



wwPDB X-ray Structure Validation Summary Report ⓘ

Mar 18, 2026 – 03:48 AM UTC

PDB ID : 1VZ0 / pdb_00001vz0
Title : Chromosome segregation protein Spo0J from *Thermus thermophilus*
Authors : Leonard, T.A.; Butler, P.J.G.; Lowe, J.
Deposited on : 2004-05-12
Resolution : 2.30 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

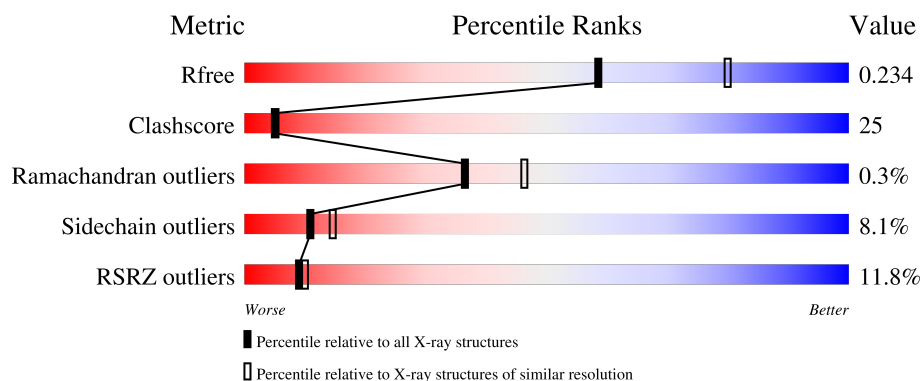
1 Overall quality at a glance

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.30 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.



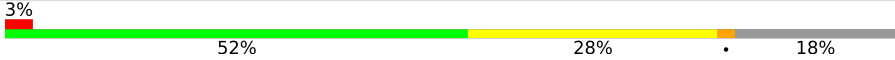
Metric	Whole archive (#Entries)	Similar resolution (#Entries, resolution range(Å))
R_{free}	180053	6319 (2.30-2.30)
Clashscore	190562	6919 (2.30-2.30)
Ramachandran outliers	187476	6854 (2.30-2.30)
Sidechain outliers	187428	6854 (2.30-2.30)
RSRZ outliers	180081	6325 (2.30-2.30)

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	230	7% 54% 21% 5% 19%
1	B	230	12% 46% 35% • 16%
1	C	230	10% 50% 28% • • 17%
1	D	230	11% 57% 26% • 16%
1	E	230	13% 53% 25% 5% 17%

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Mol	Chain	Length	Quality of chain
1	F	230	
1	G	230	
1	H	230	

2 Entry composition

There are 4 unique types of molecules in this entry. The entry contains 12878 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 Chromosome-partitioning protein Spo0J.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
1	A	187	Total	C	N	O	S	0	0	1
			1459	911	272	273	3			
1	B	193	Total	C	N	O	S	0	0	1
			1511	943	284	281	3			
1	C	190	Total	C	N	O	S	0	0	1
			1487	928	278	278	3			
1	D	193	Total	C	N	O	S	0	0	1
			1511	943	284	281	3			
1	E	192	Total	C	N	O	S	0	0	1
			1506	940	283	280	3			
1	F	189	Total	C	N	O	S	0	0	1
			1478	923	277	275	3			
1	G	187	Total	C	N	O	S	0	0	1
			1459	911	272	273	3			
1	H	188	Total	C	N	O	S	0	0	1
			1467	917	273	274	3			

There are 64 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
A	223	GLY	-	expression tag	UNP Q72H91
A	224	SER	-	expression tag	UNP Q72H91
A	225	HIS	-	expression tag	UNP Q72H91
A	226	HIS	-	expression tag	UNP Q72H91
A	227	HIS	-	expression tag	UNP Q72H91
A	228	HIS	-	expression tag	UNP Q72H91
A	229	HIS	-	expression tag	UNP Q72H91
A	230	HIS	-	expression tag	UNP Q72H91
B	223	GLY	-	expression tag	UNP Q72H91
B	224	SER	-	expression tag	UNP Q72H91
B	225	HIS	-	expression tag	UNP Q72H91
B	226	HIS	-	expression tag	UNP Q72H91
B	227	HIS	-	expression tag	UNP Q72H91

