



wwPDB X-ray Structure Validation Summary Report ⓘ

Aug 14, 2023 – 07:28 PM EDT

PDB ID : 1S7W
Title : Crystal structures of the murine class I major histocompatibility complex H-2Db in complex with LCMV-derived gp33 index peptide and three of its escape variants
Authors : Velloso, L.M.; Michaelsson, J.; Ljunggren, H.G.; Schneider, G.; Achour, A.
Deposited on : 2004-01-30
Resolution : 2.40 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 : 4.02b-467
Xtriage (Phenix) : 1.13
EDS : 2.35
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) : 2.35

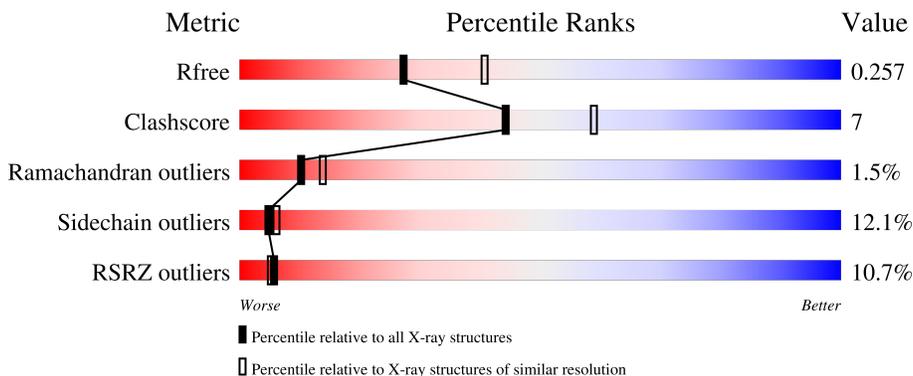
1 Overall quality at a glance i

The following experimental techniques were used to determine the structure:

X-RAY DIFFRACTION

The reported resolution of this entry is 2.40 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	3907 (2.40-2.40)
Clashscore	141614	4398 (2.40-2.40)
Ramachandran outliers	138981	4318 (2.40-2.40)
Sidechain outliers	138945	4319 (2.40-2.40)
RSRZ outliers	127900	3811 (2.40-2.40)

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	338	10% 60% 16% .. 18%
1	D	338	9% 64% 13% .. 18%
1	G	338	12% 65% 13% .. 18%
1	J	338	14% 67% 11% .. 18%
2	B	99	% 73% 20% 5% ..

Continued on next page...

Continued from previous page...

Mol	Chain	Length	Quality of chain
2	E	99	<p>2% 79% 18%</p>
2	H	99	<p>% 76% 23%</p>
2	K	99	<p>4% 76% 24%</p>
3	C	9	<p>78% 22%</p>
3	F	9	<p>89% 11%</p>
3	I	9	<p>11% 67% 33%</p>
3	L	9	<p>89% 11%</p>

2 Entry composition [i](#)

There are 4 unique types of molecules in this entry. The entry contains 13148 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 H-2 class I histocompatibility antigen, D-B alpha chain.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
1	A	276	Total 2269	C 1432	N 401	O 427	S 9	0	1	0
1	D	276	Total 2264	C 1430	N 400	O 425	S 9	0	0	0
1	G	276	Total 2264	C 1430	N 400	O 425	S 9	0	0	0
1	J	276	Total 2264	C 1430	N 400	O 425	S 9	0	0	0

- Molecule 2 is a protein called Beta-2-microglobulin.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
2	B	98	Total 812	C 519	N 137	O 150	S 6	0	0	0
2	E	99	Total 818	C 523	N 138	O 151	S 6	0	0	0
2	H	99	Total 818	C 523	N 138	O 151	S 6	0	0	0
2	K	99	Total 818	C 523	N 138	O 151	S 6	0	0	0

- Molecule 3 is a protein called Glycoprotein 9-residue peptide.

