



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 9, 2026 – 09:19 AM UTC

PDB ID : 6P5T / pdb_00006p5t
Title : Surface-layer (S-layer) RsaA protein from *Caulobacter crescentus* bound to strontium and iodide
Authors : Chan, A.C.; Herrmann, J.; Smit, J.; Wakatsuki, S.; Murphy, M.E.
Deposited on : 2019-05-30
Resolution : 2.10 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

<https://www.wwpdb.org/validation/2017/XrayValidationReportHelp>

with specific help available everywhere you see the ⓘ symbol.

The types of validation reports are described at

<http://www.wwpdb.org/validation/2017/FAQs#types>.

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

MolProbity	:	4-5-2 with Phenix2.0
Xtriage (Phenix)	:	2.0
EDS	:	3.0
Percentile statistics	:	20250101.v01 (using entries in the PDB archive January 1st 2025)
CCP4	:	9.0.010 (Gargrove)
Density-Fitness	:	1.0.12
Ideal geometry (proteins)	:	Engh & Huber (2001)
Ideal geometry (DNA, RNA)	:	Parkinson et al. (1996)
Validation Pipeline (wwPDB-VP)	:	2.49

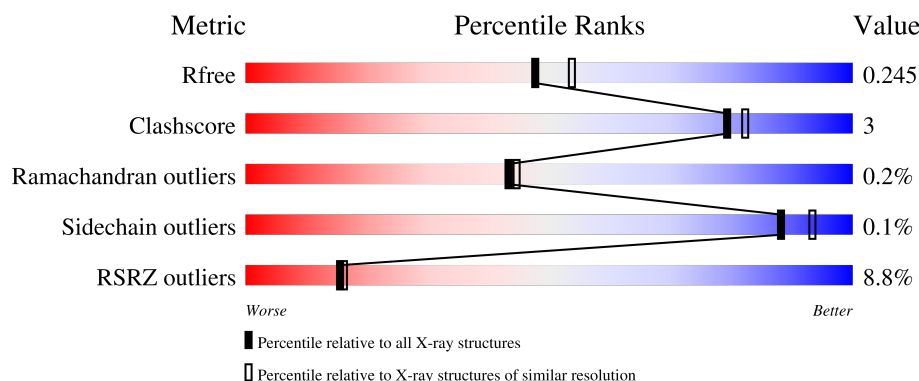
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.10 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}	180053	6658 (2.10-2.10)
Clashscore	190562	7164 (2.10-2.10)
Ramachandran outliers	187476	7099 (2.10-2.10)
Sidechain outliers	187428	7100 (2.10-2.10)
RSRZ outliers	180081	6662 (2.10-2.10)

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	814	93%
1	B	814	90%
1	C	814	90%
1	D	814	90%
1	E	814	90%

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
1	F	814	

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 criteria:

Mol	Type	Chain	Res	Chirality	Geometry	Clashes	Electron density
2	IOD	A	1128	-	-	X	-
2	IOD	B	1117	-	-	X	-
2	IOD	C	1110	-	-	X	-
2	IOD	D	1119	-	-	X	-
2	IOD	E	1122	-	-	X	-
2	IOD	F	1127	-	-	X	-
2	IOD	F	1130	-	-	X	-

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 36028 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 S-layer protein.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	782	Total	C	N	O	S	0	1	0
			5162	3140	867	1153	2			
1	B	776	Total	C	N	O	S	0	2	0
			5135	3125	862	1146	2			
1	C	781	Total	C	N	O	S	0	1	0
			5156	3137	866	1151	2			
1	D	780	Total	C	N	O	S	0	1	0
			5152	3135	865	1150	2			
1	E	781	Total	C	N	O	S	0	0	0
			5150	3134	865	1149	2			
1	F	782	Total	C	N	O	S	0	1	0
			5162	3140	867	1153	2			

There are 60 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	213	MET	-	initiating methionine	UNP P35828
A	214	THR	-	expression tag	UNP P35828
A	215	MET	-	expression tag	UNP P35828
A	216	ILE	-	expression tag	UNP P35828
A	217	THR	-	expression tag	UNP P35828
A	218	ASN	-	expression tag	UNP P35828
A	219	SER	-	expression tag	UNP P35828
A	220	ARG	-	expression tag	UNP P35828
A	221	GLY	-	expression tag	UNP P35828
A	222	SER	-	expression tag	UNP P35828
B	213	MET	-	initiating methionine	UNP P35828
B	214	THR	-	expression tag	UNP P35828
B	215	MET	-	expression tag	UNP P35828
B	216	ILE	-	expression tag	UNP P35828
B	217	THR	-	expression tag	UNP P35828
B	218	ASN	-	expression tag	UNP P35828
B	219	SER	-	expression tag	UNP P35828

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
B	220	ARG	-	expression tag	UNP P35828
B	221	GLY	-	expression tag	UNP P35828
B	222	SER	-	expression tag	UNP P35828
C	213	MET	-	initiating methionine	UNP P35828
C	214	THR	-	expression tag	UNP P35828
C	215	MET	-	expression tag	UNP P35828
C	216	ILE	-	expression tag	UNP P35828
C	217	THR	-	expression tag	UNP P35828
C	218	ASN	-	expression tag	UNP P35828
C	219	SER	-	expression tag	UNP P35828
C	220	ARG	-	expression tag	UNP P35828
C	221	GLY	-	expression tag	UNP P35828
C	222	SER	-	expression tag	UNP P35828
D	213	MET	-	initiating methionine	UNP P35828
D	214	THR	-	expression tag	UNP P35828
D	215	MET	-	expression tag	UNP P35828
D	216	ILE	-	expression tag	UNP P35828
D	217	THR	-	expression tag	UNP P35828
D	218	ASN	-	expression tag	UNP P35828
D	219	SER	-	expression tag	UNP P35828
D	220	ARG	-	expression tag	UNP P35828
D	221	GLY	-	expression tag	UNP P35828
D	222	SER	-	expression tag	UNP P35828
E	213	MET	-	initiating methionine	UNP P35828
E	214	THR	-	expression tag	UNP P35828
E	215	MET	-	expression tag	UNP P35828
E	216	ILE	-	expression tag	UNP P35828
E	217	THR	-	expression tag	UNP P35828
E	218	ASN	-	expression tag	UNP P35828
E	219	SER	-	expression tag	UNP P35828
E	220	ARG	-	expression tag	UNP P35828
E	221	GLY	-	expression tag	UNP P35828
E	222	SER	-	expression tag	UNP P35828
F	213	MET	-	initiating methionine	UNP P35828
F	214	THR	-	expression tag	UNP P35828
F	215	MET	-	expression tag	UNP P35828
F	216	ILE	-	expression tag	UNP P35828
F	217	THR	-	expression tag	UNP P35828
F	218	ASN	-	expression tag	UNP P35828
F	219	SER	-	expression tag	UNP P35828
F	220	ARG	-	expression tag	UNP P35828
F	221	GLY	-	expression tag	UNP P35828

