181	TRP	3.4
1	B	189	PRO	3.4
1	D	186	CYS	3.3
1	C	133	TYR	3.2
1	C	67	ARG	3.0
1	D	133	TYR	3.0
1	A	193	PRO	2.8
1	D	175	ILE	2.8
1	A	190	ARG	2.8
1	C	186	CYS	2.7
1	D	204	CYS	2.7

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Mol	Chain	Res	Type	RSRZ
1	D	124	PHE	2.7
1	C	185	LEU	2.6
1	A	189	PRO	2.6
1	B	187	LYS	2.6
1	A	192	ASN	2.5
1	B	4	LEU	2.4
1	D	205	THR	2.3
1	A	195	ILE	2.3
1	B	181	TRP	2.2
1	A	194	ASP	2.2
1	C	128	GLU	2.2
1	D	130	LEU	2.2
1	C	158	ARG	2.2
1	C	181	TRP	2.1
1	C	157	PHE	2.0
1	C	5	SER	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 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.