



# Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 06:00 am BST

PDB ID : 6I5J  
Title : Crystal structure of SOCS2:Elongin C:Elongin B in complex with growth hormone receptor peptide  
Authors : Kung, W.W.; Ramachandran, S.; Makukhin, N.; Bruno, E.; Ciulli, A.  
Deposited on : 2018-11-13  
Resolution : 2.80 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

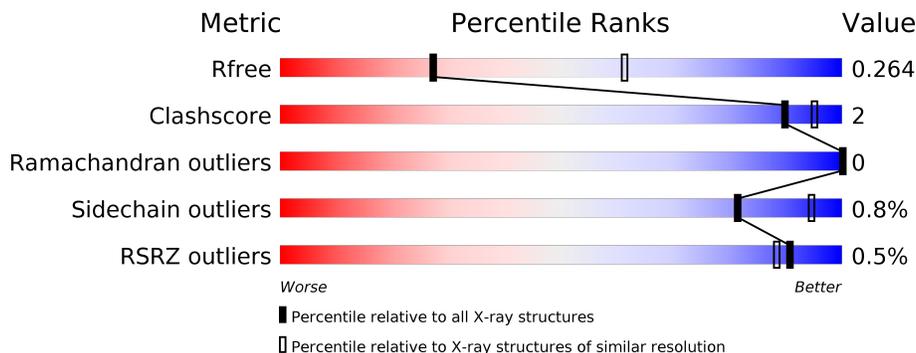
# 1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

*X-RAY DIFFRACTION*

The reported resolution of this entry is 2.80 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	3140 (2.80-2.80)
Clashscore	141614	3569 (2.80-2.80)
Ramachandran outliers	138981	3498 (2.80-2.80)
Sidechain outliers	138945	3500 (2.80-2.80)
RSRZ outliers	127900	3078 (2.80-2.80)

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	169	96% (0% red, 0% orange, 0% yellow, 96% green, 4% grey)
2	B	104	88% (0% red, 0% orange, 12% yellow, 88% green, 0% grey)
2	E	104	92% (0% red, 0% orange, 7% yellow, 92% green, 1% grey)
3	C	97	95% (0% red, 0% orange, 5% yellow, 95% green, 0% grey)
3	F	97	94% (0% red, 0% orange, 5% yellow, 94% green, 1% grey)
4	D	169	95% (2% red, 0% orange, 0% yellow, 95% green, 3% grey)

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Mol	Chain	Length	Quality of chain
5	I	11	 82% 18%
5	J	11	 91% 9%
5	K	11	 91% 9%
5	L	11	 82% 18%

## 2 Entry composition [i](#)

There are 7 unique types of molecules in this entry. The entry contains 6135 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 Suppressor of cytokine signaling 2.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	As	C	N	O				S
1	A	168	1324	2	848	227	240	7	0	1	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	31	MET	PRO	engineered mutation	UNP O14508

- Molecule 2 is a protein called Elongin-B.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace	
			Total	As	C	N	O				S
2	B	104	812	1	517	136	153	5	0	0	0
2	E	103	801	1	509	135	151	5	0	0	0

- Molecule 3 is a protein called Elongin-C.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	97	765	490	123	146	6	0	0	0
3	F	97	760	489	122	142	7	0	0	0

There are 2 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	16	MET	-	initiating methionine	UNP Q15369
F	16	MET	-	initiating methionine	UNP Q15369

- Molecule 4 is a protein called Suppressor of cytokine signaling 2.

Mol	Chain	Residues	Atoms						ZeroOcc	AltConf	Trace
			Total	As	C	N	O	S			
4	D	169	1313	1	839	222	245	6	0	0	0

There is a discrepancy between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
D	31	MET	PRO	engineered mutation	UNP O14508

- Molecule 5 is a protein called Growth hormone receptor peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	P			
5	I	11	92	58	14	19	1	0	0	0
5	J	10	75	47	10	17	1	0	0	0
5	K	10	83	51	13	18	1	0	0	0
5	L	9	75	47	12	15	1	0	0	0

- Molecule 6 is COBALT (II) ION (three-letter code: CO) (formula: Co).

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
6	A	1	Total	Co	0	0
			1	1		
6	D	1	Total	Co	0	0
			1	1		

- Molecule 7 is water.