Mol	Chain	Residues	Atoms					ZeroOcc	AltConf	Trace
			Total	C	N	O	S			
3	C	9	Total 74	C 49	N 11	O 13	S 1	0	0	0
3	F	9	Total 74	C 49	N 11	O 13	S 1	0	0	0
3	I	9	Total 74	C 49	N 11	O 13	S 1	0	0	0
3	L	9	Total 74	C 49	N 11	O 13	S 1	0	0	0

There are 8 discrepancies between the modelled and reference sequences:

Chain	Residue	Modelled	Actual	Comment	Reference
C	3	LEU	VAL	engineered mutation	UNP P07399
C	9	MET	CYS	SEE REMARK 999	UNP P07399
F	3	LEU	VAL	engineered mutation	UNP P07399
F	9	MET	CYS	SEE REMARK 999	UNP P07399
I	3	LEU	VAL	engineered mutation	UNP P07399
I	9	MET	CYS	SEE REMARK 999	UNP P07399
L	3	LEU	VAL	engineered mutation	UNP P07399
L	9	MET	CYS	SEE REMARK 999	UNP P07399

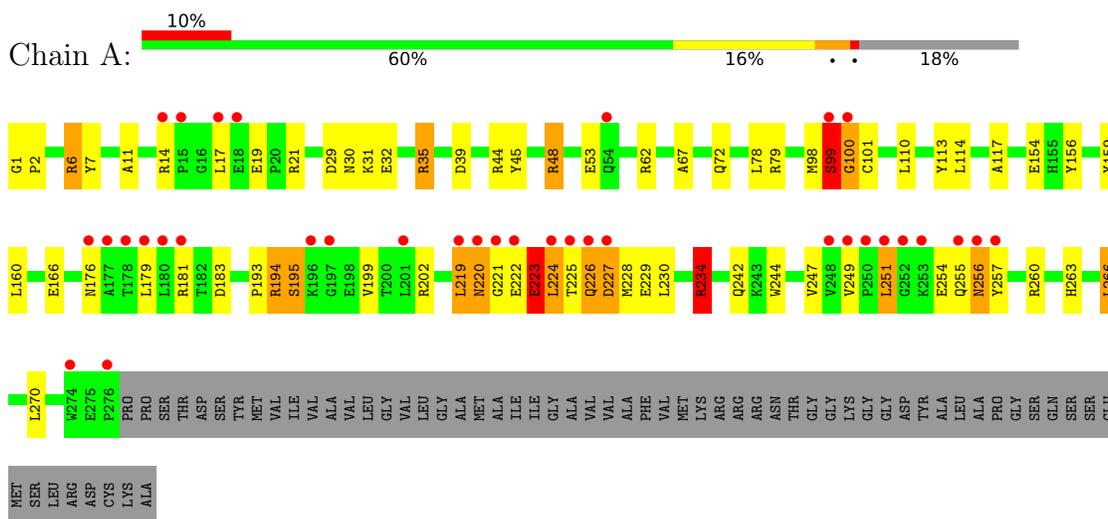
- Molecule 4 is water.

Mol	Chain	Residues	Atoms	ZeroOcc	AltConf
4	A	87	Total O 87 87	0	0
4	B	57	Total O 57 57	0	0
4	C	2	Total O 2 2	0	0
4	D	80	Total O 80 80	0	0
4	E	35	Total O 35 35	0	0
4	F	3	Total O 3 3	0	0
4	G	84	Total O 84 84	0	0
4	H	44	Total O 44 44	0	0
4	I	2	Total O 2 2	0	0
4	J	83	Total O 83 83	0	0
4	K	44	Total O 44 44	0	0
4	L	4	Total O 4 4	0	0

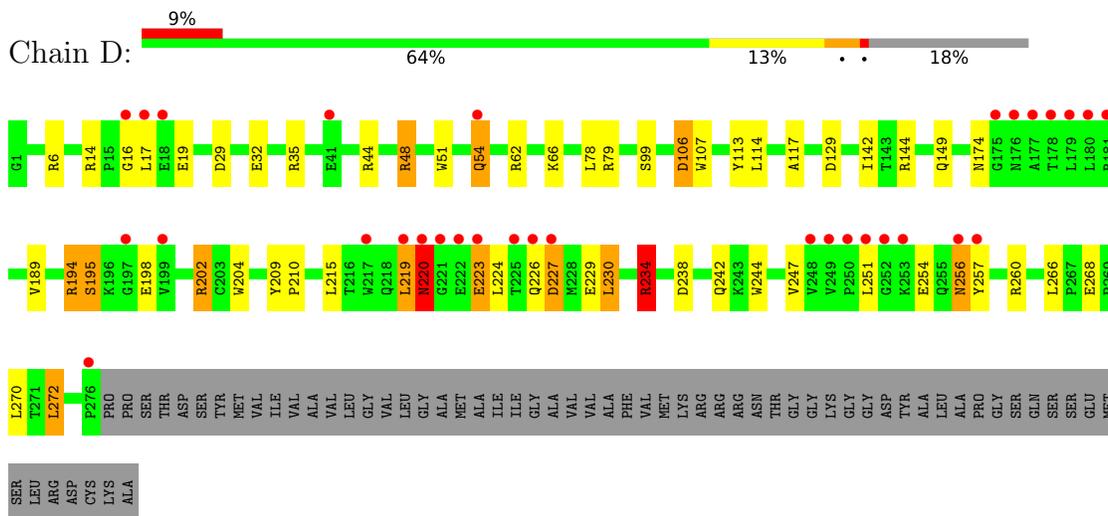
3 Residue-property plots [i](#)