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Chain	Residue	Modelled	Actual	Comment	Reference
B	228	HIS	-	expression tag	UNP Q72H91
B	229	HIS	-	expression tag	UNP Q72H91
B	230	HIS	-	expression tag	UNP Q72H91
C	223	GLY	-	expression tag	UNP Q72H91
C	224	SER	-	expression tag	UNP Q72H91
C	225	HIS	-	expression tag	UNP Q72H91
C	226	HIS	-	expression tag	UNP Q72H91
C	227	HIS	-	expression tag	UNP Q72H91
C	228	HIS	-	expression tag	UNP Q72H91
C	229	HIS	-	expression tag	UNP Q72H91
C	230	HIS	-	expression tag	UNP Q72H91
D	223	GLY	-	expression tag	UNP Q72H91
D	224	SER	-	expression tag	UNP Q72H91
D	225	HIS	-	expression tag	UNP Q72H91
D	226	HIS	-	expression tag	UNP Q72H91
D	227	HIS	-	expression tag	UNP Q72H91
D	228	HIS	-	expression tag	UNP Q72H91
D	229	HIS	-	expression tag	UNP Q72H91
D	230	HIS	-	expression tag	UNP Q72H91
E	223	GLY	-	expression tag	UNP Q72H91
E	224	SER	-	expression tag	UNP Q72H91
E	225	HIS	-	expression tag	UNP Q72H91
E	226	HIS	-	expression tag	UNP Q72H91
E	227	HIS	-	expression tag	UNP Q72H91
E	228	HIS	-	expression tag	UNP Q72H91
E	229	HIS	-	expression tag	UNP Q72H91
E	230	HIS	-	expression tag	UNP Q72H91
F	223	GLY	-	expression tag	UNP Q72H91
F	224	SER	-	expression tag	UNP Q72H91
F	225	HIS	-	expression tag	UNP Q72H91
F	226	HIS	-	expression tag	UNP Q72H91
F	227	HIS	-	expression tag	UNP Q72H91
F	228	HIS	-	expression tag	UNP Q72H91
F	229	HIS	-	expression tag	UNP Q72H91
F	230	HIS	-	expression tag	UNP Q72H91
G	223	GLY	-	expression tag	UNP Q72H91
G	224	SER	-	expression tag	UNP Q72H91
G	225	HIS	-	expression tag	UNP Q72H91
G	226	HIS	-	expression tag	UNP Q72H91
G	227	HIS	-	expression tag	UNP Q72H91
G	228	HIS	-	expression tag	UNP Q72H91
G	229	HIS	-	expression tag	UNP Q72H91

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Chain	Residue	Modelled	Actual	Comment	Reference
G	230	HIS	-	expression tag	UNP Q72H91
H	223	GLY	-	expression tag	UNP Q72H91
H	224	SER	-	expression tag	UNP Q72H91
H	225	HIS	-	expression tag	UNP Q72H91
H	226	HIS	-	expression tag	UNP Q72H91
H	227	HIS	-	expression tag	UNP Q72H91
H	228	HIS	-	expression tag	UNP Q72H91
H	229	HIS	-	expression tag	UNP Q72H91
H	230	HIS	-	expression tag	UNP Q72H91

- Molecule 2 is COBALT (II) ION (CCD ID: CO) (formula: Co).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
2	A	3	Total Co 3 3	0	0
2	B	2	Total Co 2 2	0	0
2	C	2	Total Co 2 2	0	0
2	D	2	Total Co 2 2	0	0
2	E	2	Total Co 2 2	0	0
2	G	1	Total Co 1 1	0	0
2	H	1	Total Co 1 1	0	0

- Molecule 3 is MAGNESIUM ION (CCD ID: MG) (formula: Mg).