Continued on next page...

Continued from previous page...

Chain	Residue	Modelled	Actual	Comment	Reference
F	222	SER	-	expression tag	UNP P35828

- Molecule 2 is IODIDE ION (CCD ID: IOD) (formula: I).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	29	Total I 29 29	0	0
2	B	24	Total I 24 24	0	0
2	C	20	Total I 20 20	0	0
2	D	23	Total I 23 23	0	0
2	E	24	Total I 24 24	0	0
2	F	30	Total I 30 30	0	0

- Molecule 3 is STRONTIUM ION (CCD ID: SR) (formula: Sr).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	A	20	Total Sr 20 20	0	0
3	B	20	Total Sr 20 20	0	0
3	C	21	Total Sr 21 21	0	0
3	D	19	Total Sr 19 19	0	0
3	E	21	Total Sr 21 21	0	0
3	F	23	Total Sr 23 23	0	0

- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	1058	Total O 1058 1058	0	0
4	B	924	Total O 924 924	0	0

Continued on next page...

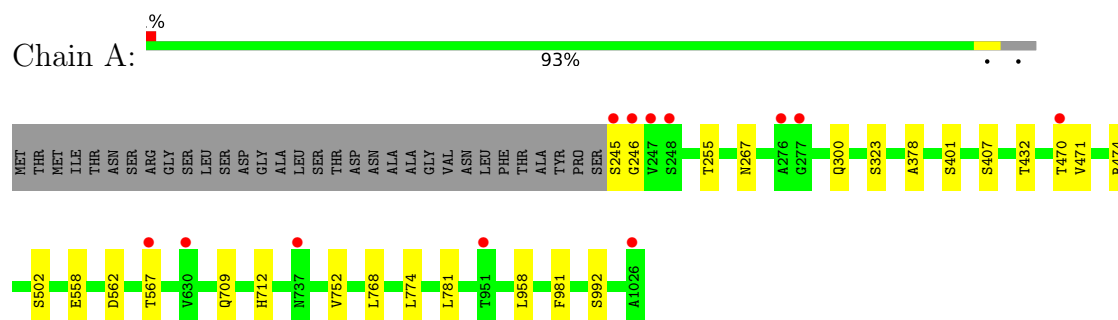
Continued from previous page...

Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	C	599	Total 599	O 599	0	0
4	D	690	Total 690	O 690	0	0
4	E	730	Total 730	O 730	0	0
4	F	836	Total 836	O 836	0	0

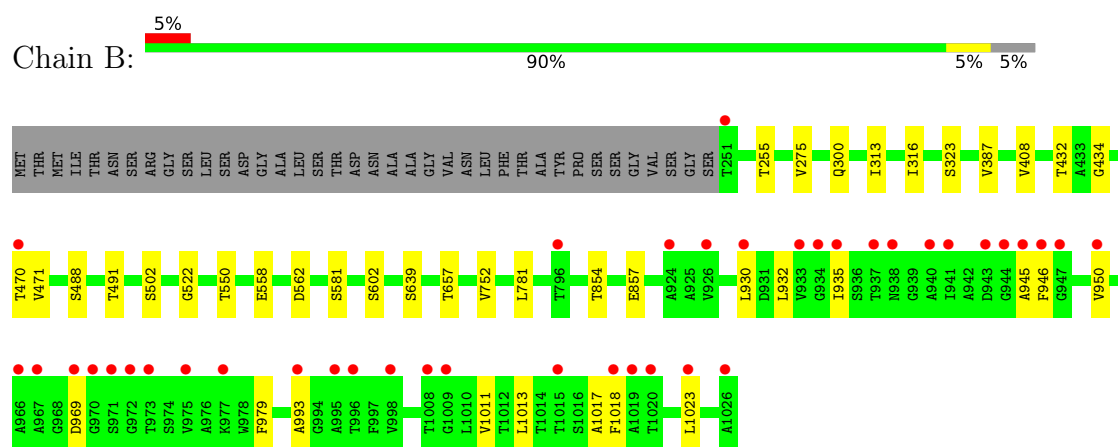
3 Residue-property plots [i](#)

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.