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: H-2 class I histocompatibility antigen, D-B alpha chain

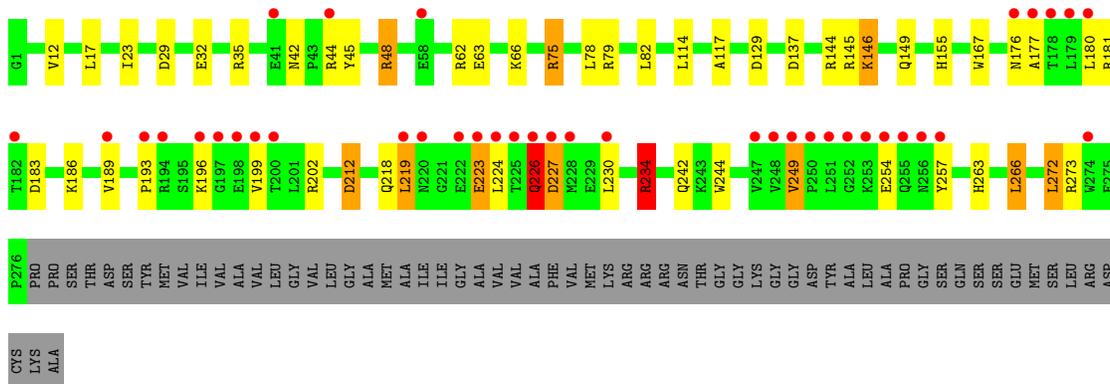


- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

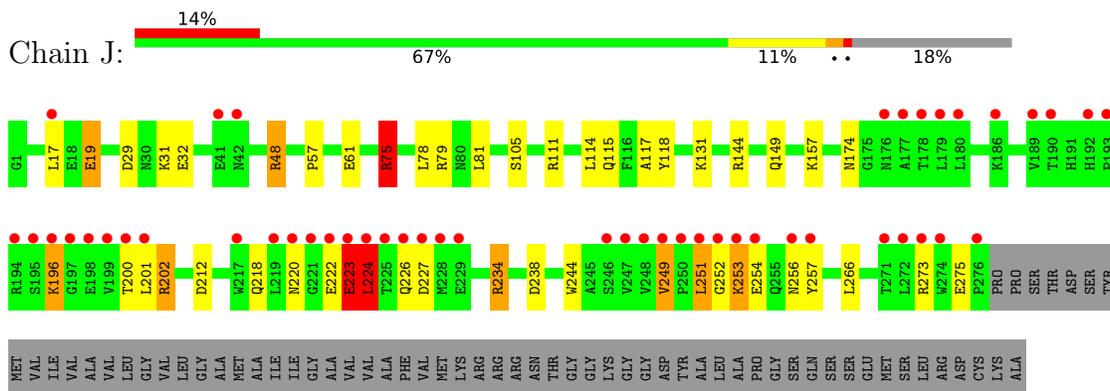


- Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain

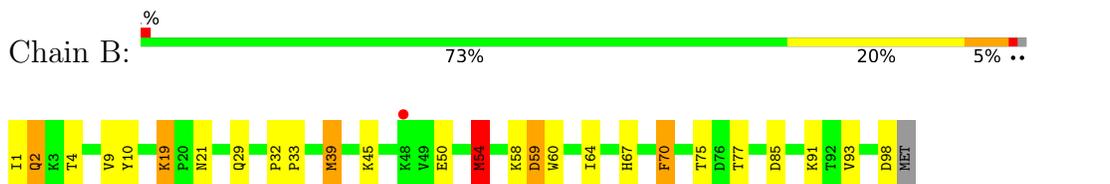




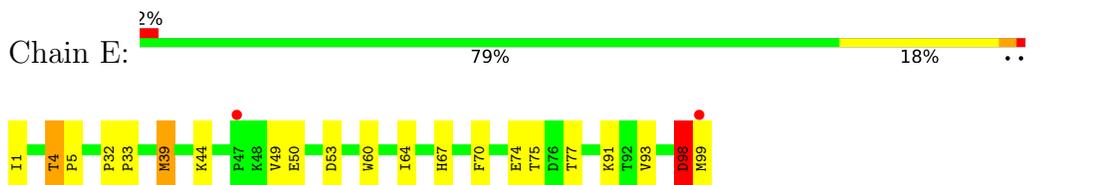
• Molecule 1: H-2 class I histocompatibility antigen, D-B alpha chain



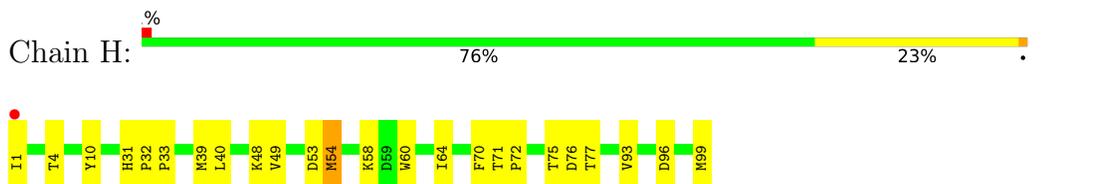
• Molecule 2: Beta-2-microglobulin



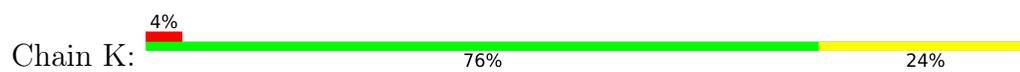
• Molecule 2: Beta-2-microglobulin



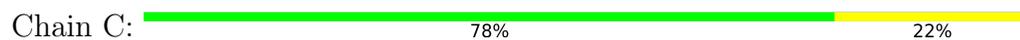
• Molecule 2: Beta-2-microglobulin



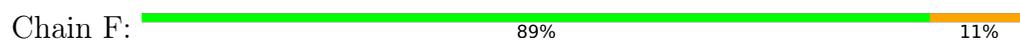
• Molecule 2: Beta-2-microglobulin



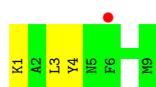
- Molecule 3: Glycoprotein 9-residue peptide



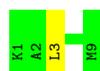
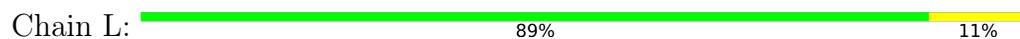
- Molecule 3: Glycoprotein 9-residue peptide



- Molecule 3: Glycoprotein 9-residue peptide



