



Full wwPDB X-ray Structure Validation Report ⓘ

May 13, 2020 – 01:51 am BST

PDB ID : 2X8K
Title : Crystal Structure of SPP1 Dit (gp 19.1) Protein, a Paradigm of Hub Adsorption Apparatus in Gram-positive Infecting Phages.
Authors : Veessler, D.; Robin, G.; Lichiere, J.; Auzat, I.; Tavares, P.; Bron, P.; Campanacci, V.; Cambillau, C.
Deposited on : 2010-03-10
Resolution : 2.95 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 : 2.11
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

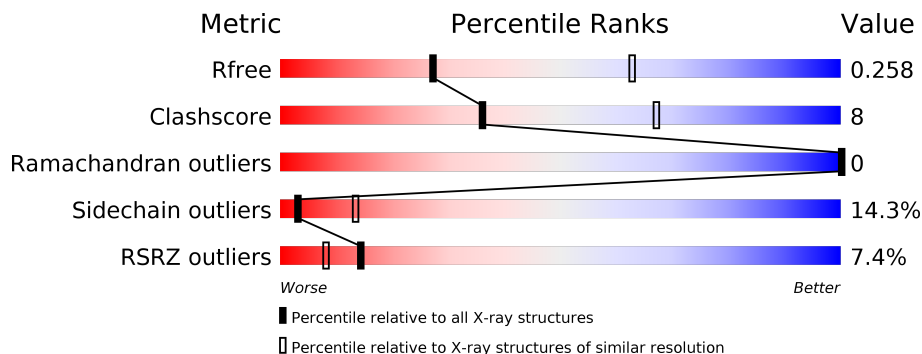
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.95 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	3104 (3.00-2.92)
Clashscore	141614	3462 (3.00-2.92)
Ramachandran outliers	138981	3340 (3.00-2.92)
Sidechain outliers	138945	3343 (3.00-2.92)
RSRZ outliers	127900	2986 (3.00-2.92)

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 ≥ 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	 12% 73% 21% . .
1	B	252	 2% 75% 17% . .
1	C	252	 7% 70% 23% . .

2 Entry composition

There is only 1 type of molecule in this entry. The entry contains 5710 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 HYPOTHETICAL PROTEIN 19.1.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	242	1902	1210	306	378	8	0	0	0
1	B	242	1902	1210	306	378	8	0	0	0
1	C	243	1906	1212	307	379	8	0	0	0

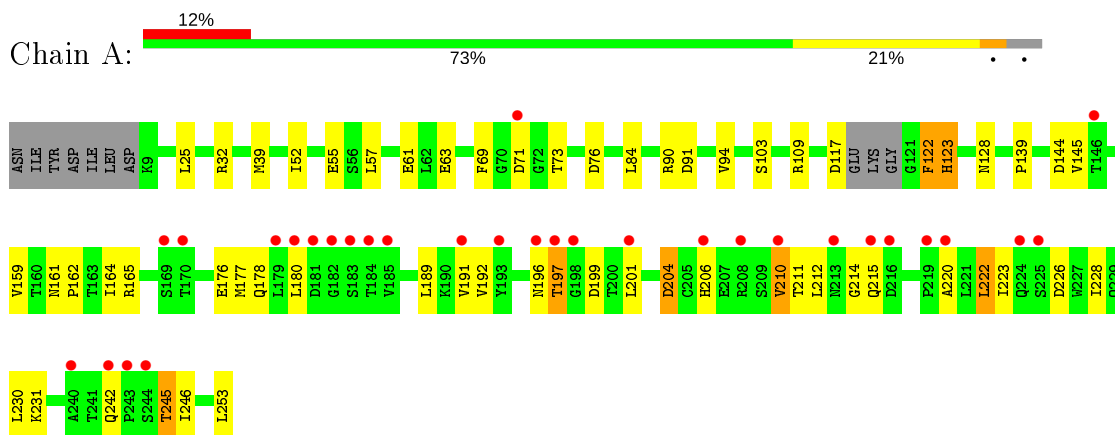
There are 3 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	192	VAL	LYS	conflict	UNP O48459
B	192	VAL	LYS	conflict	UNP O48459
C	192	VAL	LYS	conflict	UNP O48459