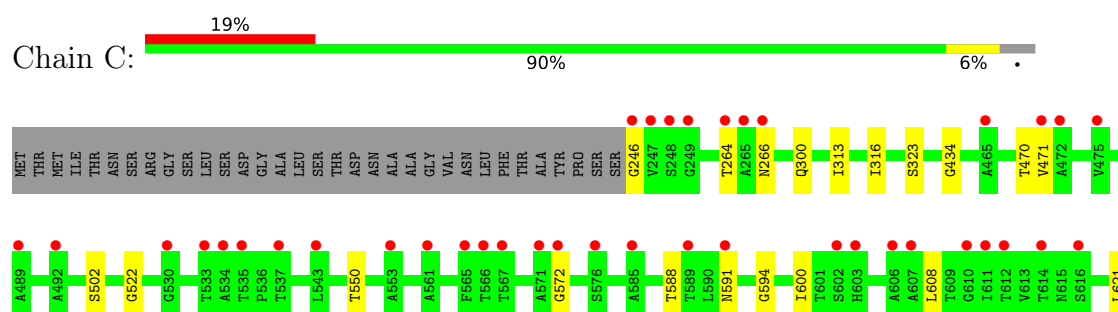
- Molecule 1: S-layer protein

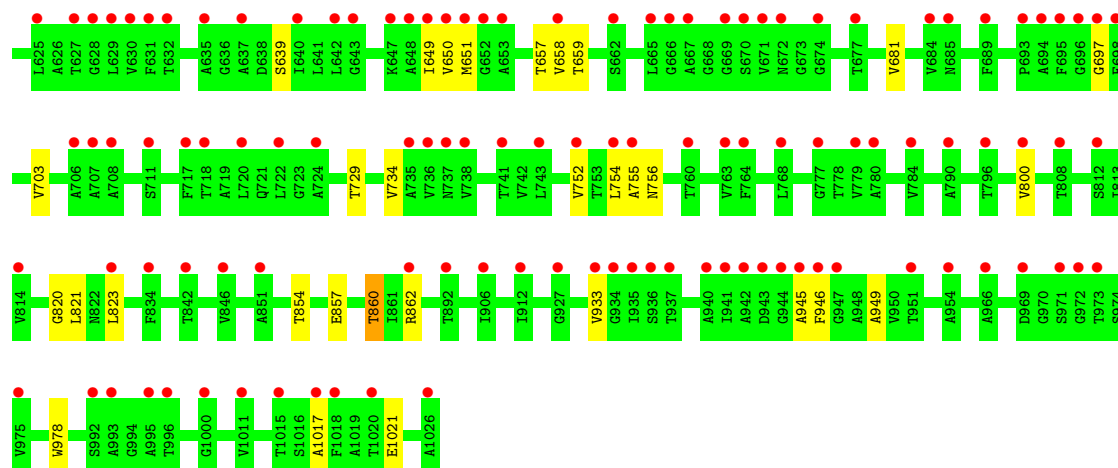


- Molecule 1: S-layer protein

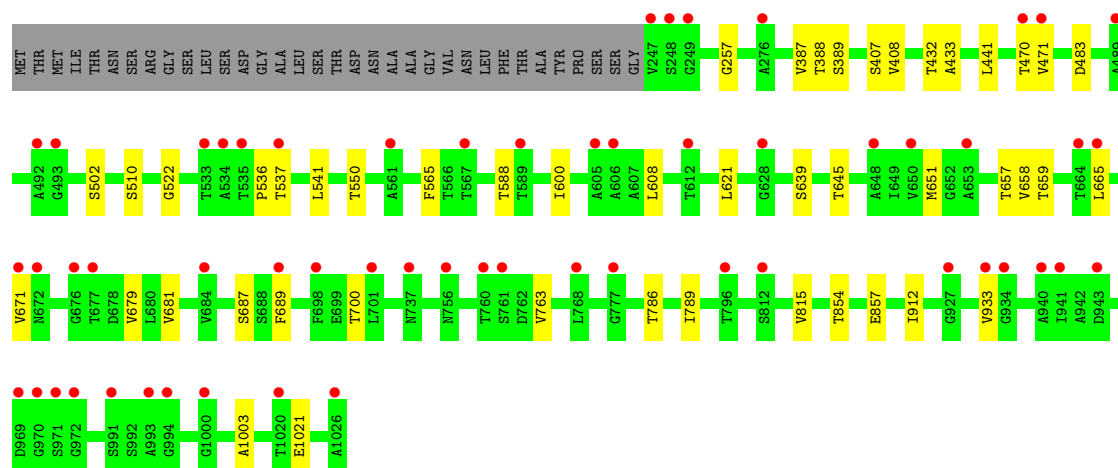
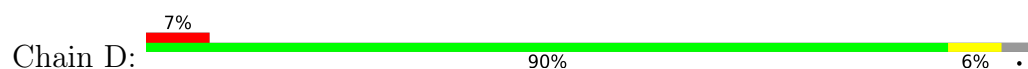


- Molecule 1: S-layer protein

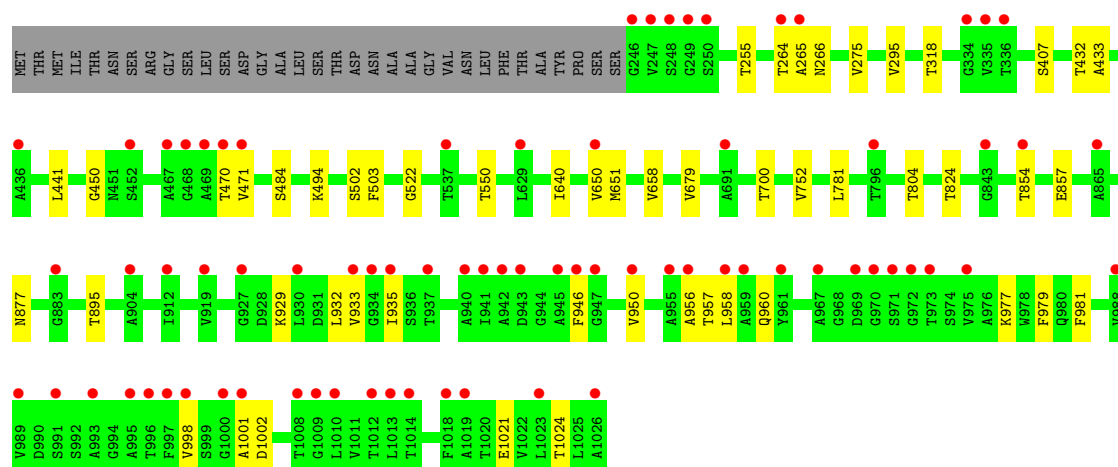
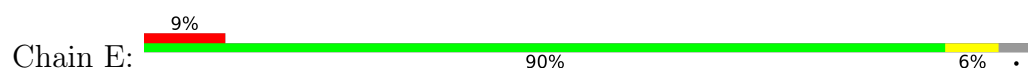