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
7	A	7	Total	O	0	0
			7	7		
7	B	6	Total	O	0	0
			6	6		
7	C	5	Total	O	0	0
			5	5		
7	D	6	Total	O	0	0
			6	6		
7	E	4	Total	O	0	0
			4	4		
7	F	2	Total	O	0	0
			2	2		

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<b>Mol</b>	<b>Chain</b>	<b>Residues</b>	<b>Atoms</b>		<b>ZeroOcc</b>	<b>AltConf</b>
7	K	3	Total	O	0	0
			3	3		

### 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: Suppressor of cytokine signaling 2

Chain A:  96%



- Molecule 2: Elongin-B

Chain B:  88%



- Molecule 2: Elongin-B

Chain E:  92%



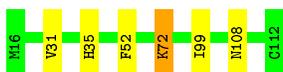
- Molecule 3: Elongin-C

Chain C:  95%

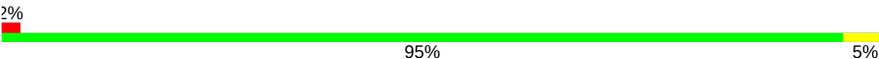


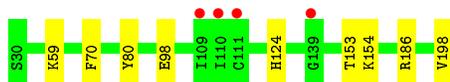
- Molecule 3: Elongin-C

Chain F:  94%

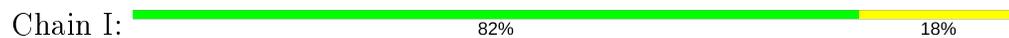


- Molecule 4: Suppressor of cytokine signaling 2

Chain D:  95%



- Molecule 5: Growth hormone receptor peptide



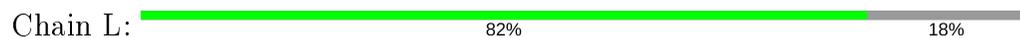
- Molecule 5: Growth hormone receptor peptide



- Molecule 5: Growth hormone receptor peptide



- Molecule 5: Growth hormone receptor peptide



## 4 Data and refinement statistics

Property	Value	Source
Space group	P 2 21 21	Depositor
Cell constants a, b, c, $\alpha$ , $\beta$ , $\gamma$	57.84Å 113.71Å 156.94Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	64.58 – 2.80 64.58 – 2.80	Depositor EDS
% Data completeness (in resolution range)	100.0 (64.58-2.80) 99.9 (64.58-2.80)	Depositor EDS
$R_{merge}$	(Not available)	Depositor
$R_{sym}$	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ <sup>1</sup>	2.55 (at 2.81Å)	Xtrriage
Refinement program	PHENIX (1.13_2998: ???)	Depositor
R, $R_{free}$	0.210 , 0.264 0.210 , 0.264	Depositor DCC
$R_{free}$ test set	1305 reflections (4.97%)	wwPDB-VP
Wilson B-factor (Å <sup>2</sup> )	42.5	Xtrriage
Anisotropy	0.531	Xtrriage
Bulk solvent $k_{sol}$ (e/Å <sup>3</sup> ), $B_{sol}$ (Å <sup>2</sup> )	0.34 , 32.3	EDS
L-test for twinning <sup>2</sup>	$\langle  L  \rangle = 0.49$ , $\langle L^2 \rangle = 0.33$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
$F_o, F_c$ correlation	0.92	EDS
Total number of atoms	6135	wwPDB-VP
Average B, all atoms (Å <sup>2</sup> )	42.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.80% 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

### 5.1 Standard geometry

Bond lengths and bond angles in the following residue types are not validated in this section: CAS, CO, VLM, PTR

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	0.23	0/1333	0.40	0/1803
2	B	0.25	0/818	0.45	0/1105
2	E	0.24	0/807	0.43	0/1090
3	C	0.24	0/782	0.38	0/1057
3	F	0.24	0/777	0.38	0/1050
4	D	0.23	0/1333	0.40	0/1809
5	I	0.22	0/69	0.43	0/93
5	J	0.21	0/59	0.42	0/79
5	K	0.20	0/59	0.43	0/79
5	L	0.19	0/51	0.34	0/67
All	All	0.24	0/6088	0.40	0/8232

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
5	I	0	1

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

All (1) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
5	I	5	ILE	Peptide

## 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	1324	0	1302	3	0
2	B	812	0	802	7	0
2	E	801	0	790	4	0
3	C	765	0	751	3	0
3	F	760	0	747	4	0
4	D	1313	0	1265	5	0
5	I	92	0	86	1	0
5	J	75	0	60	0	0
5	K	83	0	72	0	0
5	L	75	0	68	0	0
6	A	1	0	0	0	0
6	D	1	0	0	0	0
7	A	7	0	0	0	0
7	B	6	0	0	0	0
7	C	5	0	0	0	0
7	D	6	0	0	0	0
7	E	4	0	0	0	0
7	F	2	0	0	0	0
7	K	3	0	0	0	0
All	All	6135	0	5943	22	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 2.