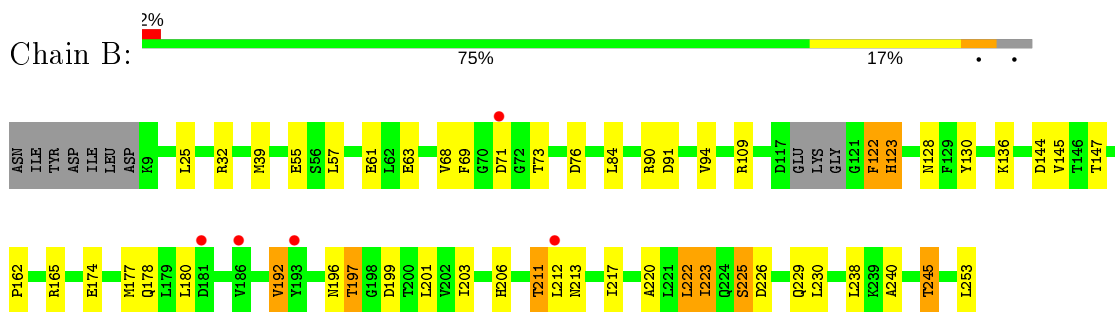
3 Residue-property plots [i](#)

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.

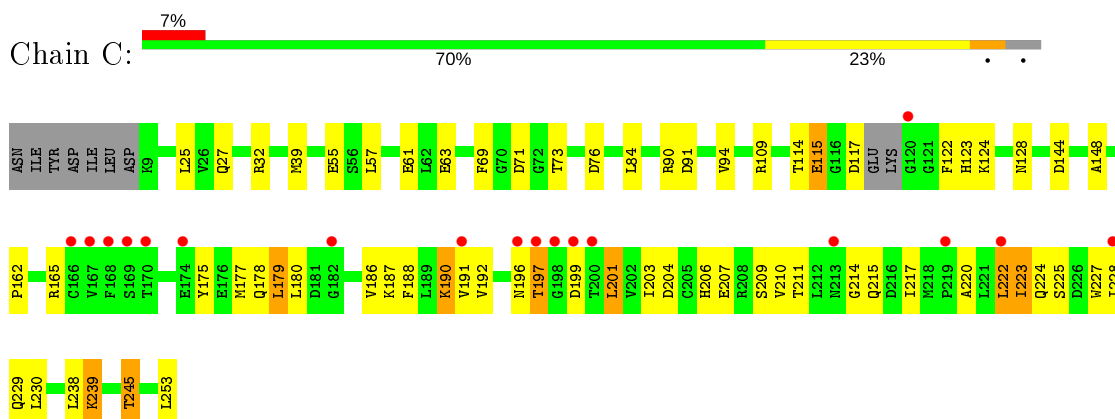
- Molecule 1: HYPOTHETICAL PROTEIN 19.1



- Molecule 1: HYPOTHETICAL PROTEIN 19.1



- Molecule 1: HYPOTHETICAL PROTEIN 19.1



4 Data and refinement statistics

Property	Value	Source
Space group	I 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	107.19Å 125.75Å 189.35Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	34.37 – 2.95 34.37 – 2.95	Depositor EDS
% Data completeness (in resolution range)	(Not available) (34.37-2.95) 99.5 (34.37-2.95)	Depositor EDS
R_{merge}	0.06	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.06 (at 2.95Å)	Xtrriage
Refinement program	BUSTER 2.9.2	Depositor
R, R_{free}	0.200 , 0.236 0.222 , 0.258	Depositor DCC
R_{free} test set	958 reflections (3.53%)	wwPDB-VP
Wilson B-factor (Å ²)	84.0	Xtrriage
Anisotropy	0.615	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.31 , 88.8	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	5710	wwPDB-VP
Average B, all atoms (Å ²)	109.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 3.66% 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	0.49	0/1940	0.80	5/2639 (0.2%)
1	B	0.49	0/1940	0.84	5/2639 (0.2%)
1	C	0.51	0/1944	0.83	4/2644 (0.2%)
All	All	0.50	0/5824	0.82	14/7922 (0.2%)

There are no bond length outliers.

All (14) bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	223	ILE	N-CA-C	-9.51	85.32	111.00
1	C	223	ILE	N-CA-C	-9.33	85.80	111.00
1	A	223	ILE	N-CA-C	-8.61	87.75	111.00
1	B	222	LEU	N-CA-C	8.41	133.71	111.00
1	C	222	LEU	N-CA-C	7.91	132.36	111.00
1	A	222	LEU	N-CA-C	6.75	129.22	111.00
1	B	223	ILE	N-CA-CB	6.74	126.31	110.80
1	B	222	LEU	CB-CA-C	-6.66	97.55	110.20
1	C	222	LEU	CB-CA-C	-6.62	97.62	110.20
1	A	223	ILE	N-CA-CB	5.42	123.26	110.80
1	B	213	ASN	N-CA-C	5.40	125.59	111.00
1	C	225	SER	N-CA-C	-5.38	96.48	111.00
1	A	222	LEU	CB-CA-C	-5.35	100.03	110.20
1	A	226	ASP	CB-CG-OD2	5.18	122.97	118.30

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	1902	0	1847	26	0
1	B	1902	0	1847	21	0
1	C	1906	0	1850	44	0
All	All	5710	0	5544	90	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 8.