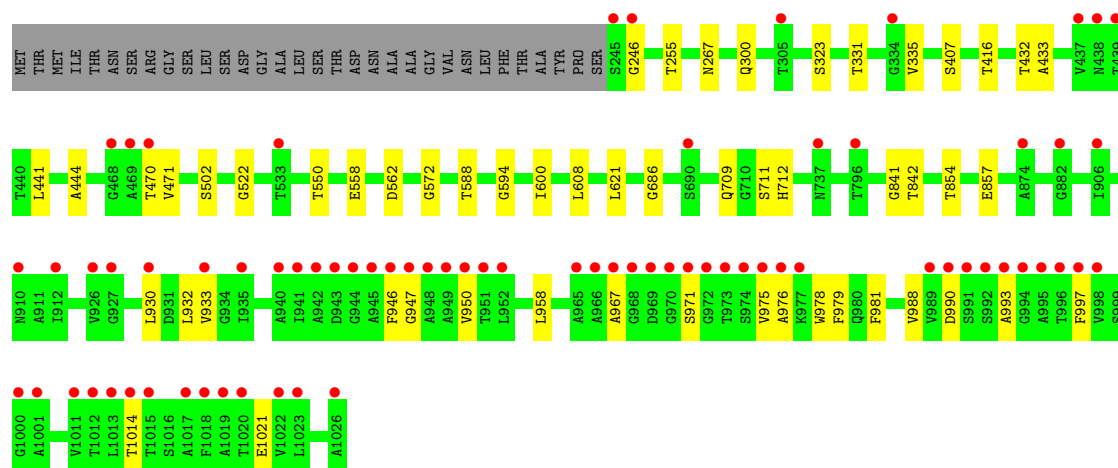
• Molecule 1: S-layer protein



• Molecule 1: S-layer protein



Chain F: 9% 89% 7%



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	210.73Å 80.56Å 221.83Å 90.00° 117.44° 90.00°	Depositor
Resolution (Å)	49.30 – 2.10 49.30 – 2.10	Depositor EDS
% Data completeness (in resolution range)	99.7 (49.30-2.10) 99.8 (49.30-2.10)	Depositor EDS
R_{merge}	0.23	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	1.97 (at 2.10Å)	Xtriage
Refinement program	PHENIX	Depositor
R, R_{free}	0.205 , 0.243 0.210 , 0.245	Depositor DCC
R_{free} test set	19236 reflections (4.99%)	wwPDB-VP
Wilson B-factor (Å ²)	22.1	Xtriage
Anisotropy	1.164	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.37 , 65.4	EDS
L-test for twinning ²	$\langle L \rangle = 0.49$, $\langle L^2 \rangle = 0.33$	Xtriage
Estimated twinning fraction	0.000 for h,-k,-h-l	Xtriage
F_o, F_c correlation	0.95	EDS
Total number of atoms	36028	wwPDB-VP
Average B, all atoms (Å ²)	38.0	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 29.33 % 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 1.5780e-03. The detected translational NCS is most likely also responsible for the elevated intensity ratio.*

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 ⓘ

5.1 Standard geometry ⓘ

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

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	0.24	0/5195	0.42	0/7151
1	B	0.25	0/5168	0.43	0/7115
1	C	0.25	0/5189	0.44	1/7143 (0.0%)
1	D	0.24	1/5185 (0.0%)	0.41	0/7138
1	E	0.20	0/5183	0.39	0/7135
1	F	0.25	0/5195	0.42	0/7151
All	All	0.24	1/31115 (0.0%)	0.42	1/42833 (0.0%)

All (1) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	D	536	PRO	C-O	-5.15	1.18	1.23

All (1) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	C	860	THR	CA-CB-OG1	-5.26	101.71	109.60

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	5162	0	5096	17	0
1	B	5135	0	5070	23	0
1	C	5156	0	5090	34	0
1	D	5152	0	5088	25	0
1	E	5150	0	5086	37	0
1	F	5162	0	5096	30	0
2	A	29	0	0	4	0
2	B	24	0	0	4	0
2	C	20	0	0	3	0
2	D	23	0	0	2	0
2	E	24	0	0	5	0
2	F	30	0	0	6	0
3	A	20	0	0	0	0
3	B	20	0	0	0	0
3	C	21	0	0	0	0
3	D	19	0	0	0	0
3	E	21	0	0	0	0
3	F	23	0	0	0	0
4	A	1058	0	0	2	0
4	B	924	0	0	1	0
4	C	599	0	0	5	0
4	D	690	0	0	0	0
4	E	730	0	0	2	0
4	F	836	0	0	1	0
All	All	36028	0	30526	168	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 3.

The worst 5 of 168 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:F:1116:IOD:I	2:F:1117:IOD:I	3.31	0.88
1:E:650:VAL:HG13	2:E:1103:IOD:I	2.43	0.88
2:C:1109:IOD:I	2:C:1110:IOD:I	3.35	0.85
1:C:650:VAL:HG13	2:C:1105:IOD:I	2.48	0.83
2:E:1110:IOD:I	2:E:1115:IOD:I	3.39	0.81

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	781/814 (96%)	759 (97%)	20 (3%)	2 (0%)	36	36
1	B	776/814 (95%)	750 (97%)	25 (3%)	1 (0%)	48	50
1	C	780/814 (96%)	752 (96%)	27 (4%)	1 (0%)	48	50
1	D	779/814 (96%)	755 (97%)	23 (3%)	1 (0%)	48	50
1	E	779/814 (96%)	753 (97%)	24 (3%)	2 (0%)	36	36
1	F	781/814 (96%)	754 (96%)	26 (3%)	1 (0%)	48	50
All	All	4676/4884 (96%)	4523 (97%)	145 (3%)	8 (0%)	43	44

5 of 8 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	265	ALA
1	A	246	GLY
1	A	502	SER
1	D	502	SER
1	E	502	SER

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	530/554 (96%)	530 (100%)	0	100	100
1	B	527/554 (95%)	526 (100%)	1 (0%)	87	93
1	C	529/554 (96%)	528 (100%)	1 (0%)	87	93

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
1	D	529/554 (96%)	528 (100%)	1 (0%)	87	93
1	E	528/554 (95%)	528 (100%)	0	100	100
1	F	530/554 (96%)	530 (100%)	0	100	100
All	All	3173/3324 (96%)	3170 (100%)	3 (0%)	88	93

All (3) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	B	1011	VAL
1	C	862	ARG
1	D	537	THR

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 11 such sidechains are listed below:

Mol	Chain	Res	Type
1	E	591	ASN
1	E	877	ASN
1	F	397	ASN
1	E	960	GLN
1	D	733	ASN

5.3.3 RNA ⓘ

There are no RNA molecules in this entry.