All (22) 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)
2:B:25:PHE:HB2	2:B:53:ASP:HB3	1.70	0.73
1:A:109:ILE:HG23	1:A:110:ILE:HG22	1.81	0.62
2:B:41:GLU:HG2	2:B:80:ARG:HD2	1.84	0.59
4:D:186:ARG:NH2	3:F:108:ASN:OD1	2.38	0.56
2:E:23:THR:HA	2:E:56:THR:HA	1.89	0.55
2:E:52:ASP:HB3	2:E:55:LYS:HG3	1.90	0.53
2:B:24:VAL:HG13	2:B:44:LEU:HD12	1.91	0.52
3:C:98:GLU:N	3:C:98:GLU:OE2	2.37	0.49

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:116:LEU:HD11	5:I:3:ILE:HD11	1.95	0.48
4:D:153:THR:OG1	4:D:154:LYS:N	2.46	0.47
2:B:36:LYS:NZ	3:F:52:PHE:O	2.47	0.46
2:E:4:PHE:CE1	2:E:69:PRO:HG3	2.51	0.46
4:D:80:TYR:HE2	4:D:98:GLU:HG2	1.82	0.45
3:C:39:SER:HA	3:C:112:CYS:HB3	1.98	0.44
2:E:15:PHE:HB2	3:F:31:VAL:HG12	1.99	0.44
1:A:46:THR:HB	1:A:48:TRP:CE2	2.54	0.43
4:D:59:LYS:HE2	4:D:59:LYS:HB3	1.84	0.41
2:B:23:THR:HA	2:B:56:THR:HA	2.03	0.41
4:D:70:PHE:HZ	4:D:198:VAL:HG21	1.84	0.41
3:F:72:LYS:HD2	3:F:99:ILE:HD11	2.02	0.41
2:B:4:PHE:CE1	2:B:69:PRO:HG3	2.54	0.41
2:B:69:PRO:HB3	3:C:78:THR:HG22	2.04	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	163/169 (96%)	160 (98%)	3 (2%)	0	100	100
2	B	101/104 (97%)	97 (96%)	4 (4%)	0	100	100
2	E	100/104 (96%)	96 (96%)	4 (4%)	0	100	100
3	C	95/97 (98%)	91 (96%)	4 (4%)	0	100	100
3	F	95/97 (98%)	94 (99%)	1 (1%)	0	100	100
4	D	166/169 (98%)	161 (97%)	5 (3%)	0	100	100
5	I	8/11 (73%)	8 (100%)	0	0	100	100
5	J	7/11 (64%)	6 (86%)	1 (14%)	0	100	100
5	K	7/11 (64%)	7 (100%)	0	0	100	100

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Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
5	L	6/11 (54%)	5 (83%)	1 (17%)	0	100	100
All	All	748/784 (95%)	725 (97%)	23 (3%)	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	137/147 (93%)	137 (100%)	0	100	100
2	B	86/91 (94%)	85 (99%)	1 (1%)	71	92
2	E	85/91 (93%)	85 (100%)	0	100	100
3	C	85/86 (99%)	84 (99%)	1 (1%)	71	92
3	F	83/86 (96%)	81 (98%)	2 (2%)	49	81
4	D	134/148 (90%)	133 (99%)	1 (1%)	84	95
5	I	9/9 (100%)	9 (100%)	0	100	100
5	J	6/9 (67%)	6 (100%)	0	100	100
5	K	7/9 (78%)	7 (100%)	0	100	100
5	L	6/9 (67%)	6 (100%)	0	100	100
All	All	638/685 (93%)	633 (99%)	5 (1%)	81	94

All (5) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	B	1	MET
3	C	34	GLU
4	D	124	HIS
3	F	35	HIS
3	F	72	LYS

Some sidechains can be flipped to improve hydrogen bonding and reduce clashes. There are no such sidechains identified.

### 5.3.3 RNA [i](#)

There are no RNA molecules in this entry.

## 5.4 Non-standard residues in protein, DNA, RNA chains [i](#)

12 non-standard protein/DNA/RNA residues are 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
5	VLM	K	6	5	6,7,7	0.18	0	7,9,9	0.14	0
2	CAS	E	89	2	5,8,9	1.18	0	1,9,11	1.47	0
5	VLM	L	6	5	6,7,7	0.18	0	7,9,9	0.13	0
1	CAS	A	133	1	5,8,9	1.12	0	1,9,11	1.61	0
5	PTR	L	0	5	15,16,17	1.36	1 (6%)	19,22,24	0.56	0
4	CAS	D	133	4	5,8,9	1.11	0	1,9,11	1.01	0
5	PTR	K	0	5	15,16,17	1.36	1 (6%)	19,22,24	0.59	0
5	PTR	I	0	5	15,16,17	1.36	1 (6%)	19,22,24	0.49	0
5	PTR	J	0	5	15,16,17	1.36	1 (6%)	19,22,24	0.50	0
2	CAS	B	89	2	5,8,9	1.15	0	1,9,11	1.55	0
1	CAS	A	111	1	5,8,9	1.16	0	1,9,11	1.14	0
5	VLM	I	6	5	6,7,7	0.20	0	7,9,9	0.11	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
5	VLM	K	6	5	-	0/7/8/8	-
2	CAS	E	89	2	-	0/0/7/9	-
5	VLM	L	6	5	-	0/7/8/8	-
1	CAS	A	133	1	-	0/0/7/9	-
5	PTR	L	0	5	-	0/10/11/13	0/1/1/1
4	CAS	D	133	4	-	0/0/7/9	-
5	PTR	K	0	5	-	2/10/11/13	0/1/1/1