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
3	C	1	Total Mg 1 1	0	0
3	D	1	Total Mg 1 1	0	0

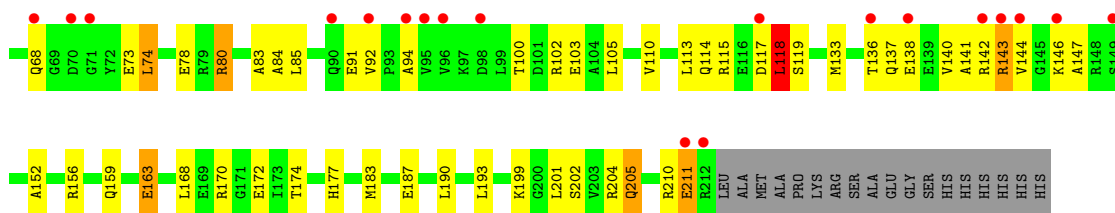
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	140	Total O 140 140	0	0

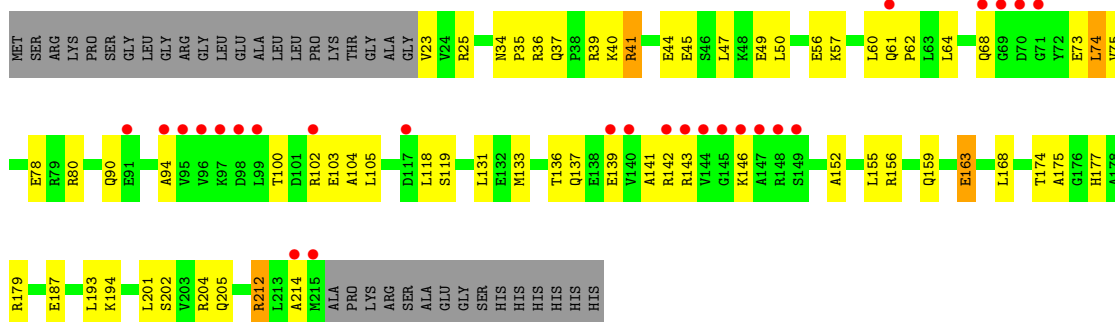
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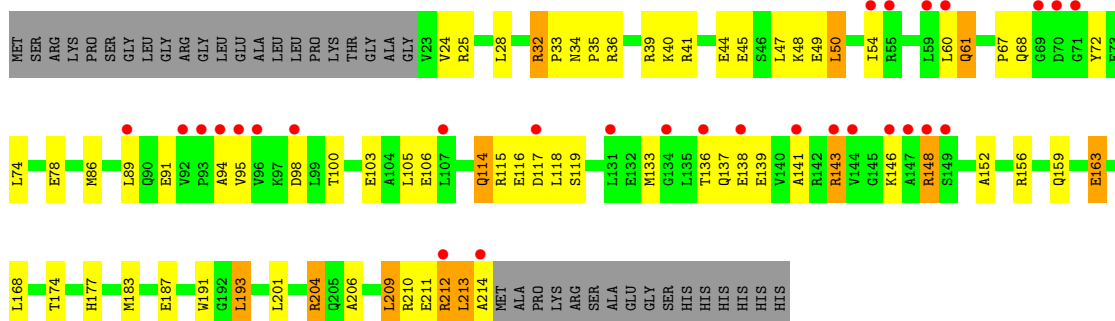
Mol	Chain	Residues	Atoms		ZeroOcc	AltConf
4	B	130	Total 130	O 130	0	0
4	C	114	Total 114	O 114	0	0
4	D	126	Total 126	O 126	0	0
4	E	110	Total 110	O 110	0	0
4	F	117	Total 117	O 117	0	0
4	G	122	Total 122	O 122	0	0
4	H	126	Total 126	O 126	0	0



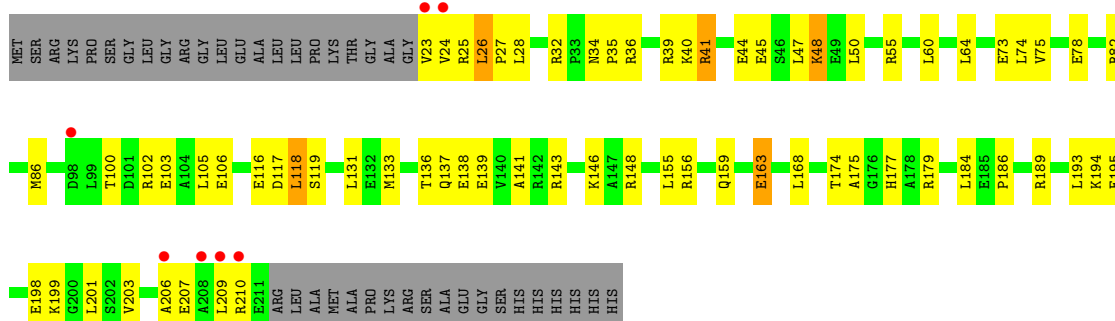
• Molecule 1: Chromosome-partitioning protein Spo0J