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

There are no non-standard protein/DNA/RNA residues in this entry.

5.5 Carbohydrates ⓘ

There are no oligosaccharides in this entry.

5.6 Ligand geometry ⓘ

Of 274 ligands modelled in this entry, 274 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 [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	782/814 (96%)	0.28	12 (1%)	72 74	12, 27, 38, 91	1 (0%)
1	B	776/814 (95%)	0.51	40 (5%)	33 35	10, 30, 57, 100	2 (0%)
1	C	781/814 (95%)	1.31	152 (19%)	3 3	18, 52, 72, 94	1 (0%)
1	D	780/814 (95%)	0.86	57 (7%)	21 22	15, 45, 60, 86	1 (0%)
1	E	781/814 (95%)	0.79	75 (9%)	13 14	19, 38, 68, 139	0
1	F	782/814 (96%)	0.68	74 (9%)	14 14	11, 34, 70, 146	1 (0%)
All	All	4682/4884 (95%)	0.74	410 (8%)	15 16	10, 36, 65, 146	6 (0%)

The worst 5 of 410 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	277	GLY	7.2
1	A	246	GLY	7.0
1	C	264	THR	5.9
1	F	245	SER	5.8
1	B	946	PHE	5.7

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 oligosaccharides in this entry.

6.4 Ligands ⓘ

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, 95th 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(Å ²)	Q<0.9
2	IOD	D	1122	1/1	0.76	0.19	130,130,130,130	1
2	IOD	F	1128	1/1	0.80	0.23	118,118,118,118	1
2	IOD	F	1130	1/1	0.88	0.20	93,93,93,93	1
2	IOD	C	1118	1/1	0.89	0.14	89,89,89,89	1
2	IOD	B	1124	1/1	0.90	0.11	94,94,94,94	1
2	IOD	B	1122	1/1	0.91	0.17	67,67,67,67	1
2	IOD	C	1115	1/1	0.92	0.16	102,102,102,102	1
2	IOD	E	1119	1/1	0.92	0.12	72,72,72,72	1
2	IOD	A	1129	1/1	0.93	0.15	84,84,84,84	1
2	IOD	F	1129	1/1	0.93	0.11	69,69,69,69	1
2	IOD	D	1118	1/1	0.93	0.14	73,73,73,73	1
3	SR	C	1139	1/1	0.93	0.08	44,44,44,44	1
3	SR	C	1141	1/1	0.93	0.09	25,25,25,25	1
3	SR	E	1142	1/1	0.93	0.08	34,34,34,34	1
3	SR	F	1147	1/1	0.93	0.07	30,30,30,30	1
2	IOD	C	1117	1/1	0.94	0.11	74,74,74,74	1
2	IOD	E	1120	1/1	0.95	0.09	63,63,63,63	1
3	SR	A	1146	1/1	0.95	0.05	26,26,26,26	1
3	SR	B	1143	1/1	0.95	0.06	32,32,32,32	1
2	IOD	E	1123	1/1	0.95	0.09	93,93,93,93	1
2	IOD	E	1124	1/1	0.95	0.15	89,89,89,89	1
2	IOD	A	1126	1/1	0.95	0.10	73,73,73,73	1
2	IOD	D	1121	1/1	0.95	0.16	101,101,101,101	1
2	IOD	C	1105	1/1	0.96	0.15	88,88,88,88	0
2	IOD	C	1119	1/1	0.96	0.11	78,78,78,78	1
2	IOD	E	1122	1/1	0.96	0.11	57,57,57,57	1
3	SR	A	1149	1/1	0.96	0.07	47,47,47,47	1
2	IOD	C	1114	1/1	0.96	0.07	63,63,63,63	1
2	IOD	B	1123	1/1	0.96	0.07	69,69,69,69	1
2	IOD	F	1125	1/1	0.96	0.09	80,80,80,80	1
3	SR	D	1142	1/1	0.96	0.08	70,70,70,70	1
3	SR	E	1141	1/1	0.96	0.05	31,31,31,31	1
2	IOD	F	1127	1/1	0.96	0.08	59,59,59,59	1
3	SR	E	1145	1/1	0.96	0.07	68,68,68,68	1
2	IOD	B	1121	1/1	0.96	0.07	46,46,46,46	1
2	IOD	F	1106	1/1	0.97	0.04	37,37,37,37	1
2	IOD	F	1115	1/1	0.97	0.07	50,50,50,50	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IOD	F	1118	1/1	0.97	0.06	51,51,51,51	1
2	IOD	F	1122	1/1	0.97	0.06	63,63,63,63	1
2	IOD	C	1120	1/1	0.97	0.15	69,69,69,69	1
2	IOD	D	1110	1/1	0.97	0.06	53,53,53,53	1
2	IOD	D	1113	1/1	0.97	0.08	58,58,58,58	1
2	IOD	D	1115	1/1	0.97	0.09	67,67,67,67	1
2	IOD	A	1122	1/1	0.97	0.06	45,45,45,45	1
2	IOD	D	1119	1/1	0.97	0.10	64,64,64,64	1
2	IOD	C	1112	1/1	0.97	0.07	54,54,54,54	1
2	IOD	B	1112	1/1	0.97	0.21	88,88,88,88	0
3	SR	C	1121	1/1	0.97	0.04	38,38,38,38	0
3	SR	C	1129	1/1	0.97	0.05	45,45,45,45	1
3	SR	C	1136	1/1	0.97	0.05	45,45,45,45	1
2	IOD	E	1117	1/1	0.97	0.06	51,51,51,51	1
2	IOD	A	1123	1/1	0.97	0.14	69,69,69,69	1
2	IOD	C	1116	1/1	0.97	0.07	72,72,72,72	1
3	SR	E	1126	1/1	0.97	0.04	38,38,38,38	0
3	SR	E	1132	1/1	0.97	0.05	27,27,27,27	1
2	IOD	E	1121	1/1	0.97	0.08	73,73,73,73	1
2	IOD	A	1125	1/1	0.97	0.07	57,57,57,57	1
3	SR	E	1143	1/1	0.97	0.05	36,36,36,36	1
2	IOD	A	1118	1/1	0.97	0.09	61,61,61,61	1
2	IOD	A	1127	1/1	0.97	0.08	76,76,76,76	1
3	SR	F	1148	1/1	0.97	0.06	28,28,28,28	1
3	SR	F	1152	1/1	0.97	0.05	36,36,36,36	1
2	IOD	F	1121	1/1	0.98	0.06	61,61,61,61	1
2	IOD	A	1115	1/1	0.98	0.05	42,42,42,42	1
2	IOD	F	1123	1/1	0.98	0.08	57,57,57,57	1
2	IOD	A	1119	1/1	0.98	0.04	45,45,45,45	1
2	IOD	A	1128	1/1	0.98	0.04	48,48,48,48	1
2	IOD	D	1123	1/1	0.98	0.07	62,62,62,62	1
2	IOD	E	1108	1/1	0.98	0.21	95,95,95,95	0
2	IOD	E	1109	1/1	0.98	0.18	94,94,94,94	0
3	SR	A	1130	1/1	0.98	0.05	31,31,31,31	0
3	SR	A	1140	1/1	0.98	0.04	39,39,39,39	0
3	SR	A	1143	1/1	0.98	0.05	31,31,31,31	0
2	IOD	E	1113	1/1	0.98	0.16	91,91,91,91	0
2	IOD	E	1114	1/1	0.98	0.07	55,55,55,55	1
3	SR	B	1126	1/1	0.98	0.07	28,28,28,28	0
3	SR	B	1131	1/1	0.98	0.04	27,27,27,27	1
3	SR	B	1132	1/1	0.98	0.05	25,25,25,25	0
3	SR	B	1136	1/1	0.98	0.09	55,55,55,55	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SR	B	1142	1/1	0.98	0.03	32,32,32,32	1
2	IOD	E	1115	1/1	0.98	0.05	54,54,54,54	1
3	SR	B	1144	1/1	0.98	0.03	27,27,27,27	1
2	IOD	E	1116	1/1	0.98	0.05	60,60,60,60	1
3	SR	C	1122	1/1	0.98	0.04	37,37,37,37	0
2	IOD	A	1124	1/1	0.98	0.06	57,57,57,57	1
3	SR	C	1132	1/1	0.98	0.04	39,39,39,39	1
3	SR	C	1134	1/1	0.98	0.10	62,62,62,62	0
2	IOD	E	1118	1/1	0.98	0.08	63,63,63,63	1