- Molecule 3: Glycoprotein 9-residue peptide



4 Data and refinement statistics

Property	Value	Source
Space group	P 1 21 1	Depositor
Cell constants a, b, c, α , β , γ	92.25Å 123.30Å 99.30Å 90.00° 103.13° 90.00°	Depositor
Resolution (Å)	19.84 – 2.40 38.05 – 2.40	Depositor EDS
% Data completeness (in resolution range)	100.0 (19.84-2.40) 99.9 (38.05-2.40)	Depositor EDS
R_{merge}	(Not available)	Depositor
R_{sym}	(Not available)	Depositor
$\langle I/\sigma(I) \rangle$ ¹	2.31 (at 2.39Å)	Xtrriage
Refinement program	REFMAC 5.1.24	Depositor
R, R_{free}	0.199 , 0.246 0.213 , 0.257	Depositor DCC
R_{free} test set	1689 reflections (2.00%)	wwPDB-VP
Wilson B-factor (Å ²)	33.1	Xtrriage
Anisotropy	0.027	Xtrriage
Bulk solvent k_{sol} (e/Å ³), B_{sol} (Å ²)	0.34 , 57.0	EDS
L-test for twinning ²	$\langle L \rangle = 0.48$, $\langle L^2 \rangle = 0.30$	Xtrriage
Estimated twinning fraction	No twinning to report.	Xtrriage
F_o, F_c correlation	0.94	EDS
Total number of atoms	13148	wwPDB-VP
Average B, all atoms (Å ²)	26.0	wwPDB-VP