All (90) 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:187:LYS:CD	1:C:228:ILE:HG22	1.67	1.22
1:C:187:LYS:HD3	1:C:228:ILE:CG2	1.89	1.01
1:A:164:ILE:HD11	1:A:228:ILE:HD11	1.49	0.93
1:C:187:LYS:HD3	1:C:228:ILE:HG22	0.92	0.91
1:C:179:LEU:HD13	1:C:228:ILE:HD12	1.59	0.85
1:C:197:THR:O	1:C:197:THR:HG23	1.77	0.85
1:A:164:ILE:HD11	1:A:228:ILE:CD1	2.11	0.80
1:B:197:THR:HG23	1:B:197:THR:O	1.81	0.79
1:A:197:THR:O	1:A:197:THR:HG23	1.83	0.78
1:C:188:PHE:CE2	1:C:190:LYS:HD3	2.24	0.73
1:C:187:LYS:CD	1:C:228:ILE:CG2	2.57	0.73
1:C:148:ALA:C	1:C:239:LYS:HG3	2.11	0.70
1:A:165:ARG:HB3	1:A:245:THR:HG22	1.74	0.69
1:C:177:MET:HE1	1:C:238:LEU:HB3	1.74	0.69
1:C:179:LEU:CD1	1:C:228:ILE:HD12	2.23	0.69
1:A:162:PRO:HD2	1:A:228:ILE:HG13	1.73	0.68
1:C:165:ARG:HB3	1:C:245:THR:HG22	1.76	0.68
1:B:165:ARG:HB3	1:B:245:THR:HG22	1.76	0.67
1:C:207:GLU:HA	1:C:227:TRP:CH2	2.30	0.67
1:B:192:VAL:HG23	1:B:220:ALA:O	1.97	0.64
1:C:197:THR:O	1:C:197:THR:CG2	2.44	0.64
1:C:220:ALA:O	1:C:222:LEU:HD12	1.97	0.64
1:C:203:ILE:HG12	1:C:206:HIS:H	1.65	0.61
1:A:191:VAL:HG13	1:A:220:ALA:HB1	1.83	0.61
1:A:196:ASN:O	1:A:197:THR:HB	2.00	0.61
1:B:145:VAL:HG11	1:B:177:MET:HE1	1.82	0.60
1:B:196:ASN:O	1:B:197:THR:HB	2.02	0.60
1:A:211:THR:HG23	1:A:212:LEU:N	2.17	0.58