2	IOD	A	1121	1/1	0.98	0.04	50,50,50,50	1
3	SR	C	1140	1/1	0.98	0.09	37,37,37,37	1
2	IOD	C	1108	1/1	0.98	0.06	70,70,70,70	1
3	SR	D	1124	1/1	0.98	0.03	32,32,32,32	0
3	SR	D	1126	1/1	0.98	0.06	48,48,48,48	0
3	SR	D	1137	1/1	0.98	0.08	29,29,29,29	1
3	SR	D	1138	1/1	0.98	0.07	57,57,57,57	0
3	SR	D	1140	1/1	0.98	0.04	33,33,33,33	1
3	SR	D	1141	1/1	0.98	0.05	32,32,32,32	1
2	IOD	C	1110	1/1	0.98	0.07	64,64,64,64	1
3	SR	E	1125	1/1	0.98	0.03	39,39,39,39	0
2	IOD	D	1112	1/1	0.98	0.05	49,49,49,49	1
3	SR	E	1127	1/1	0.98	0.05	42,42,42,42	1
2	IOD	C	1111	1/1	0.98	0.05	59,59,59,59	1
3	SR	E	1136	1/1	0.98	0.03	37,37,37,37	1
3	SR	E	1137	1/1	0.98	0.08	51,51,51,51	1
3	SR	E	1138	1/1	0.98	0.10	62,62,62,62	0
2	IOD	D	1114	1/1	0.98	0.05	61,61,61,61	1
2	IOD	F	1101	1/1	0.98	0.06	54,54,54,54	1
2	IOD	B	1117	1/1	0.98	0.04	39,39,39,39	1
2	IOD	F	1110	1/1	0.98	0.05	61,61,61,61	1
3	SR	F	1132	1/1	0.98	0.04	30,30,30,30	0
3	SR	F	1136	1/1	0.98	0.05	25,25,25,25	1
3	SR	F	1137	1/1	0.98	0.04	41,41,41,41	1
3	SR	F	1143	1/1	0.98	0.04	37,37,37,37	0
3	SR	F	1144	1/1	0.98	0.12	68,68,68,68	0
3	SR	F	1146	1/1	0.98	0.09	73,73,73,73	0
2	IOD	D	1117	1/1	0.98	0.07	62,62,62,62	1
2	IOD	B	1119	1/1	0.98	0.05	68,68,68,68	1
3	SR	F	1149	1/1	0.98	0.04	35,35,35,35	1
3	SR	F	1150	1/1	0.98	0.04	32,32,32,32	1
3	SR	F	1151	1/1	0.98	0.04	24,24,24,24	1
2	IOD	F	1119	1/1	0.98	0.04	45,45,45,45	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IOD	F	1124	1/1	0.99	0.02	38,38,38,38	0
2	IOD	D	1107	1/1	0.99	0.03	58,58,58,58	1
2	IOD	F	1126	1/1	0.99	0.07	53,53,53,53	1
2	IOD	D	1108	1/1	0.99	0.05	49,49,49,49	1
2	IOD	D	1109	1/1	0.99	0.03	37,37,37,37	1
2	IOD	B	1113	1/1	0.99	0.04	37,37,37,37	1
2	IOD	D	1111	1/1	0.99	0.04	50,50,50,50	1
2	IOD	B	1114	1/1	0.99	0.09	69,69,69,69	1
3	SR	A	1131	1/1	0.99	0.02	35,35,35,35	0
3	SR	A	1132	1/1	0.99	0.02	36,36,36,36	0
3	SR	A	1134	1/1	0.99	0.04	40,40,40,40	0
3	SR	A	1135	1/1	0.99	0.04	38,38,38,38	0
3	SR	A	1137	1/1	0.99	0.03	34,34,34,34	0
3	SR	A	1138	1/1	0.99	0.04	28,28,28,28	0
3	SR	A	1139	1/1	0.99	0.04	34,34,34,34	0
2	IOD	B	1115	1/1	0.99	0.03	39,39,39,39	1
3	SR	A	1141	1/1	0.99	0.03	32,32,32,32	0
2	IOD	B	1116	1/1	0.99	0.03	40,40,40,40	1
3	SR	A	1144	1/1	0.99	0.03	32,32,32,32	0
3	SR	A	1145	1/1	0.99	0.03	36,36,36,36	0
2	IOD	A	1108	1/1	0.99	0.03	43,43,43,43	1
3	SR	A	1147	1/1	0.99	0.03	28,28,28,28	1
3	SR	A	1148	1/1	0.99	0.06	59,59,59,59	1
2	IOD	D	1116	1/1	0.99	0.03	40,40,40,40	1
3	SR	B	1125	1/1	0.99	0.03	32,32,32,32	0
2	IOD	B	1118	1/1	0.99	0.05	54,54,54,54	1
3	SR	B	1127	1/1	0.99	0.04	26,26,26,26	0
3	SR	B	1128	1/1	0.99	0.03	40,40,40,40	0
3	SR	B	1129	1/1	0.99	0.03	37,37,37,37	0
3	SR	B	1130	1/1	0.99	0.02	43,43,43,43	0
2	IOD	A	1120	1/1	0.99	0.03	44,44,44,44	1
2	IOD	B	1120	1/1	0.99	0.04	55,55,55,55	1
3	SR	B	1134	1/1	0.99	0.03	31,31,31,31	0
3	SR	B	1135	1/1	0.99	0.03	41,41,41,41	0
2	IOD	D	1120	1/1	0.99	0.07	73,73,73,73	1
3	SR	B	1137	1/1	0.99	0.03	53,53,53,53	0
3	SR	B	1138	1/1	0.99	0.03	36,36,36,36	0
3	SR	B	1139	1/1	0.99	0.04	32,32,32,32	1
3	SR	B	1140	1/1	0.99	0.06	58,58,58,58	0
3	SR	B	1141	1/1	0.99	0.05	26,26,26,26	1
2	IOD	A	1109	1/1	0.99	0.03	38,38,38,38	1
2	IOD	A	1110	1/1	0.99	0.02	39,39,39,39	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
2	IOD	A	1111	1/1	0.99	0.03	38,38,38,38	1
2	IOD	E	1103	1/1	0.99	0.03	50,50,50,50	1
2	IOD	E	1104	1/1	0.99	0.02	35,35,35,35	1
3	SR	C	1123	1/1	0.99	0.04	48,48,48,48	0
3	SR	C	1124	1/1	0.99	0.02	43,43,43,43	1
3	SR	C	1125	1/1	0.99	0.10	53,53,53,53	0
3	SR	C	1126	1/1	0.99	0.02	43,43,43,43	1
3	SR	C	1127	1/1	0.99	0.03	43,43,43,43	1
2	IOD	E	1105	1/1	0.99	0.10	67,67,67,67	0
3	SR	C	1130	1/1	0.99	0.05	55,55,55,55	0
3	SR	C	1131	1/1	0.99	0.07	53,53,53,53	0
2	IOD	E	1106	1/1	0.99	0.04	52,52,52,52	1
3	SR	C	1133	1/1	0.99	0.08	60,60,60,60	0
2	IOD	A	1112	1/1	0.99	0.03	46,46,46,46	1
3	SR	C	1135	1/1	0.99	0.03	39,39,39,39	1
2	IOD	C	1102	1/1	0.99	0.02	53,53,53,53	1
3	SR	C	1137	1/1	0.99	0.08	48,48,48,48	0
3	SR	C	1138	1/1	0.99	0.02	36,36,36,36	1
2	IOD	E	1110	1/1	0.99	0.03	41,41,41,41	1
2	IOD	E	1111	1/1	0.99	0.03	45,45,45,45	1
2	IOD	A	1113	1/1	0.99	0.04	40,40,40,40	1
2	IOD	C	1107	1/1	0.99	0.05	55,55,55,55	1
2	IOD	A	1114	1/1	0.99	0.04	49,49,49,49	1
3	SR	D	1128	1/1	0.99	0.05	50,50,50,50	0
3	SR	D	1129	1/1	0.99	0.05	48,48,48,48	0
3	SR	D	1131	1/1	0.99	0.02	36,36,36,36	1
3	SR	D	1132	1/1	0.99	0.02	31,31,31,31	0
3	SR	D	1134	1/1	0.99	0.04	45,45,45,45	0
3	SR	D	1135	1/1	0.99	0.08	51,51,51,51	0
3	SR	D	1136	1/1	0.99	0.04	57,57,57,57	0
2	IOD	C	1109	1/1	0.99	0.02	36,36,36,36	1
2	IOD	A	1106	1/1	0.99	0.02	39,39,39,39	1
3	SR	D	1139	1/1	0.99	0.04	43,43,43,43	0
2	IOD	A	1116	1/1	0.99	0.03	34,34,34,34	1
2	IOD	A	1117	1/1	0.99	0.04	35,35,35,35	1
2	IOD	C	1113	1/1	0.99	0.07	60,60,60,60	1
2	IOD	B	1103	1/1	0.99	0.02	35,35,35,35	1
2	IOD	B	1105	1/1	0.99	0.03	51,51,51,51	1
2	IOD	B	1107	1/1	0.99	0.03	38,38,38,38	1
3	SR	E	1129	1/1	0.99	0.02	37,37,37,37	1
3	SR	E	1130	1/1	0.99	0.03	27,27,27,27	0
2	IOD	B	1108	1/1	0.99	0.03	41,41,41,41	1