Xtrriage's analysis on translational NCS is as follows: *The largest off-origin peak in the Patterson function is 17.15% 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	0.68	0/2337	0.87	8/3174 (0.3%)
1	D	0.67	0/2331	0.87	9/3166 (0.3%)
1	G	0.69	1/2331 (0.0%)	0.85	11/3166 (0.3%)
1	J	0.64	0/2331	0.85	5/3166 (0.2%)
2	B	0.78	2/838 (0.2%)	0.94	3/1138 (0.3%)
2	E	0.78	1/844 (0.1%)	0.85	2/1146 (0.2%)
2	H	0.77	0/844	0.88	3/1146 (0.3%)
2	K	0.73	0/844	0.87	2/1146 (0.2%)
3	C	0.95	0/75	1.01	0/98
3	F	0.85	0/75	0.95	0/98
3	I	0.95	0/75	0.92	0/98
3	L	0.81	0/75	0.95	0/98
All	All	0.70	4/13000 (0.0%)	0.87	43/17640 (0.2%)

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
1	A	0	4

All (4) bond length outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(Å)	Ideal(Å)
2	E	39	MET	SD-CE	-6.21	1.43	1.77
2	B	39	MET	SD-CE	-5.56	1.46	1.77
2	B	54	MET	CG-SD	5.52	1.95	1.81
1	G	146	LYS	CE-NZ	5.48	1.62	1.49

The worst 5 of 43 bond angle outliers are listed below:

Mol	Chain	Res	Type	Atoms	Z	Observed(°)	Ideal(°)
2	B	98	ASP	CB-CG-OD2	8.08	125.57	118.30
1	A	35	ARG	NE-CZ-NH1	7.65	124.13	120.30
1	G	129	ASP	CB-CG-OD2	7.46	125.01	118.30
1	D	35	ARG	NE-CZ-NH2	-7.34	116.63	120.30
1	A	29	ASP	CB-CG-OD2	7.32	124.89	118.30

There are no chirality outliers.

All (4) planarity outliers are listed below:

Mol	Chain	Res	Type	Group
1	A	6	ARG	Peptide
1	A	98	MET	Mainchain
1	A	99[B]	SER	Mainchain

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	2269	0	2138	45	0
1	D	2264	0	2136	36	0
1	G	2264	0	2136	26	0
1	J	2264	0	2136	20	0
2	B	812	0	787	13	0
2	E	818	0	791	9	0
2	H	818	0	791	11	0
2	K	818	0	791	14	0
3	C	74	0	76	2	0
3	F	74	0	76	5	0
3	I	74	0	76	3	0
3	L	74	0	76	0	0
4	A	87	0	0	7	0
4	B	57	0	0	0	0
4	C	2	0	0	0	0
4	D	80	0	0	3	0
4	E	35	0	0	1	0
4	F	3	0	0	0	0
4	G	84	0	0	7	0
4	H	44	0	0	3	0

Continued on next page...

Continued from previous page...

Mol	Chain	Non-H	H(model)	H(added)	Clashes	Symm-Clashes
4	I	2	0	0	0	0
4	J	83	0	0	3	0
4	K	44	0	0	4	0
4	L	4	0	0	0	0
All	All	13148	0	12010	163	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 7.

The worst 5 of 163 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)
4:G:347:HOH:O	2:H:99:MET:CG	2.01	1.09
1:D:219:LEU:HD13	1:D:257:TYR:OH	1.48	1.09
1:J:144:ARG:HD2	4:J:404:HOH:O	1.62	1.00
1:A:99[A]:SER:OG	1:A:100:GLY:N	1.91	0.96
1:D:219:LEU:HB2	1:D:257:TYR:CE1	2.09	0.87

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	275/338 (81%)	259 (94%)	9 (3%)	7 (2%)	5 6
1	D	274/338 (81%)	258 (94%)	12 (4%)	4 (2%)	10 14
1	G	274/338 (81%)	259 (94%)	10 (4%)	5 (2%)	8 10
1	J	274/338 (81%)	250 (91%)	18 (7%)	6 (2%)	6 7
2	B	96/99 (97%)	94 (98%)	2 (2%)	0	100 100
2	E	97/99 (98%)	93 (96%)	3 (3%)	1 (1%)	15 23