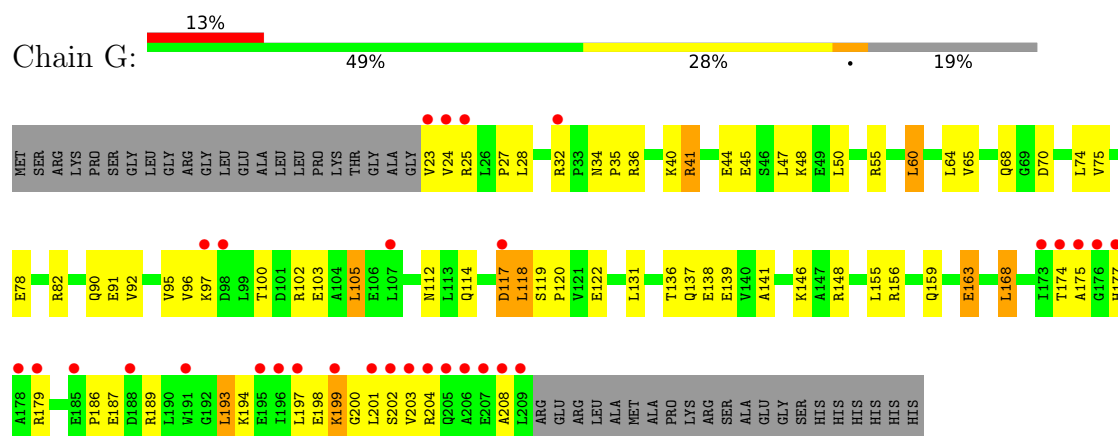
• Molecule 1: Chromosome-partitioning protein Spo0J



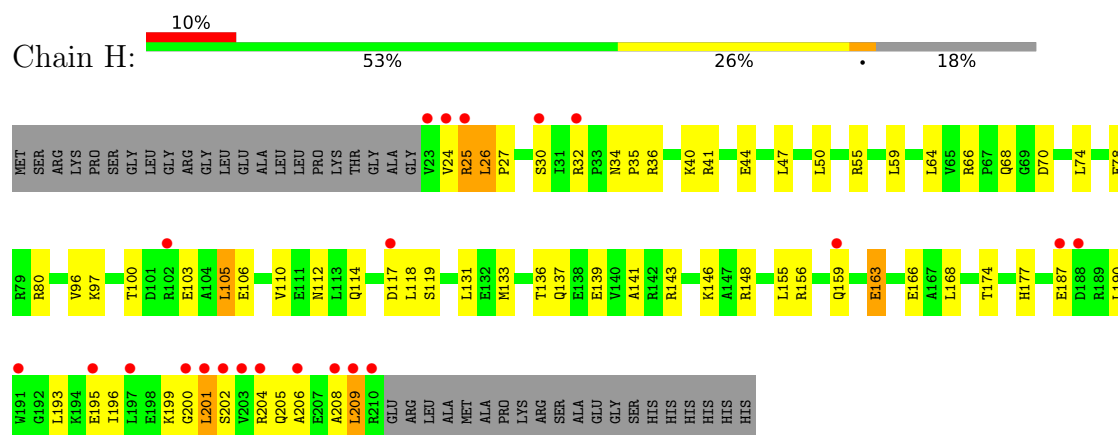
• Molecule 1: Chromosome-partitioning protein Spo0J