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SR	E	1133	1/1	0.99	0.03	35,35,35,35	1
3	SR	E	1134	1/1	0.99	0.03	37,37,37,37	1
3	SR	E	1135	1/1	0.99	0.03	39,39,39,39	0
2	IOD	B	1109	1/1	0.99	0.03	41,41,41,41	1
2	IOD	F	1103	1/1	0.99	0.04	36,36,36,36	0
2	IOD	F	1105	1/1	0.99	0.03	39,39,39,39	1
3	SR	E	1139	1/1	0.99	0.03	39,39,39,39	0
3	SR	E	1140	1/1	0.99	0.09	63,63,63,63	0
2	IOD	B	1111	1/1	0.99	0.04	48,48,48,48	1
2	IOD	F	1107	1/1	0.99	0.05	51,51,51,51	1
2	IOD	F	1108	1/1	0.99	0.03	37,37,37,37	1
3	SR	E	1144	1/1	0.99	0.06	29,29,29,29	1
2	IOD	F	1109	1/1	0.99	0.02	40,40,40,40	1
3	SR	F	1131	1/1	0.99	0.03	30,30,30,30	0
2	IOD	A	1107	1/1	0.99	0.03	39,39,39,39	1
3	SR	F	1133	1/1	0.99	0.02	37,37,37,37	0
3	SR	F	1134	1/1	0.99	0.04	25,25,25,25	0
2	IOD	F	1111	1/1	0.99	0.03	33,33,33,33	1
2	IOD	F	1112	1/1	0.99	0.03	40,40,40,40	1
3	SR	F	1138	1/1	0.99	0.02	37,37,37,37	0
3	SR	F	1140	1/1	0.99	0.02	36,36,36,36	0
3	SR	F	1141	1/1	0.99	0.03	36,36,36,36	1
3	SR	F	1142	1/1	0.99	0.04	32,32,32,32	1
2	IOD	D	1101	1/1	0.99	0.03	46,46,46,46	1
2	IOD	F	1116	1/1	0.99	0.04	45,45,45,45	1
3	SR	F	1145	1/1	0.99	0.08	66,66,66,66	0
2	IOD	F	1117	1/1	0.99	0.05	50,50,50,50	1
2	IOD	D	1102	1/1	0.99	0.03	54,54,54,54	0
2	IOD	D	1103	1/1	0.99	0.03	46,46,46,46	1
2	IOD	F	1120	1/1	0.99	0.07	48,48,48,48	1
2	IOD	D	1104	1/1	0.99	0.03	48,48,48,48	1
2	IOD	D	1105	1/1	0.99	0.06	55,55,55,55	1
2	IOD	D	1106	1/1	0.99	0.03	50,50,50,50	1
3	SR	F	1153	1/1	0.99	0.03	34,34,34,34	1
3	SR	A	1133	1/1	1.00	0.02	33,33,33,33	0
2	IOD	A	1105	1/1	1.00	0.03	46,46,46,46	1
2	IOD	F	1113	1/1	1.00	0.02	45,45,45,45	1
3	SR	A	1136	1/1	1.00	0.02	35,35,35,35	0
2	IOD	F	1114	1/1	1.00	0.02	44,44,44,44	1
2	IOD	B	1104	1/1	1.00	0.01	42,42,42,42	1
3	SR	D	1125	1/1	1.00	0.03	29,29,29,29	0
2	IOD	C	1101	1/1	1.00	0.06	57,57,57,57	0