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Favoured	Allowed	Outliers	Percentiles	
2	H	97/99 (98%)	95 (98%)	2 (2%)	0	100	100
2	K	97/99 (98%)	94 (97%)	3 (3%)	0	100	100
3	C	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	F	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	I	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
3	L	7/9 (78%)	6 (86%)	1 (14%)	0	100	100
All	All	1512/1784 (85%)	1426 (94%)	63 (4%)	23 (2%)	10	14

5 of 23 Ramachandran outliers are listed below:

Mol	Chain	Res	Type
1	A	99[A]	SER
1	A	99[B]	SER
1	G	227	ASP
1	J	196	LYS
1	J	253	LYS

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	235/280 (84%)	201 (86%)	34 (14%)	3	3
1	D	234/280 (84%)	204 (87%)	30 (13%)	4	5
1	G	234/280 (84%)	210 (90%)	24 (10%)	7	10
1	J	234/280 (84%)	203 (87%)	31 (13%)	4	4
2	B	93/94 (99%)	81 (87%)	12 (13%)	4	5
2	E	93/94 (99%)	83 (89%)	10 (11%)	6	9
2	H	93/94 (99%)	84 (90%)	9 (10%)	8	12
2	K	93/94 (99%)	84 (90%)	9 (10%)	8	12
3	C	7/7 (100%)	7 (100%)	0	100	100
3	F	7/7 (100%)	6 (86%)	1 (14%)	3	4

Continued on next page...

Continued from previous page...

Mol	Chain	Analysed	Rotameric	Outliers	Percentiles	
3	I	7/7 (100%)	6 (86%)	1 (14%)	3	4
3	L	7/7 (100%)	6 (86%)	1 (14%)	3	4
All	All	1337/1524 (88%)	1175 (88%)	162 (12%)	5	6

5 of 162 residues with a non-rotameric sidechain are listed below:

Mol	Chain	Res	Type
2	H	54	MET
1	J	234	ARG
2	H	93	VAL
1	J	105	SER
1	J	273	ARG

Sometimes sidechains can be flipped to improve hydrogen bonding and reduce clashes. 5 of 26 such sidechains are listed below:

Mol	Chain	Res	Type
1	G	97	GLN
1	G	218	GLN
1	J	220	ASN
1	G	192	HIS
2	H	31	HIS

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 monosaccharides in this entry.

5.6 Ligand geometry [i](#)

There are no ligands in this entry.

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, 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	276/338 (81%)	0.64	35 (12%) 3 3	8, 20, 46, 56	0
1	D	276/338 (81%)	0.69	32 (11%) 4 4	8, 23, 54, 64	0
1	G	276/338 (81%)	0.76	39 (14%) 2 2	6, 23, 48, 59	0
1	J	276/338 (81%)	0.89	49 (17%) 1 1	11, 28, 60, 66	0
2	B	98/99 (98%)	0.07	1 (1%) 82 80	9, 16, 23, 28	0
2	E	99/99 (100%)	0.22	2 (2%) 65 63	8, 18, 26, 29	0
2	H	99/99 (100%)	0.07	1 (1%) 82 80	10, 18, 27, 32	0
2	K	99/99 (100%)	0.13	4 (4%) 38 37	12, 25, 34, 40	0
3	C	9/9 (100%)	0.24	0 100 100	11, 13, 17, 17	0
3	F	9/9 (100%)	0.20	0 100 100	13, 18, 25, 30	0
3	I	9/9 (100%)	0.45	1 (11%) 5 4	13, 18, 24, 28	0
3	L	9/9 (100%)	0.05	0 100 100	35, 37, 45, 46	0
All	All	1535/1784 (86%)	0.57	164 (10%) 6 5	6, 22, 53, 66	0

The worst 5 of 164 RSRZ outliers are listed below:

Mol	Chain	Res	Type	RSRZ
1	J	178	THR	11.7
1	D	177	ALA	11.3
1	D	178	THR	10.6
1	A	178	THR	10.5
1	A	177	ALA	10.2

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 monosaccharides 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.