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:164:ILE:CD1	1:A:228:ILE:HD11	2.30	0.57
1:C:179:LEU:HB2	1:C:228:ILE:HD13	1.87	0.55
1:C:196:ASN:O	1:C:197:THR:HB	2.05	0.55
1:C:165:ARG:HE	1:C:201:LEU:HD21	1.73	0.54
1:C:207:GLU:HG2	1:C:227:TRP:CE2	2.43	0.53
1:C:191:VAL:HG22	1:C:220:ALA:HB1	1.90	0.53
1:C:207:GLU:HA	1:C:227:TRP:CZ3	2.44	0.53
1:C:204:ASP:HA	1:C:227:TRP:CE3	2.44	0.52
1:B:211:THR:HB	1:B:217:ILE:HG13	1.91	0.52
1:C:179:LEU:HB2	1:C:228:ILE:CD1	2.40	0.51
1:A:145:VAL:HG11	1:A:177:MET:HE1	1.93	0.50
1:A:162:PRO:HG3	1:A:230:LEU:HD13	1.93	0.50
1:A:162:PRO:HG2	1:A:228:ILE:HD12	1.94	0.49
1:C:204:ASP:OD2	1:C:227:TRP:HB3	2.12	0.49
1:C:187:LYS:CB	1:C:228:ILE:CG2	2.90	0.49
1:C:148:ALA:CA	1:C:239:LYS:HG3	2.42	0.49
1:A:122:PHE:N	1:A:122:PHE:CD1	2.79	0.49
1:A:210:VAL:HG13	1:A:214:GLY:HA2	1.95	0.49
1:C:179:LEU:HD23	1:C:186:VAL:HB	1.94	0.49
1:B:71:ASP:HB3	1:B:76:ASP:HB3	1.96	0.48
1:C:27:GLN:HE22	1:C:124:LYS:NZ	2.12	0.48
1:A:71:ASP:HB3	1:A:76:ASP:HB3	1.97	0.47
1:A:214:GLY:O	1:A:215:GLN:NE2	2.48	0.47
1:B:68:VAL:O	1:B:123:HIS:ND1	2.47	0.47
1:C:175:TYR:O	1:C:190:LYS:HA	2.16	0.46
1:C:71:ASP:HB3	1:C:76:ASP:HB3	1.97	0.46
1:B:203:ILE:HG12	1:B:206:HIS:H	1.79	0.46
1:C:187:LYS:HB2	1:C:228:ILE:HG21	1.97	0.46
1:A:196:ASN:O	1:A:197:THR:CB	2.65	0.45
1:B:147:THR:HA	1:B:240:ALA:O	2.16	0.45
1:C:187:LYS:HB3	1:C:228:ILE:CG2	2.47	0.44
1:B:177:MET:HE2	1:B:238:LEU:HB3	2.00	0.44
1:C:115:GLU:HG3	1:C:123:HIS:CE1	2.52	0.44
1:C:162:PRO:HG3	1:C:230:LEU:HD13	1.99	0.44
1:B:196:ASN:O	1:B:197:THR:CB	2.65	0.44
1:C:187:LYS:CB	1:C:228:ILE:HG21	2.48	0.44
1:C:222:LEU:HD12	1:C:222:LEU:H	1.83	0.43
1:A:161:ASN:HB3	1:A:204:ASP:HB3	2.01	0.43
1:A:39:MET:HG2	1:A:55:GLU:HG3	2.01	0.43
1:B:39:MET:HG2	1:B:55:GLU:HG3	1.99	0.43
1:A:61:GLU:OE2	1:A:128:ASN:HB3	2.19	0.42

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:B:197:THR:CG2	1:B:197:THR:O	2.47	0.42
1:B:177:MET:CE	1:B:238:LEU:HB3	2.49	0.42
1:C:39:MET:HG2	1:C:55:GLU:HG3	2.00	0.42
1:C:196:ASN:O	1:C:197:THR:CB	2.67	0.42
1:C:223:ILE:HG22	1:C:224:GLN:N	2.34	0.42
1:C:207:GLU:CA	1:C:227:TRP:CH2	3.01	0.42
1:B:122:PHE:CD1	1:B:122:PHE:N	2.86	0.42
1:C:210:VAL:HG13	1:C:214:GLY:HA2	2.02	0.42
1:B:122:PHE:HB2	1:B:123:HIS:H	1.70	0.42
1:A:52:ILE:HD11	1:B:130:TYR:HD2	1.85	0.42
1:A:122:PHE:HB2	1:A:123:HIS:H	1.62	0.41
1:A:159:VAL:HG22	1:A:231:LYS:HA	2.03	0.41
1:B:61:GLU:OE2	1:B:128:ASN:HB3	2.20	0.41
1:A:103:SER:HB3	1:A:139:PRO:HG3	2.03	0.41
1:B:223:ILE:O	1:B:225:SER:N	2.54	0.41
1:C:188:PHE:HE2	1:C:190:LYS:HD3	1.77	0.41
1:C:187:LYS:HD2	1:C:228:ILE:HG22	1.84	0.41
1:A:176:GLU:HA	1:A:189:LEU:O	2.20	0.40
1:B:162:PRO:HG3	1:B:230:LEU:HD13	2.04	0.40
1:C:61:GLU:OE2	1:C:128:ASN:HB3	2.20	0.40
1:A:162:PRO:HG2	1:A:228:ILE:CD1	2.52	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	238/252 (94%)	220 (92%)	18 (8%)	0	100	100
1	B	238/252 (94%)	219 (92%)	19 (8%)	0	100	100
1	C	239/252 (95%)	220 (92%)	19 (8%)	0	100	100
All	All	715/756 (95%)	659 (92%)	56 (8%)	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	212/225 (94%)	183 (86%)	29 (14%)	3	15
1	B	212/225 (94%)	182 (86%)	30 (14%)	3	13
1	C	212/225 (94%)	180 (85%)	32 (15%)	3	12
All	All	636/675 (94%)	545 (86%)	91 (14%)	3	13