Continued on next page...

Continued from previous page...

Mol	Type	Chain	Res	Atoms	RSCC	RSR	B-factors($\text{\AA}^2$)	Q<0.9
3	SR	D	1127	1/1	1.00	0.03	40,40,40,40	1
2	IOD	E	1101	1/1	1.00	0.02	47,47,47,47	1
2	IOD	E	1102	1/1	1.00	0.02	45,45,45,45	0
3	SR	D	1130	1/1	1.00	0.02	45,45,45,45	0
3	SR	A	1142	1/1	1.00	0.02	29,29,29,29	1
2	IOD	A	1101	1/1	1.00	0.03	42,42,42,42	0
3	SR	D	1133	1/1	1.00	0.03	35,35,35,35	1
2	IOD	C	1103	1/1	1.00	0.05	53,53,53,53	1
3	SR	F	1135	1/1	1.00	0.01	36,36,36,36	0
2	IOD	C	1104	1/1	1.00	0.03	47,47,47,47	1
2	IOD	B	1106	1/1	1.00	0.03	37,37,37,37	1
2	IOD	E	1107	1/1	1.00	0.02	42,42,42,42	1
3	SR	F	1139	1/1	1.00	0.02	34,34,34,34	1
2	IOD	F	1102	1/1	1.00	0.03	47,47,47,47	0
2	IOD	C	1106	1/1	1.00	0.02	50,50,50,50	1
2	IOD	F	1104	1/1	1.00	0.01	41,41,41,41	1
3	SR	C	1128	1/1	1.00	0.02	31,31,31,31	0
2	IOD	A	1102	1/1	1.00	0.02	45,45,45,45	0
2	IOD	A	1103	1/1	1.00	0.02	42,42,42,42	1
2	IOD	A	1104	1/1	1.00	0.01	42,42,42,42	1
2	IOD	E	1112	1/1	1.00	0.02	45,45,45,45	1
3	SR	E	1128	1/1	1.00	0.02	41,41,41,41	0
2	IOD	B	1110	1/1	1.00	0.02	41,41,41,41	1
2	IOD	B	1101	1/1	1.00	0.01	42,42,42,42	0
3	SR	E	1131	1/1	1.00	0.02	36,36,36,36	0
2	IOD	B	1102	1/1	1.00	0.02	44,44,44,44	0
3	SR	B	1133	1/1	1.00	0.07	45,45,45,45	0

6.5 Other polymers [i](#)

There are no such residues in this entry.