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Mol	Type	Chain	Res	Link	Chirals	Torsions	Rings
5	PTR	I	0	5	-	2/10/11/13	0/1/1/1
5	PTR	J	0	5	-	2/10/11/13	0/1/1/1
2	CAS	B	89	2	-	0/0/7/9	-
1	CAS	A	111	1	-	0/0/7/9	-
5	VLM	I	6	5	-	0/7/8/8	-

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
5	I	0	PTR	OH-CZ	-4.54	1.30	1.40
5	K	0	PTR	OH-CZ	-4.51	1.30	1.40
5	J	0	PTR	OH-CZ	-4.48	1.30	1.40
5	L	0	PTR	OH-CZ	-4.47	1.30	1.40

There are no bond angle outliers.

There are no chirality outliers.

All (6) torsion outliers are listed below:

Mol	Chain	Res	Type	Atoms
5	K	0	PTR	CZ-OH-P-O1P
5	I	0	PTR	C-CA-CB-CG
5	I	0	PTR	N-CA-CB-CG
5	K	0	PTR	CZ-OH-P-O2P
5	J	0	PTR	N-CA-CB-CG
5	J	0	PTR	C-CA-CB-CG

There are no ring outliers.

No monomer is involved in short contacts.

## 5.5 Carbohydrates [i](#)

There are no carbohydrates in this entry.

## 5.6 Ligand geometry [i](#)

Of 2 ligands modelled in this entry, 2 are monoatomic - leaving 0 for Mogul analysis.

There are no bond length outliers.

There are no bond angle outliers.

There are no chirality outliers.

There are no torsion outliers.

There are no ring outliers.

No monomer is involved in short contacts.

## 5.7 Other polymers

There are no such residues in this entry.

## 5.8 Polymer linkage issues

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, 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	166/169 (98%)	-0.20	0 100 100	23, 37, 79, 105	0
2	B	103/104 (99%)	-0.08	0 100 100	25, 38, 71, 83	0
2	E	102/104 (98%)	-0.17	0 100 100	25, 37, 64, 89	0
3	C	97/97 (100%)	-0.18	0 100 100	21, 32, 71, 100	0
3	F	97/97 (100%)	-0.20	0 100 100	24, 36, 58, 62	0
4	D	168/169 (99%)	0.19	4 (2%) 59 49	26, 45, 91, 108	0
5	I	9/11 (81%)	0.11	0 100 100	33, 36, 49, 85	0
5	J	9/11 (81%)	0.65	0 100 100	49, 67, 93, 98	0
5	K	8/11 (72%)	-0.19	0 100 100	33, 48, 56, 71	0
5	L	7/11 (63%)	0.91	0 100 100	63, 77, 86, 105	0
All	All	766/784 (97%)	-0.07	4 (0%) 91 88	21, 38, 79, 108	0

All (4) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
4	D	139	GLY	3.4
4	D	111	CYS	2.1
4	D	109	ILE	2.1
4	D	110	ILE	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
5	PTR	L	0	16/17	0.90	0.20	76,80,84,87	0
2	CAS	E	89	9/10	0.92	0.18	28,34,89,90	0
2	CAS	B	89	9/10	0.92	0.18	44,46,124,125	0
5	PTR	J	0	16/17	0.94	0.19	39,47,55,61	0
5	VLM	L	6	8/8	0.94	0.29	54,58,62,68	0
5	VLM	I	6	8/8	0.94	0.23	43,50,54,57	0
1	CAS	A	111	9/10	0.95	0.14	38,43,106,107	0
4	CAS	D	133	9/10	0.95	0.18	50,58,86,87	0
5	VLM	K	6	8/8	0.96	0.25	35,39,43,44	0
5	PTR	K	0	16/17	0.97	0.14	34,44,52,53	0
5	PTR	I	0	16/17	0.97	0.16	33,42,46,50	0
1	CAS	A	133	9/10	0.97	0.16	41,57,67,67	0

### 6.3 Carbohydrates [i](#)

There are no carbohydrates in this entry.

### 6.4 Ligands [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
6	CO	D	201	1/1	0.81	0.09	89,89,89,89	0
6	CO	A	201	1/1	0.97	0.15	52,52,52,52	0

### 6.5 Other polymers [i](#)

There are no such residues in this entry.