All (91) residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	A	25	LEU
1	A	32	ARG
1	A	57	LEU
1	A	63	GLU
1	A	69	PHE
1	A	73	THR
1	A	84	LEU
1	A	90	ARG
1	A	91	ASP
1	A	94	VAL
1	A	109	ARG
1	A	117	ASP
1	A	122	PHE
1	A	123	HIS
1	A	144	ASP
1	A	178	GLN
1	A	180	LEU
1	A	192	VAL
1	A	197	THR
1	A	199	ASP
1	A	201	LEU
1	A	204	ASP
1	A	206	HIS

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Mol	Chain	Res	Type
1	A	210	VAL
1	A	222	LEU
1	A	242	GLN
1	A	245	THR
1	A	246	ILE
1	A	253	LEU
1	B	25	LEU
1	B	32	ARG
1	B	57	LEU
1	B	63	GLU
1	B	69	PHE
1	B	73	THR
1	B	84	LEU
1	B	90	ARG
1	B	91	ASP
1	B	94	VAL
1	B	109	ARG
1	B	122	PHE
1	B	123	HIS
1	B	136	LYS
1	B	144	ASP
1	B	174	GLU
1	B	178	GLN
1	B	180	LEU
1	B	192	VAL
1	B	197	THR
1	B	199	ASP
1	B	201	LEU
1	B	211	THR
1	B	212	LEU
1	B	222	LEU
1	B	225	SER
1	B	226	ASP
1	B	229	GLN
1	B	245	THR
1	B	253	LEU
1	C	25	LEU
1	C	32	ARG
1	C	57	LEU
1	C	63	GLU
1	C	69	PHE
1	C	73	THR

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Mol	Chain	Res	Type
1	C	84	LEU
1	C	90	ARG
1	C	91	ASP
1	C	94	VAL
1	C	109	ARG
1	C	114	THR
1	C	115	GLU
1	C	117	ASP
1	C	122	PHE
1	C	144	ASP
1	C	178	GLN
1	C	179	LEU
1	C	180	LEU
1	C	190	LYS
1	C	192	VAL
1	C	197	THR
1	C	199	ASP
1	C	201	LEU
1	C	209	SER
1	C	211	THR
1	C	215	GLN
1	C	217	ILE
1	C	229	GLN
1	C	239	LYS
1	C	245	THR
1	C	253	LEU

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	89	HIS
1	B	242	GLN
1	C	27	GLN
1	C	229	GLN

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, 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	242/252 (96%)	0.59	31 (12%) 3 2	52, 107, 188, 202	0
1	B	242/252 (96%)	0.15	5 (2%) 63 46	57, 93, 171, 191	0
1	C	243/252 (96%)	0.30	18 (7%) 14 8	57, 98, 185, 194	0
All	All	727/756 (96%)	0.35	54 (7%) 14 8	52, 98, 184, 202	0

All (54) RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	A	191	VAL	7.0
1	A	183	SER	5.9
1	A	243	PRO	5.3
1	C	167	VAL	5.0
1	A	201	LEU	4.9
1	A	181	ASP	4.8
1	C	198	GLY	4.7
1	A	184	THR	4.6
1	C	197	THR	4.5
1	A	180	LEU	4.5
1	A	197	THR	4.3
1	A	213	ASN	4.3
1	A	182	GLY	4.3
1	A	220	ALA	4.2
1	A	224	GLN	3.9
1	B	212	LEU	3.8
1	A	198	GLY	3.7
1	C	169	SER	3.6
1	C	191	VAL	3.2
1	A	216	ASP	3.2
1	C	170	THR	3.1
1	A	210	VAL	3.1
1	A	225	SER	2.9

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Mol	Chain	Res	Type	RSRZ
1	A	169	SER	2.8
1	A	170	THR	2.8
1	A	242	GLN	2.8
1	C	174	GLU	2.8
1	A	219	PRO	2.8
1	C	168	PHE	2.7
1	A	71	ASP	2.7
1	A	179	LEU	2.7
1	C	199	ASP	2.7
1	C	219	PRO	2.6
1	C	196	ASN	2.6
1	C	182	GLY	2.6
1	A	244	SER	2.5
1	C	213	ASN	2.4
1	A	215	GLN	2.4
1	A	240	ALA	2.3
1	C	120	GLY	2.3
1	B	71	ASP	2.3
1	B	193	TYR	2.3
1	A	193	TYR	2.3
1	A	206	HIS	2.3
1	C	166	CYS	2.2
1	B	186	VAL	2.2
1	A	185	VAL	2.2
1	A	196	ASN	2.1
1	B	181	ASP	2.1
1	A	208	ARG	2.1
1	A	146	THR	2.1
1	C	200	THR	2.1
1	C	228	ILE	2.1
1	C	222	LEU	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

There are no ligands in this entry.

6.5 Other polymers

There are no such residues in this entry.