● Molecule 1: Chromosome-partitioning protein Spo0J



● Molecule 1: Chromosome-partitioning protein Spo0J



4 Data and refinement statistics

Property	Value	Source
Space group	C 2 2 2	Depositor
Cell constants a, b, c, α , β , γ	182.24Å 295.15Å 73.49Å 90.00° 90.00° 90.00°	Depositor
Resolution (Å)	38.72 – 2.30 38.72 – 2.30	Depositor EDS
% Data completeness (in resolution range)	98.9 (38.72-2.30) 98.9 (38.72-2.30)	Depositor EDS
R_{merge}	0.08	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.47 (at 2.29Å)	Xtriage
Refinement program	CNS 1.1	Depositor
R, R_{free}	0.235 , 0.278 0.232 , 0.234	Depositor DCC
R_{free} test set	4470 reflections (5.01%)	wwPDB-VP
Wilson B-factor (Å ²)	30.9	Xtriage
Anisotropy	0.327	Xtriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 61.2	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.31$	Xtriage
Estimated twinning fraction	No twinning to report.	Xtriage
F_o, F_c correlation	0.93	EDS
Total number of atoms	12878	wwPDB-VP
Average B, all atoms (Å ²)	39.0	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 25.31 % 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 3.2475e-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: CO, MG

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	0.47	1/1476 (0.1%)	0.90	3/1993 (0.2%)
1	B	0.45	1/1528 (0.1%)	0.93	4/2062 (0.2%)
1	C	0.45	1/1504 (0.1%)	0.93	3/2030 (0.1%)
1	D	0.44	1/1528 (0.1%)	0.89	2/2062 (0.1%)
1	E	0.44	1/1523 (0.1%)	0.93	3/2055 (0.1%)
1	F	0.46	1/1495 (0.1%)	0.88	3/2018 (0.1%)
1	G	0.46	1/1476 (0.1%)	0.89	4/1993 (0.2%)
1	H	0.45	1/1484 (0.1%)	0.90	2/2004 (0.1%)
All	All	0.45	8/12014 (0.1%)	0.91	24/16217 (0.1%)

The worst 5 of 8 bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
1	E	213	LEU	C-N	-5.92	1.25	1.33
1	A	208	ALA	C-N	-5.79	1.25	1.33
1	F	210	ARG	C-N	-5.69	1.25	1.33
1	H	209	LEU	C-N	-5.58	1.25	1.33
1	C	211	GLU	C-N	-5.49	1.25	1.33

The worst 5 of 24 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
1	B	199	LYS	N-CA-C	-7.64	99.52	110.59
1	H	118	LEU	N-CA-C	7.39	121.87	110.20
1	C	118	LEU	N-CA-C	7.35	121.33	110.30
1	D	118	LEU	N-CA-C	7.33	120.88	109.96
1	C	119	SER	N-CA-C	-7.13	100.80	110.36

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	1459	0	1517	84	0
1	B	1511	0	1576	100	0
1	C	1487	0	1547	96	0
1	D	1511	0	1576	73	0
1	E	1506	0	1571	87	0
1	F	1478	0	1541	71	0
1	G	1459	0	1517	94	0
1	H	1467	0	1528	85	0
2	A	3	0	0	0	0
2	B	2	0	0	0	0
2	C	2	0	0	0	0
2	D	2	0	0	0	0
2	E	2	0	0	0	0
2	G	1	0	0	0	0
2	H	1	0	0	0	0
3	C	1	0	0	0	0
3	D	1	0	0	0	0
4	A	140	0	0	7	0
4	B	130	0	0	19	0
4	C	114	0	0	11	0
4	D	126	0	0	8	0
4	E	110	0	0	11	0
4	F	117	0	0	8	0
4	G	122	0	0	12	0
4	H	126	0	0	3	0
All	All	12878	0	12373	605	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 25.

The worst 5 of 605 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:25:ARG:HH21	1:C:25:ARG:HB3	1.12	1.11
1:G:64:LEU:HG	1:G:97:LYS:HZ1	1.05	1.08

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Atom-1	Atom-2	Interatomic distance (Å)	Clash overlap (Å)
1:A:142:ARG:HE	1:A:142:ARG:HA	1.20	1.01
1:D:94:ALA:HB3	1:H:26:LEU:HD21	1.42	1.01
1:B:202:SER:H	1:B:205:GLN:HE21	1.03	0.98

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	185/230 (80%)	183 (99%)	0	2 (1%)	11	13
1	B	191/230 (83%)	186 (97%)	5 (3%)	0	100	100
1	C	188/230 (82%)	185 (98%)	2 (1%)	1 (0%)	24	31
1	D	191/230 (83%)	188 (98%)	3 (2%)	0	100	100
1	E	190/230 (83%)	186 (98%)	3 (2%)	1 (0%)	24	31
1	F	187/230 (81%)	181 (97%)	6 (3%)	0	100	100
1	G	185/230 (80%)	178 (96%)	7 (4%)	0	100	100
1	H	186/230 (81%)	182 (98%)	4 (2%)	0	100	100
All	All	1503/1840 (82%)	1469 (98%)	30 (2%)	4 (0%)	36	46

All (4) Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	E	212	ARG
1	A	208	ALA
1	C	60	LEU
1	A	207	GLU

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	151/184 (82%)	135 (89%)	16 (11%)	6	8
1	B	156/184 (85%)	143 (92%)	13 (8%)	10	14
1	C	154/184 (84%)	139 (90%)	15 (10%)	8	10
1	D	156/184 (85%)	148 (95%)	8 (5%)	21	32
1	E	156/184 (85%)	140 (90%)	16 (10%)	7	8
1	F	153/184 (83%)	143 (94%)	10 (6%)	15	22
1	G	151/184 (82%)	142 (94%)	9 (6%)	17	25
1	H	152/184 (83%)	140 (92%)	12 (8%)	11	15
All	All	1229/1472 (84%)	1130 (92%)	99 (8%)	11	14

5 of 99 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
1	E	61	GLN
1	F	48	LYS
1	E	105	LEU
1	E	193	LEU
1	F	163	GLU

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 65 such sidechains are listed below:

Mol	Chain	Res	Type
1	H	34	ASN
1	H	90	GLN
1	D	34	ASN
1	C	177	HIS
1	H	128	GLN

5.3.3 RNA [i](#)

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 oligosaccharides in this entry.

5.6 Ligand geometry [i](#)

Of 15 ligands modelled in this entry, 15 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	187/230 (81%)	0.38	15 (8%) 18 20	15, 32, 69, 88	0
1	B	193/230 (83%)	0.70	27 (13%) 6 7	16, 37, 71, 95	0
1	C	190/230 (82%)	0.59	22 (11%) 9 10	15, 37, 67, 80	0
1	D	193/230 (83%)	0.72	26 (13%) 7 8	15, 38, 71, 84	0
1	E	192/230 (83%)	0.74	29 (15%) 5 6	17, 38, 74, 87	0
1	F	189/230 (82%)	0.41	7 (3%) 45 48	14, 33, 75, 101	0
1	G	187/230 (81%)	0.68	31 (16%) 4 5	17, 33, 77, 120	0
1	H	188/230 (81%)	0.53	22 (11%) 9 10	16, 33, 76, 93	0
All	All	1519/1840 (82%)	0.60	179 (11%) 9 10	14, 35, 73, 120	0

The worst 5 of 179 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	G	175	ALA	7.8
1	G	201	LEU	5.5
1	E	94	ALA	5.1
1	E	95	VAL	5.0
1	G	174	THR	4.8

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 [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, 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($\text{\AA}^2$)	Q<0.9
3	MG	C	1214	1/1	0.92	0.30	24,24,24,24	0
3	MG	D	1217	1/1	0.93	0.32	27,27,27,27	0
2	CO	H	1210	1/1	0.94	0.16	64,64,64,64	0
2	CO	A	1211	1/1	0.97	0.12	56,56,56,56	0
2	CO	E	1215	1/1	0.97	0.09	52,52,52,52	0
2	CO	G	1209	1/1	0.97	0.13	61,61,61,61	0
2	CO	A	1209	1/1	0.98	0.04	46,46,46,46	0
2	CO	E	1214	1/1	0.99	0.05	34,34,34,34	0
2	CO	A	1210	1/1	0.99	0.01	22,22,22,22	0
2	CO	B	1215	1/1	0.99	0.04	33,33,33,33	0
2	CO	B	1216	1/1	0.99	0.02	24,24,24,24	0
2	CO	C	1213	1/1	0.99	0.07	34,34,34,34	0
2	CO	D	1215	1/1	0.99	0.07	26,26,26,26	0
2	CO	C	1212	1/1	1.00	0.02	23,23,23,23	0
2	CO	D	1216	1/1	1.00	0.01	20,20,20,20	0

6.5 Other polymers [i](#)

There are no such residues in this entry.